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/db_xref="taxon:32644" 336 a 541 c 453 g 299 t	NICOLA NI	AMANGALY. ALEXANDER, W., HILTON, D.J., KOJIMA, T., Maeda, M. and Kikuchiy. A NOVEL HAEMOPOIETIN RECEPTOR AND GENETIC SEQUENCES ENCODING SAME Patent: WO 9811225-A 19-MAR-1998;	unclassified. 1 (bases 1 to 1629) Nicola N.A., Fabri, L., Farley, A., Nash, A., Willson, T., Rakar, S.,	unidentified. unidentified	94774663 A70382.1 GI:4774663	A70382 1629 bp DNA Sequence 12 from Patent WO9811225. A70382
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Nicola, N.A., Fabri, L., Farley, A., Nash, A., Willson, T., Zhang, J., Alexander, W., Hilton, D.J., Kojima, T., Maeda, Kikuchi, Y.
                                      A NOVEL HAEMOPOIETIN RECEPTOR AND GENETIC PATENT: WO 9811125-A 19-MAR-1998; NICOLA NICOS ANTONY (AU)

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                                           A NOVEL HARMOPOIETIN RECEPTOR AND PATENT: WO 9811225-A 19 MAR-1998; NICOLA NICOS ANTONY (AU)
Location/Qualifiers
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NICOLA,N.A., Fabri,L., Farley,A., Nash,A., Willson,T., Zhang,J., Alexander,W., Hilton,D.J., Kojima,T., Maeda,J.KikuChi,Y.
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2 (bases 1 to 1716)
Elson,G.C.A., Graber,P., Losberger,P., Herren,
Menoud,L.N., Wells,T.N.C., Kosco-Vilbols,M.H.
Direct Submission
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getfelfivslkyklrwygonvcereferbybhyshetpkdlaletprdlaletprepholyveraturlg
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119. 229
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                                                                                                                                                                                                                 similar to the sequence Number AC003112"
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/map="19p12"
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/db_xref="taxon:9606"
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                                   /Translation-"PTLLIGSSLQATCSIHGDTPGATAEGLYWTLNGRRLPSELSRLL NTSTLALALANLMGSRQQSGDNLVCHAEDGS ILAGSCLYVGLPPEKPENISCWSRNMK DLTCRWTPGAHGETFLHTNYSLKYKLRWYGQDNTCEEYHTVGPHSCHIPKDLALFTPY EIWVEATNRLGSRRSDVLTLDVLDVYTTDPPDVHVSRVGGLEDQLSVRWVSPPALKD FLFQAKYQIRYRVEDSYDWKYVDDVSNQTSCRLAGLKPGTVYFVQVRCNPFGIYGSKK AG"
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/note="unnamed protein product"
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/db_xref="PID:e1433696"
/db_xref="PID:g4774668"
/db_xref="GI:4774668"
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                                                                 tgggtctcaccaccagctctcaaggatttcctcttccaagccaagtaccagatccgctac
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//Protein_id="CAB42576.1"
/db_xref="PID: e1433703"
/db_xref="PID: e4774673"
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Nicola, N.A., Fabri, L., Farley, A.,
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/protein_id="CAB42574.1"
/db_xref="PID:e1433693"
/db_xref="PID:g4774666"
/db_xref="GI:4774666"
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GGVCEPRGGEPSSGPVRRELKQFLGWLKKHAYCSNLSFRLYDQWRAWMQKSHKTRNQV
GKLGEACVGGKGAEEERDPGEQPPQHRTLLSKHRTRGSCPRADGVRREVRGSG"
245 c 272 g 178 t
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                                                                                                           Score 305; DB 5; Pred. No. 3.8e-54; 0; Mismatches 0;
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Hilton, D.J., Kojima
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1 (bases 1 to 6663)
Nicola,N.A., Fabri,L., Farley,A., Nash,A., Willson,T., Rakar,S.,
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Kikuchi,Y.
                                                                                                                                                                                                          Similarity 99.
81; Conservative
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/db_xref="taxon:32644"
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AC003112.1
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Kikuchi,Y.
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Nicola, N.A., Fabri, L.
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                                                                                                           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 40668)

Lamerdin, J. E., McCready, P. M., Adamson, A. W., Burkhart-Schultz, K., Gordon, L., Christensen, M., Kyle, A., Ramirez, M., Stilwagen, S., Garnes, J., Danganan, L., Bruce, R., Quan, G., Montgomery, M., Ow, D., Kobayashi, A., Olsen, A.O. and Carrano, A.V.
                                                                                                                                                                                                                                                                                            Human DNA from chromosome 19 sequence, complete sequence.
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Lamerdin, J.E.
Direct Submission
Submitted (21-NOV-1997) Hu
National Laboratory, 7000
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2 (bases 1 to
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/db_xref="taxon:32644"
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Livermore, CA 94551, USA
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                                                                                                                                                               frame: 1, quality: excellent, score: 100.000-DDS similarity to AA047548 zf15e02.rl Soares fetal heart NbH119W Homo sapiens cDNA clone 377018 5' (139. 221); 100% identity. -DDS similarity to AA136115 z490b04.rl Soares pregnant uterus NbHPU Homo sapiens cDNA clone 490063 5' (111. 192); 99% identity. -DDS similarity to AA452628 x33f04.rl Soares total fetus NbHFB 9W Homo sapiens cDNA clone 788287 5' (83. .165); 100% identity. -DDS similarity to AA009412 ze82h02.rl Soares fetal heart NbHH19W Homo sapiens cDNA clone 365523 5' (62. .144); 100% identity."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /note-"DDS similarity to AA047548 zf15e02.rl Soares fetal heart NbHH19W Homo saplens cDNA clone 377018 5′ (1. 138); 96% identity. --Other overlapping matches: -(10435. 10548) DDS similarity to AA156115 zk90b04.rl Soares pregnant uterus NbHPU Homo saplens cDNA clone 490063 5′ (1. 110); 93% identity. --(10466. 10548) DDS similarity to AA455628 zx33f04.rl Soares total fetus NbHPB 9w Homo saplens cDNA clone 78828 75′ (1. 82); 95% identity. --(10486. 10548) DDS similarity to AA009412 ze82h02.rl Soares fetal heart MbHH19W Homo saplens cDNA clone 365523 5′ (1. .61); 97%
/note-"DDS similarity to AA136115 zk90b04.rl Soares /note-"DDS similarity to AA136115 zk90b04.rl Soares pregnant uterus NbHPU Homo sapiens cDNA clone 490063 5' (193. .394); 94% identity.~~DDS similarity to AA009412 ze82h02.rl Soares fetal heart NbHH19W Homo sapiens cDNA clone 365523 5' (145. .346); 96% identity.~~(11121. .11331)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        complement(9445. .9505)
/note="predicted exon,
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/rpt_family="Alu"
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/rpt_family="Alu"
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/note="LL19NC03 cosmid library constructed at LLNL from
flow-sorted chromosomes from hybrid 5HL2-B, which carries
chromosome 19 as its only human chromosome."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        complement(
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/db_xref="taxon:9606"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    nue: 1, quality: good, program: grail2exons_human_1.3, plement(9629. 9672)
te="predicted exon, program: grail2exons_human_1.3, ne: 1, quality: excellent, score: 75.000"
lement(9928. .10123)
family="Alu"
j. .n6%,"
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._family="Alu"
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_line="5HL2-B"
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"predicted exon, program: 1, quality:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   .10725
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Inote DDS similarity to AA406406 zv11e07.sl Soares NhHMPu Sl Homo sapiens cDNA clone 753148 3′ (1. 433); Score: 858 Identity: 431/433 (99%).--(14884. 1.5237) DDS similarity to W37175 zb21a02.rl Soares fetal lung NbHL19W Homo sapiens cDNA clone 302666 5′ (1. 355); 94% identity.--(15227. .14885) DDS similarity to AA121532 zk89c11.sl Soares pregnant uterus NbHPU Homo sapiens cDNA clone 490004 3′ (342. .1); 99% identity.--(15227. .14885) DDS similarity to AA127694 zk89c11.rl Soares pregnant uterus NbHPU Homo sapiens cDNA clone 490004 5′ (126. .467); 99% identity.--(15227. .14897) DDS similarity to W46603 zc32h10.rl Soares senescent fibroblasts NbHSF Homo sapiens cDNA clone 324067 5′ (328. .1); 98% identity.--(15227. .15088) DDS similarity to W46604 zc32h10.sl Soares senescent fibroblasts NbHSF Homo sapiens cDNA clone 324067 3′ (322. .465); 96% identity."
                                               /note-*DDS similarity to AA121532 zk89c11.s1 Soares /note-*DDS similarity to AA121532 zk89c11.s1 Soares pregnant uterus NbHPU Homo saplens cDNA clone 490004 3' (389. .343); 99% identity.--DDS similarity to AA127694 zk89c11.r1 Soares pregnant uterus NbHPU Homo saplens cDNA clone 490004 5' (77. .125); 90% identity.--(15735. .15713) DDS similarity to W46603 zc32h10.r1 Soares senescent fibroblasts NbHSF Homo saplens cDNA clone 324067 5' (351. .329); 100% identity.--(15735. .15713) DDS similarity to W46604 zc32h10.s1 Soares senescent fibroblasts NbHSF Homo saplens cDNA clone 324067 3' (299. .321); 100%
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /note-"predicted exon, program: grail2exons_human_1.3, frame: 2, quality: good, score: 61.000--Other overlapping matches:-(13756. 13826) DDS smilarity to AA009412 ze82h02.r1 Soares fetal heart NbHH19W Homo sapiens cDNA clone 365523 5' (428. 496); 97% identity.--(13756. 13984) DDS similarity to AA009693 ze82h02.s1 Soares fetal heart NbHH19W Homo sapiens cDNA clone 365523 3' (227. 1); 98% identity.--(13756. 13984) DDS similarity to AA450010 zx33f04.s1 Soares total fetus Nb2HF8 9W Homo sapiens cDNA clone 788287 3' (228. 1); 99% identity.--"
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14885.
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/note-"DDS similarity to AA136115 zk90b04.rl Soares
pregnant uterus NbHPU Homo sapiens CDNA clone 490063
pregnant uterus NbHPU Homo sapiens CDNA clone 490063
(395. .477); 928 identity.--DDS similarity to AA00941
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/rpt_family="Alu"
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/rpt_family="Alu"
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/rpt_family="Alu"
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complement(15895.
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    .16082)
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/note-"predicted exon, program: grail2exons_human_1.3, frame: 0, quality: excellent, score: 81.000~-Other overlapping matches:~(15936. .15895) DDS similarity to

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REFERENCE
AUTHORS
TITLE
                                                                                                                                                                                                                                                    SOURCE
ORGANISM
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                                          FEATURES
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Best Local Sim
Matches 244;
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                                                                        1 (bases 1 to 7218)
Dorner, F., Scheiflinger, F. and Falkner, F.
Recombinant fowlpox virus
Patent: US 5670367-A 14.23-SEP-1997;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence
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The complete DNA sequence of the long unique region in the genome of herpes simplex virus type 1
J. Gen. Virol. 69 (Pt 7), 1531-1574 (1988)
                                                                                                                                                                                                                                                                                                                                                       Submitted (17-JAN-1989) McGeoch D.J., Institute of Virology, Church Street, Revised by [7]
2 (bases 9001 to 117360)
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Herpes simplex virus
X14112 D00317 D00374
                     Perry, L.J. and McGeoch, D.J.

The DNA sequences of the long repeat region and adjoining the long unique region in the genome of herpes simplex vin J. Gen. Virol. 69 (Pt 11), 2831-2846 (1988)
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See also x06461 and x02138.

Residues 1 - 8661 and 148674 - 152260 of TR-L and TR-S, resp. have not been sequenced but are derived from IR-L and IR-S sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Dolan,A., McKie,E., MacLean,A.R. and McGeoch,D.J. Status of the ICP34.5 gene in herpes simplex virus type I strain J. Gen. Virol. 73 (Pt 4), 971-973 (1992)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                McGeoch,D.J., Dolan,A., Donald,S. and Brauer,D.H. Complete DNA sequence of the short repeat region herpes simplex virus type 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  McGeoch,D.J., Dolan,A., Donald,S. and Rixon,F.J.
Sequence determination and genetic content of the short unique region in the genome of herpes simplex virus type 1
J. Mol. Biol. 181 (1), 1-13 (1985)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   4 (bases 132605 to 145583)
McGeoch, D.J., Dolan, A., Don
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAPPPPPAGGPPPSCSLLLROWLHVPESASDDDDDDDDDDDDDPPSPPPEPAPEARPTAAAPR
PRPPPPGVGPGGGADPSHPPSRPFRLPPRLALRLRVTAEHLARLRLRRAGGEGAPEPP
ATPATPATPATPATPARVRESPHVRVRHLVVWASAARLARRGSWARERADRARFRRRV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /product="neurovirulence
/protein_id="CAA32348.1"
/db_xref="PID:e312308"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /db_xref="taxon:10298"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 'note="a sequence(terminal redundancy)"
                 /db_xref="SWISS-PROT:P08393"
/translation="MEPROGASTREPEGREQREPAPDVWVFPCDRDLPDSSDSEAETE
/translation="MEPROGASTREPEGREQGVDGGAVSGGSPPREEDPGSCGGA
VGGRGDADHHDDDSASEADSTPTELFETGLLGPQGVDGGAVSGGSPPREEDPGSCGGA
PPREDGGSDEGDVCAVCTDEIAPHLRCDTFPCMHRFCIPCMKTWMQLRNTCPLCNAKL
PPREDGGSDEGDVCAVCTDEIAPHLRCDTFPCMHRFCIPCMKTWMQLRNTCPLCNAKL
VYLIVGVTPSGSFSTIPIVNDPQTRMEAEAVRAGTAVDFINFONARAPRVLITLGGH
                                                                                                                                                                                                                                                                                   <sub>J</sub>∪ın(2261. .2317,3083. .3749,3886.
⁄gene≖"RL2"
                                                                                                                                                                                                                                                                                                                                                                                                               /note="reiteration set 6"
1534. .1539
                                                                                                                                                                                                                                                                                                                                                                                                                                                            /gene="RL1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AEAEAVIGPCLGPEARARALARGAGPANSV"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /db_xref="SPTREMBL:012396"
/translation="MARRRRHRGPRRPRPPGPTGAVPTAQSQVTSTPNSEPAVRSAPA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /db_xref="GI:1944537"
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                                                                                                                                                                                        /protein_id="CAA32336.1"
/db_xref="PID:e312309"
                                                                                                                                        /db_xref="GI:59500"
                                                                                                                                                                 /db_xref="PID:g59500"
                                                                                                                                                                                                                                           codon_start=
rvralspthpepttdeddddlddadyvppaprrtprapprrgaaappvtggashaapq
                                                                                                                                                                                                                                                                 function="modulator of cell state and gene expression"
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TSAPLDWTTFRRVELLIDDAWRPLMEPELANPLTAHLLAEYNRRCQTEEVLPPREDVFS WTRYCTPDEVRVVIIGQDPYHHPGQAHGLAFSVRANVPPPPSLRNVLAAVKNCYPEAR MSGHGCLEKWARDGVLLLNTTLTVKRGAAASHSRIGWDRFVGGVIRRLAARRPGLVFM

astetrpgsggepaacrssgpaallaaleagpagvtfsssappdppmdltnggvspaa

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misc_feature
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5676. .5681
/gene="RL2"
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EQSLCRARATVARGSGGPGVEGGHGPSRGAAPSGAAPLPSAASVEQEAAVRPRKRRGS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               eaeagrprgrtgplvnrpaplannrdpivisdsppasphrppaapmpgsaprpgppas
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                                         /protein_id="CAA32338.1"
/db_xref="PID:e312316"
/db_xref="PID:959503"
/db_xref="GI:59503"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /note="reiteration
9032. .9212
/gene="RL2"
                                                                                                                                                                                                                                                                                                 /translation="MGILGWYGLIAYGVLCVRGGLPSTEYVIRSRVAREYGDILKVPC
/translation="MGILGWYGLIAYGVLCVRGGLDTVLWDRHAQKAYWVNPFLFVAG
VPLPSDDLDWRYETPSAINYALIDGIFLRYHCPGLDTVLWDRHAQKAYWVNPFLFVAG
FLEDLSYPAFPANTQETETRLALYKEIRQALDSRKQAASHTPVKAGCVUFDYSRTRRC
VGRQDLGPTNGTSGRTPVLPPDDEAGLQPKPLTTPPPIIATSDPTPRRDAATKSRRRR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /gene="RL2"
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/note="reiteration
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                     'db_xref="SWISS-PROT:P10186"
                                                                                                                                       product="uracil-DNA glycosylase"
                                                                                                                                                                                                                                                                                                                                                                                                 db_xref="SWISS-PROT:P10185"
                                                                                                                                                                                                                                                                                                                                                                                                                                             db_xref="PID:g59502"
                                                                                                                                                                                                                                                                                                                                                                                                                                                       protein_id="CAA32337.1"
protein_id="CAA32337.1"
ib_xref="piD:e312315"
ib_vref="piD:e312315"
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translation="MKRACSRSPSPRRRPSSPRRTPPRDGTPPQKADADDPTPGASND
                                                                                                                                                                                                                                  gene-"UL2"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      codon_start=1
                                                                                                                                                          codon_start=1
                                                                                                                                                                                       gene="UL2"
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                      AUTHORS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     . 109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        149461 CCCGGGCCGCCGCGCAGGCCCGCCCCCGTGGCCGTGTCGCGCCGGCCCGCCG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 49 ccccaatctgcaccccgcagactcgcccccgccccataccggcgttgcagtcaccgcccg 108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ccgccgcggccgctgtcctcgctgtggtcgcctc 202
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ttgcgcgccaccccatgcccgcgggtcgcccgggcccgtcgcccatccgcgcggcgg 168
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CGCCCGCCGCCCCCTGGAGGCCTACTGCTC 149614
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          91;
  3 (bases 113322 to 126373)
Perry.L.J. and McGeoch,D.J.
The DNA sequences of the long repeat region and adjoining parts of the long unique region in the genome of herpes simplex virus type :
J. Gen. Virol. 69 (Pt 11), 2831-2846 (1988)
                                                                                                            Chases 9001 to 117360)

(Chases 9001 to 117360)

McGeoch,D.J., Dalrymple,M.A., Davison,A.J., Dolan,A., Frame,M.C., McGeoch,D.J., Perry,L.J., Scott,J.E. and Taylor,P.

The complete DNA sequence of the long unique region in the genome of herpes simplex virus type 1

J. Gen. Virol. 69 (Pt 7), 1531-1574 (1988)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        capsid protein; complete genome; desoxyribonuclease; desoxyuridine triphosphatase; DNA polymerase; DNA-binding protein; genome; glycoprotein; kinase; long terminal repeat; origin of replication; regulatory protein; repetitive sequence; ribonucleotide reductase;
                                                                                                                                                                                                                                                                                                                                                     Viruses; dsDNA viruses, no RNA stage; Alphaherpesvirinae; Simplexvirus.
1 (bases 1 to 152261)
                                                                                                                                                                                                                                                                                                                                                                                                               human herpesvirus 1 human herpesvirus 1
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Herpes simplex virus
X14112 D00317 D00374
                                                                                                                                                                                                                                                                     Submitted (17-JAN-1989) McGeoch D.J., Institute of Virology, Church Street,
                                                                                                                                                                                                                                                                                                                 Direct Submission
                                                                                                                                                                                                                                                                                                                                  McGeoch, D.J
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           X14112.1 GI:1944536
                                                                                                                                                                                                                                                      Revised by
                                                                                                                                                                                                                                                                                                                                                                                                                                                 regument protein; thymidine kinase.
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10957.
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/gene="RL2"
complement(11753. .11758)
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VSSIDELGRROLTDTIKDLRLSLAKESIACTKTSSFSGNAPRHFYGAFGREAPR
SNKSLOMFVLCKRAHAARVREQLRVVIQSRKPRKYYTRSSDGRLCPAVPVFVHEFVSS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /protein_id="CAA32339.1"
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/db_xref="PID:g59504"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EPMRLHRDNVMLASGAE*
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Pred. No. 0.094;
0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         of Virology, Church Street, Glasgow G11 5JR, GB
On Apr 18, 1997 this sequence version replaced g1:59499.
See also x06461 and x02138.
Residues 1 - 8661 and 148674 - 152260 of TR-L and TR-S,
not been sequenced but are derived from IR-L and IR-S se
Location/Qualifiers
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85160822
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        McGeoch,D.J., Dolan,A., Donald,S. and Brauer,D.H. Complete DNA sequence of the short repeat region herpes simplex virus type 1
Nucleic Acids Res. 14 (4), 1727-1745 (1986)
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McGeoch, D.J., Dolan, A., Donald, S. and Rixon, F.J.
Sequence determination and genetic content of the short unique region in the genome of herpes simplex virus type 1
J. Mol. Biol. 181 (1), 1-13 (1985)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Submitted (16-APR-1997) Dolan A., MRC Virology Institute, of Virology, Church Street, Glasgow G11 5JR, GB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Direct Submission
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /product-"neurovirulence f
/protein_id="CAA32348.1"
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                                                                                                                                                                                                                                                                                                                                                                 AEAEAVIGPCLGPEARARALARGAGPANSV"
                                                                                                                                                                                                                                                                                                                                                                                      at pat pat pat par parvrf sphvrvrhlvvwa saarlarrg sware radrarf rrrv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /organism="human herpesvirus
/strain="17"
                                                                                                                                                                                                                                /gene="RL2"
                                                                                                                                                                                                                                                                 /gene="RL
                                                                                                                                                                                                                                                                                                                         /gene="RL1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /gene="RL1"
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                                                                                                                                                      codon_start=
                                                                                                                                                                                                              oin(2261
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            'note="reiteration set
                                                                                                                                                                                        oin(2261. .2317,3083. .3749,3886. .5489)
ene="RL2"
                                                                                                                                                                        unction="modulator of cell state and gene
                                                                                                                                                                                                                                                   24110
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                                                                                                                                                                      expression"
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                                                                                                                                                                                                                  /product="uracil-DNA gly
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MSGHGCLEKWARDGVLLLNTTLTVKRGAAASHSRIGWDRFVGGVIRRLAARRPGLVFM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /note="start of UL(Long Unique region)"
9337. .10011
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                                                                                                                                                                                                                                                                                                                                                     9884. .10888
'gene="UL2"
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/gene="RL2"
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PAAARTAPPSAPIGPHGSSNTNTTTNSSGGGGSRQSRAAAPRGASGPSGGVGVGVGVV
EAEAGRPRGRTGPLVNRPAPLANNRDDTVISDSPPASPHRPPAAPMPGSAPRPGPPAS
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                                                                                                                                                                    db_xref="SWISS-PROT:P10186"
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protein_id="CAA32337.1"
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                                                                                                                                                                                               db_xref="GI:59503"
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806. .8826
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            xref-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LGPTNGTSGRTPVLPPDDEAGLQPKPLTTPPPIIATSDPTPRRDAATKSRRRR
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                                                                                                                                                                                                                                        Viruses; dsDNA viruses, no RNA stage; Herpesviridae; Alphaherpesvirinae; Simplexvirus.

1 (bases 1 to 6633)

McGeoch, D. J., Dolan, A., Donald, S. and Brauer, D. H. Complete DNA sequence of the short repeat region in herpes simplex virus type 1
                                                                                                                                                                                                                                                                                                                                          human herpesvirus 1 human herpesvirus 1
                                                                                                                                                                                                                                                                                                                                                                        IE gene 3; IE175 protein; transcriptional activator
                                                                                                                                                                                                                                                                                                                                                                                                                                                   TEHSVIGS 6033 bp DNA VRL 30-APR-19
Herpes simplex virus type I immediate early (IE) gene 3 for transcriptional activator IE175 (= ICP 4).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ch. 3.3%; similarity 59.1%; 91; Conservative
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                                                                                                                                                                                                                          eic Acids Res. 14 (4), 1727-1745 (1986)
                    complement(65. .232)
/note="Thttps://notes.pubmediagraphics."
                                                               /map="R(s) region"

complement(<1. .479)

/note="primary transcript of IE68

complement(<1. .64)
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10957.
complement(113. .217)
                                                                                                                           /organism="human herpesvirus
/strain="17"
/db_xref="taxon:10298"
                                                                                                                                                                            1. .6633
                                                                                                                                                                                            Location/Qualifiers
                  'note="Intron
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/gene="RL2"
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VSSIDELGRRQLTDTIRKDLRLSLAKFSIACTKTSSFSGNAPRHHRRGAFQRGTRAPR
SNKSLQMFVLCKRAHAARVREQLRVVIQSRKPRKYYTRSSDGRLCPAVPVFVHEFVSS
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11715. .11720
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'translation="MYKPLVSYGSVMSGVGGEGVPSALAILASWGWTFDTPNHESGIS
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'db_xref="GI:59504
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/db_xref="PID:e312317"
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/note="repetitious region 3"
6232. .6232
/note="a' sequenco"
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/note="Exon 2 IE68"
complement(502. .509)
/note="TATA-Box (IE68 gene)"
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/note="repetitious region 4"
1 2453 c 2818 g 677 t
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ALMEDPRALAS IAARCAGPAPAAQAACGGGDDDDNPHPHGAAGRLFGPLRASGPLRR
MAAMMRQ IEDPEDVRVVVLYSPLPGEDLAGGGASGPPEWSAERGGLEGCLLAALANRL
CGPDTAAWAGMWTGAPDVSALGAQGVLLLSTRDLAFAGAVEFLGLLASGDRRLIVVN
TVRACDWPADGPÄVSRQHAYLACELLPAVQCAVRWPAARDLRRTVLASGRVFGPGVFA
RVEAAHARLYPDAPPLRLCRGGNVXYRVRTREGPDTPVPMSPREYRRAVLPALDGRAA
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VAASPPRT PAF RADDDDGDEYDDAADAAGDRAPARGREREAPLRGAY PDPTDRLSPRP
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db_xref="PID:g59849"
db_xref="GI:59849"
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ranslation="MASENKORPGSPGPTDGPPPTPSPDRDERGALGWGAETEEGGDD
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hte="IE175 mRNA"
7. .5373
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Search completed: September 28, 1999, 16:36:58
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US-08-520-678A-30
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NFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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MEDIUM TYPE: Floppy
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                                                             TOPOLUGE: DN
OLECULE TYPE: DN
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NAME: Leary Ph.D., Kathryn R.
REGISTRATION NUMBER: 36,317
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URRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/458,568A
                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER: IBM PC
OPERATING SYSTEM:
                                                 NTI-SENSE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COUNTRY: UZIP: 19103
                  ORGANISM:
                                                                                                             STRANDEDNESS:
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                                                                                                                              nucleic acid
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Herpes simplex virus
Herpes Simplex Virus Type 1
                                                                                                                                             12001 base pairs

    Woodcock, Washburn, Kurtz, Mackiewicz & No. 5821339ris
    One Liberty Place, 46th floor

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                                                                               DNA (genomic)
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SEQUENCE CHARACTERISTICS:
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                                                                                                                                                                                                                                                                                             ATTORNEY/AGENT
                                                                                                                                                                                                                                                                                                                                              SOFTWARE: Patentin Re
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MEDIUM TYPE: Floppy
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                           49
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                                                                Local
                                                                                                                                               TYPE: nuclei
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CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                          COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                     APPLICATION NUMBER:
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                ccccaatctgcaccccgcagactcgccccccccataccggcgttgcagtcaccgcccg 108
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                                                                                                                                                                      4257 base pairs
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О.
                                                     Conservative
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59.1%;
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                                                Score 53.2; DB 4,
Pred. No. 0.0024;
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Pred. No. 0.0031;
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                                                                           Length 4257;
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; LOCATION:
US-08-056-051-5
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Best Local :
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INFORMATION FOR SEQ ID NO:
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NAME: NO. 5516683nan, Kevin E
REGISTRATION NUMBER: 35,303
REFERENCE/DOCKET NUMBER: 90,1092-C
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MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE CHARACTERISTICS:
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                                                                                                                                                                                                                                                                               FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                MOLECULE TYPE:
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                                                                                                                                                                                                                                                                                                                         EATURE:
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951 CCGGCCTCCCCCGGACCCCTGCGGCCCCGACTGTGCGCCCCCCGCGCCCCGGGCCTCCCCC
                                                                                                       891
                                                                                                                                                                         Local
                                                           65 gcagactcgccccccccccataccggcgttgcagtcaccgccgttgcgcccgttgcgcccccta 124
                                                                                                                                                                                                                                                                                                          NAME/KEY:
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                                                                                                                          5 cgagcttcgctgtccgcgcccagtgacgcgcgtgcggaccccgagccccaatctgcacccc 64
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                                                                                                  CGCCCCCCGCGCCCTTCCCCGGGGTCCCTGCGGCCCCGACTGTGCGCCCCGCCGCCGC
                                                                                                                                                              144;
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                                                                                                                                                                                                                                                                                                                                                                                                                                       1610 base pairs
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10 South Wacker Drive, Suite 3000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                USA
                                                                                                                                                             Conservative
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James R
                                                                                                                                                                         3.1%;
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                                                                                                                                                          Score 49.8; DB Pred. No. 0.01; 0; Mismatches 1
                                                                                                                                                             0;
                                                                                                                                                                                     DB 1;
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                                                                                                                                                                                                                                                                                                                                                                                                                               NFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE CHARACTERISTICS:
LENGTH: 803 base pairs
TYPE: NUCLEIC ACID
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MEDIUM TYPE: Floppy
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CITY: Chicago
Illinois
TATE: Illinois
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CURRENT APPLICATION DATA
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                                                                                                                                                                                                                                                                                                                           MOLECULE TYPE:
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OPERATING SYSTEM:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         REFERENCE/DOCKET NUMBER:
                                                   IDENTIFICATION METHOD: experimental THER INFORMATION: /function= "PstI site" THER INFORMATION: /evidence= EXPERIMENTAL
                                                                                                            NAME/KEY: misc_feature LOCATION: 257..262
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                                                                                                                                                                                                                               DENTIFICATION METHOD: /ev
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                                                                                                                                                                                                                                                                                      exon
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                                                                                                                                                           gene"
                                                                                                                                                                        /evidence= EXPERIMENTAL
/standard_name= "Alternate Exon 3: D4.7"
/note= "This sequence represents the third exon
allele D4.7 of the human D4 dopamine receptor
                    /standard_name= "PstI site"
/label= PstI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            US/07/928,611
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           No. 5569601el Human Dopamine Receptor and Uses
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"This sequence is a PstI site whereby
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US-07-928-611-21
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 21, Applicat Patent No. 5569601 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Best Local Similarity Matches 144; Conserv
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                                                                                                                                                                                                                                                                         COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
ODERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                  CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STREET: 10 SOUTH
CITY: Chicago
STATE: Illinois
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         630
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PPLICANT: Van Tol, Hubert H.M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      570 GCCCCGACTGTGCGCCCCGCGGGCCCGGGCCTCCCCAGGACCCCTGCGGCCCCGACTGTG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           390 CGCCCCCGCGCCCGGCCTTCCCCGGGGTCCCTGCGGCCCCGACTGTGCGCCCCGCCGCGC 449
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                                                                                  CLASSIFICATION:
                                                                                                                        APPLICATION NUMBER: UPPLICATION NUMBER: UPPLIC
                                                                                                                                                                                                                                            SOFTWARE: PatentIn Release #1.0, Version
                                                                                                                                                                                                                                                                                                                                                                                                                                                   COUNTRY: U
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ADDRESSEE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    E: Allegretti & Witcoff, Ltd.
10 South Wacker Drive, Suite 3000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    USA
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/rpt_unit= 346 . 394
/note= "This sequence is a repeat found in 7 known
                                                                                                                                                             US/07/928,611
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Pred. No. 0.0087;
D; Mismatches 157;
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US-07-928-611-21
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Best Local S
                                                                                                                                                                                                                            Sequence 12,
                                                                                                                                                                                                                Patent No.
                                                                                                                                                                                                 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   INFORMATION FOR SEQ ID NO:
           COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                 1191 C 1191
                                                                                                                                                                  APPLICANT: Van Tol,
                                                                                                                                                                                                                                                                                                                                                        1131 CGCCCCCCGCGCCCCGGCCTCCCCGGACCCCTGCGGCTCCAACTGTGCTCCCCCCGACG 1190
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                                                                            STREET: 300 Sc
CITY: Chicago
                                          ZIP: 60606
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LECULE TYPE:
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E: cDNA
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compatible
                                                                                                 Wacker Drive
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No. 5883226el
                                                                                                              Boehnen Hulbert & Berghoff
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                                                                                                                                                      Human Dopamine Receptor and Uses
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US-08-487-811A-12
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Best Local Similarity
Matches, 144; Conserv
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SEQUENCE CHARACTERISTICS:
LENGTH: 803 base pairs
TYPE: nucleic acid
STRANDENESS: single
                                                                                                                                                                                                                                                                                                                                                            OTHER INFORMATION: FEATURE:
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                                                                                              450 CCGGCCTCCCCCGGACCCCTGCGGCCCCGACTGTGCGCCCCCGCGCCCCGGCCTCCCCC 509
                                                                                                                                                            CURRENT APPLICATION DATA
185 cctcgctgtggtcgcctctgttgctctgtgtcctcggggtgcctcggggcggatcgggag 244
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                                                                                                                   NAME/KEY:
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SOFTWARE: Patent
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                                 AGGACCCCTGCGGCCCCGACTGTGCGCCCCCCGCCCCGGCCTTCCCCGGGGTCCCTGCG 569
                                                             tycccycyyytcycccyycycccytcyccaatccycycygogogogocycycycytyt 184
                                                                                                                                                                                cgagcttcgctgtccgcgcccagtgacgcgcgtgcggacccgagccccaatctgcacccc 64
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Release #1.0, Version #1.25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /label= PstI
/note= "This sequence is a PstI site whereby
digestion of human genomic DNA produces a RFLP"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /evidence= EXPERIMENTAL /standard_name= "PstI site"
                                                                                                                                                                                                                                                                                                                                                                         encoding a 16 amino acid sequence
                                                                                                                                                                                                                                                                                                                                                                                          alleles of the human D4
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/note= "This sequence is a repeat
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/standard_name= "Alternate Exon 3: D4.7"
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/rpt_type= "tandem"
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Pred. No. 0.0087;
0; Mismatches 157;
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       tent No.
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LENGTH: 1610 base pair
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TITLE OF INVENTION: A No. 5883226el Human Dopamine Receptor and Uses
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SYSTEM: PC-DOS/MS-DOS
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PCT-US93-07370-12
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NFORMATION FOR SEQ ID NO:
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CURRENT APPLICATION DATA
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MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS
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NAME/KEY:
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                                        FEATURE:
                                                                                                                                  OTHER INFORMATION: OTHER INFORMATION:
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TYPE: nucleic acid
STRANDEDNESS: single
                                                             OTHER INFORMATION:
                                                                                                                                                                                                              NAME/KEY:
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LOCATION: 257..262
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/evidence=EXPERIMENTAL
/standard_name= "Alternate Exon 3: D4.7"

/note= "This sequence represents the third exon
allele D4.7 of the human D4 dopamine receptor
                                                                                                                                                                                                                                            /label= PstI
/note= "This sequence is a PstI site whereby
digestion of human genomic DNA produces a RFLP"
                                                                                                                                                                                                                                                                                                                                                                                                                                     gene"
                                                         /note= "This sequence is a repeat found in 7 known alleles of the human D4 dopamine receptor gene encoding a 16 amino acid sequence repeated 7 times
                                                                                                             D: experimental
/rpt_type= "tandem"
/evidence= EXPERIMENTAL
/rpt_unit= 346 . 394
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'function= "PstI site"
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PCT-US93-07370-21
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Best Local Similarity
 Matches 144;
                             Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 21, Application PC/TUS9307370
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                            MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0.
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                     NUMBER OF SEQUENCES: 2: COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                 SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                  TITLE OF INVENTION: A Novel Human Dopamine
                                                                                                                     FEATURE:
                                                                                                                                                                 FEATURE:
                                                                                                                                                                                                            FEATURE:
                                                                                                                                                                                                                          MOLECULE TYPE: CDNA
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                                                                                       NAME/KEY:
LOCATION:
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                Local Similarity
                                                                                                                                                                                                                                                     STRANDEDNESS:
                                                                                                                                    LOCATION:
                                                                                                                                                  NAME/KEY:
                                                                                                                                                                                               NAME/KEY:
                                                                                                                                                                                                                                          TOPOLOGY:
                                                                                                                                                                                                                                                                    TYPE: nucleic acid
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1508..1610
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Pred. No. 0.0087;
0; Mismatches 157
               Score 49.8; DB Pred. No. 0.01;
 Mismatches
                             DB 5;
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 157;
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                                                                                 Query Match
Best Local Similarity
                                                                   Matches 141;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 8, Application US/08623471 Patent No. 5846823
                                                                                                                                                                                                                                                 INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                  PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/
FILING DATE: 27-SEP-1994
                                                                                                                                                                                                                                SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                             REFERENCE/DOCKET NUMBER: AL TELECOMMUNICATION INFORMATION: TELEPHONE: (416)-868-1482
                                                                                                                                                                                                                                                                                                                                                                 ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TITLE OF INVENTION: STABLE D4 CELL LINES NUMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                 CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                      FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
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                                                                                                                                                                                    STRANDEDNESS:
                                                                                                                                                                                                                  LENGTH:
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CGCCCCCCCCCCCCCCCCCCCCGGGGTCCCTGCGGCCCCGACTGTGCGCCCCGCCGCGC 109
                           cgagettegetgteegegeceagtgaegegegtgeggaeeeegageeecaatetgeaeee 64
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                                                                  Conservative
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                                                                              Score 49.2; DB 4
                                                                Mismatches
                                                                                               DB 4;
                                                                153;
                                                                                             Length 345;
                                                              Indels
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Best Local S
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       tent No.
                                                                                                                                           HYPOTHETICAL:
                                                                                                                                                        MOLECULE TYPE:
                                                                                                                                                                                                                                 SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                           ATTORNEY/AGENT INFORMATION: NAME: White, John P.
                                                                                                                                                                                                                                                                                                                                                                                                   CURRENT APPLICATION DATA: APPLICATION NUMBER: US
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER READABLE FORM: MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                            TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT:
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58 gcaccccgcagactcgcccccqccccataccggcgttgcagtcaccgccgttgcgcgcc 117
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                                                                                                                                                                                                                                                                                                                        NAME: White, John P. REGISTRATION NUMBER: 28,678
                                                                                                                                                                                                                                                                                                                                                                                                                             SOFTWARE: PatentIn Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
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                                                                                                                                                                                                                                                                                                             REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                         FILING DATE:
                                                                                                                                                                                                                                                                  TELEFAX:
                                                                                                                                                                                                                                                                                                                                                                       CLASSIFICATION: 435
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                                                                                                                                                                                                  nucleic acid
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1185 Avenue of the Americas
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                                                                                                                                                                         linear
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                                                                                                                                                        DNA (genomic)
                                                                                                                                                                                       single
                                                   2.7%;
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                                Score 44.6; DB 4;
Pred. No. 0.12;
0; Mismatches 84
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                                                              Length 801;
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GCCCCGGGGCCTGCGCCGCCGGCGGCGGGGGGCCCTCGCGCTCCGCTGCCGCG 181

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accccatgcccgcggtcgcccgggcccgtcgcccattccgcgcggcggccgccgcgcg 177

Ranum,

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US-07-669-171-3
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                                                    US-08-267-803B-8
         Sequence 8, Application US/08267803B Patent No. 5834183
GENERAL INFORMATION:
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                                                                                                                                                                                                                               Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                TELEX: 66141 PENNIE
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-669-171-3
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                                                                                                                                                                                                                                                                                                                                                       SEQUENCE CHARACTERISTICS:
LENGTH: 1569 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ATTORNEY/AGENT INFORMATION:
*PPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                          TELECOMMUNICATION INFORMATION: TELEPHONE: 212-790-9090
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                                                                                                           281
                                                                                                                                                               102 ccgcccgttgcgcgccacccccatgcccgcgggtcgcccggggccccgtcgcccaatccgc 161
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER: U: FILING DATE: 19910314
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDIUM TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CITY: NEW YORK
                                                                                                                                                                                                                                                                                                                                                                                                                                                     REGISTRATION NUMBER: 18,872 REFERENCE/DOCKET NUMBER: 56
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                                                                                                                                                                                                                                                                                                                            STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                              TELEFAX:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                 TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                         TYPE: NUCLEIC ACID
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                                                                                                                                                                                                                   Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Patentin Release #1.0, Version #1.25
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SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                  linear
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Pred. No.
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US-07-669-171-1

GENERAL INFORMATION:

PPLICANT: PPLICANT:

MADISEN, LINDA

MERWIN, JUNE RAE PURCHIO, ANTHONY F

NUMBER OF SEQUENCES:

& EDMONDS

ITLE OF INVENTION:

TGF-b1/b2: A NOVEL CHIMERIC TRANSFORMING GROWTH FACTOR-BETA

tent No.

Application US/07669171

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; LOCATION: US-08-267-803B-8
                                                                                                                                                                                          Query Match
Best Local Similarity
Matches 80; Conserv
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                                                                                                                              10498 TTTGATTCAAAATTTGAACAAAATTGTTTTAAATAAATTGTCTGTATACCAGTACAAGTT 10557
10618 AAAAAAAAAAAAAAAAAAA 10637
                                                               1490 tttggtccacatgatggtcacacttggatatacccccagtgtgggtaaggttggggtattg 1549
                  1610 aaaaaaaaaaaaaaaaaaa 1629
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0,
CURRENT APPLICATION DATA:
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MEDIUM TYPE: Floppy disk
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                     REFERENCE/DOCKET NUMBER: 11
LECOMMUNICATION INFORMATION:
TELEPHONE: 612-305-1217
                                                                                                                                                                                                                                                                                                       NAME/KEY:
                                                                                                                                                                                                                                                                                                                                                        TOPOLOGY:
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P.O. Box 581415
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Pred. No. 0.31;
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STREET: 1155 AVENUE OF THE AMERICAS

COTY: NEW YORK

STATE: N.Y.

COUNTRY. U.S.A.

LIP: 10036

COMPUTER PLOPY disk

COUNTRY: PF. PO.DY disk

COMPUTER PREADABLE FORM:

MEDIUM TYPE: PC.DDS/MS-DOS

COMPUTER: IMP C.COMPAILDIR

OPERATION SYSTEM: PC.DDS/MS-DOS

SOFTWARRE: PACTON INDEER: U.S/07/669,171

FILING DATE: 19910314

CLASSIFICATION NUMBER: U.S/07/669,171

FILING DATE: 19910314

CLASSIFICATION NUMBER: 15,872

REFERENCE_DOCKT NUMBER: 15,872

REFERENCE_DOCKT NUMBER: 13,872

REFERENCE_DOCKT NUMBER: 13,872
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GenCore version 4.5 Copyright (c) 1993 - 1998 Compugen Ltd.

OM nucleic - nucleic search, using sw model

on: September 28, 1999, 14:43:35; Search time 303.81 Seconds (without alignments)
1341.506 Million cell updates/sec

Title: US-09-037-657-12
Perfect score: 1629
Sequence: 1 99cacgagcttcgctgt

Scoring table: IDENTITY_NUC

ched: 311585 seqs, 125096042 residues

Database : N_Geneseq_36:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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Batten disease gen Batten disease gen

ALIGNMENTS

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The haemonojetin receptor (HR) NR6.11 is a form of the novel HR NR6. Interaction between the novel HR and a ligand facilitates proliferation, differentiation and survival of a wide variety of cells. The HR and it's derivatives can be used for modulating the activity of the receptors e.g. to regulate development, maintenance or regeneration in an array of different cells and tissues in vitro and in vivo. They can be present in therapeutics used for modulating neuronal proliferation, differentiation and survival. The products can also be used for detection and diagnosis, e.g. for cancers or predisposition to cancers, or for drug screening. Sequence 1629 BP; 336 A; 541 C; 453 G; 299 T;
                                                                                                                                                                            P-PSDB; W55011.

New isolated haemopoletin receptor - used for developing products for modulating proliferation, differentiation and survival of cells, e.g. neuronal cells

Claim 4; Page 77-81; 182pp; English.

Claim 4; Page 77-81; 182pp; NR6.1 is a form of the novel HR NR6.
                                                                                                                                                                                                                                                                                                                    19-MAR-1998.
11-SEP-1997; G02479.
11-SEP-1996; AU-002246.
(AMRA-) AMRAD OPERATIONS PTY LTD.
(DZIE/) DZIEGLEWSKA H E.
Alexander W, Fabri L, Farley A, Hilton DJ, Kikuchi Y,
KOjima T, Maeda M, Nash A, Nicola NA, Rakar S, Willson
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Novel haemopoletin receptor NR6.1 gene. Haemopoletin receptor; cell proliferation; cell survival; therapeutic; neuronal proliferation;
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Best Local Similarity Matches 1629; 301 241 181 121 121 cccatgcccgcgggtcgcccgggccccgtcgcccaatccgcgcggggcggccgccgccgccgg 180 181 61 61 μ. 1 ggcacgagcttcgctgtccgcgcccagtgacgcgcgtgcgggacccgagccccaatctgca caagctacctgctctatacatggagacacacctggggccaccgctgaggggctctactgg GGAGCCCACACAGCTGTAATCAGCCCCCAGGACCCCACCCTTCTCATCGGCTCCTCCCTG ggagcccacacagctgtaatcagcccccaggaccccacccttctcatcggctcctccctg CTGTCCTCGCTGTGGTCGCCTCTGTTGTCTCTCTCGGGGTGCCTCGGGGCGGATCG CCCATGCCGCGGGTCGCCGGGGCCCCAATCCGCGCGGCGGCGCCGCGGCGGCCG CCCCGCAGACTCGCCCCCCCCCATACCGGCGTTGCAGTCACCGCCCGTTGCGCGCCACC CCCCGCAGACTCGCCCCCGCCCCCATACCGGCGGTTGCAGTCCACCGTTGCGCGCCCCACCC 120 GGCACGAGCTTCGCTGTCCGCGCCCAGTGACGCGCGTGCGGACCCGAGCCCCAATCTGCA 60 Conservative 100.0%; 0 Score 1629; Pred. No. 0; Mismatches DB .. 1; Length 1629; Indels 0 Gaps 180 120 300 300 240 240 60 0

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                                                                                                                       PT New isolated haemopoletin receptor - used for developing products
PT for modulating proliferation, differentiation and survival of cells,
PT e.g. neuronal cells
PT e.g. neuronal cells
PT claim 5; Page 84-87; 182pp; English.
CC Interaction between the novel HR and a ligand facilitates proliferation,
CC Interaction between the novel HR and a ligand facilitates proliferation,
CC derivatives can be used for modulating the activity of the receptors e.g.
CC derivatives can be used for modulating the activity of the receptors e.g.
CC to regulate development, maintenance or regeneration in an array of
CC different cells and tissues in vitro and in vivo. They can be present in
CC therapeutics used for modulating neuronal proliferation, differentiation
CC and survival. The products can also be used for detection and diagnosis,
CC e.g. for cancers or predisposition to cancers, or for drug screening.
SQ Sequence 1673 BP; 344 A; 550 C; 474 G; 305 T;
                           Query Match
Best Local :
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11-SEP-1997; G02479.
11-SEP-1996; AU-002246.
11-SEP-1996; AU-002246.
(AMRA-) ANRAD OPERATIONS PTY (DZIEZ) DZIEGLEWSKA H E. Alexander W, Fabri L, Farley Kojima T, Maeda M, Nash A, N
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CDS
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Novel haemopoietin receptor NR6.2 gene.
Haemopoietin receptor; cell proliferation; cell different
Gell survival; therapeutic; neuronal proliferation; drug
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PT New nucleic acid encoding U4 haematopoletin receptor superfamily PT chain - potentially useful, e.g. for modulating cell proliferation PT or immune response, for treating cancer and auto: immune disease PS Claim 1; Pages 25-26; 38pp; English.

CC This is the nucleotide sequence encoding the murine U4 protein from CC the haematopoletin receptor superfamily, used in the method of the CC invention for the modulation of cell proliferation, or the immune CC response. Transformed mammalian cells are used to produce recombinant CC U4 protein. The U4 protein is used to screen for specific binding CC agents, raise antibodies. It is also used as reagents for assays and CC at issue markers for isolation of cognate ligands and receptors, and CC in pharmaceutical compositions which may modulate cell proliferation, cell differentiation, and the immune system (e.g. for treating immune CC deficiency, inherited or the result of infection, autoimmune diseases, Sequence 1656 BP; 318 A; 552 C; 478 G; 308 T;
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15-JAN-1998; U00334.
16-JAN-1997; US-784863.
(GEMY ) GENETICS INST INC.
COllins M, Donaldson DD, N
WPI; 98-414109/35.
P-PSDB; W59804.
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Key
CDS
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Nucleotide sequence of the murine U4 gene.
Murine; U4 protein; haematopoietin receptor superfamily;
cell proliferation; humune response; antibody; cell diff
autoimmune disease; cancer; allergy; ds.
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Nov.1998.

Phys. 1998; U08865.

Phys. 13-FEB-1998; US-074721.

Nov.1997; US-045287.

Nov.1997; US-045287.

Nov.1997; US-023890.

Nov.1997; US-023890.

Nov.1997; US-023890.

Nov.1997; US-023890.

Nov.1997; Nov.1997; US-023890.

Nov.1997; Nov.199862,03.

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Nov.1999; Nov.1999; Nov.199862,03.

Nov.1999; Nov.
down-regulating in blood
Disclosure; Page
The present seque
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Best Local Similarity 90.
Matches 1520; Conservative
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Sequence 1724 BP; 350 A; 550 C; 500 G; 324 T;
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Kojima T, Maeda
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WPI; 98-260970/;
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NR6 is a novel haemopoletin receptor (HR). Interaction between the nove HR and a ligand facilitates proliferation, differentiation and survival of a wide variety of cells. The HR and it's derivatives can be used for modulating the activity of the receptors e.g. to regulate development, maintenance or regeneration in an array of different cells and tissues i vitro and in vivo. They can be present in therapeutics used for modulating neuronal proliferation, differentiation and survival. The products can also be used for detection and disgnosis, e.g. for cancers or predisposition to cancers, or for drug screening.

Sequence 1930 Bp; 375 A; 623 C; 561 G; 371 T;
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          gaagtcacacaagacccgaaaccaggt 1346
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RESULT
V70894
 WO9849307-A1.
05-NOV-1998.
01-MAY-1998; U8-074721.
13-FEB-1997; US-045287.
01-MAY-1997; US-05030.
13-FEB-1998; US-023890.
                           (ZYMO) ZYMOGENETICS INC.
Adams RI, Foster DC, Gilbert
Lok S, Presnell SR, Whitmore
WPI; 99-034662/03.
P-PSDB; W70860.
                                                                                                                                                                        Key
CDS
                                                                                                                                                                                                              cDNA encoding human zcytor5.
Zcytor5; cytokinin-like receptor;
maintenance factor; thyroid; heari
                                                                                                                                                                                                                                                       V70894;
down-regulating
in blood
                                                                                                                                                                                                    cardiac pathology;
                                                                                                                                                                                                                                  cDNA encoding
                   New mammalian
                                                                                                                                                                                                                                             17-MAR-1999
                                                                                                                                                                                          sapiens.
                                                                                                                                                                                                                                                                  standard;
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       cytokinin-like receptor Zcytor5 - useful for,
ng Zcytor5 natural ligands or detecting cardio
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/product=
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enlargement; Zcytor!
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                                                                                                                                                                                                  down-regulation; growth factor;
t; skeletal muscle; cardiotrophin-1;
ent; %cytor5 ligand; ss.
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                                                         Lehner
      cardiotrophin-1
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The present sequence encodes a protein designated Zcytor5, which is a cytokinin-like receptor. Soluble Zcytor5 may be administered to down-regulate the effects of a growth and/or maintenance factor in thyroid, heart, and skeletal muscle for example to lessen the effect of cardiotrophin-l on cardiac pathologies, so preventing heart enlargement. Zcytor5 could be used to detect cardiotrophin-l in the blood, and to discover other possible Zcytor5 ligands. A probe comprising Zcytor5 DNA or RNA can be used to determine the presence and integrity of the Zcytor5 gene on chromosome 19. Antibodies and the anti-idiotypic antibody could be used to purify Zcytor5 and the argument and the modify Zcytor5 ligand effects.

Sequence 1690 BP; 319 A; 592 C; 505 G; 274 T;
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Best Local Similarity
Matches 1090; Conser
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                                     CAACACATGTGAGGAGTACCACACAGTGGGGCCCCACTCCTGCCACATCCCCAAGGACCT
99ccctcttcactccctatgagatctgggtggaagccaccaatcgcctaggctcagcaag
                                                                                                                                                                                                  GGAGACCTTCCTCCACACCAACTACTCCCTCAAGTACAAGCTTAGGTGGTATGGCCAGGA
                                                                                                                                                                                                                99agacattettacataccaactactececteaagtacaagetgaggtggtacggtcagga
                                                                                                                                                                                                                                                     CAGCTGCTGGTCCAAGAACATGAAGGACTTGACCTGCCGCTGGACGCCAGGGGCCCACGG
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Pred. No. 1.5e-191;
0; Mismatches 174;
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In blood
Disclosure; Page 68-70; 55pp; English.
The present sequence encodes an allelic varaint of protein designated Zcytor5, which is a cytokinin-like receptor. Soluble Zcytor5 may be administered to down-regulate the effects of a growth and/or maintenance factor in thyroid, heart, and skeletal muscle for example to lessen the effect of cardiotrophin-1 on cardiac pathologies, so preventing heart enlargement. Zcytor5 could be used to detect cardiotrophin-1 in the
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05-NOV-1998.
01-MAY-1998; U08865.
13-FEB-1998; U5-074721.
01-MAY-1997; U5-045287.
01-MAY-1997; U5-850030.
13-FEB-1998; U5-023890.
                                                                                                                                                                                                                                                                                                                                                             Homo sapiens.
Key
CDS
                                                                                                                                                                        (ZYMO) ZYMOGENETICS INC.
Adams Rt, Foster DC, Gilbert
Lok S, Presnell SR, Whitmore
WPI; 99-034662/03.
P-PSDB; W70861.
                                                                                                                                                                                                                                                                                                                                                                                                         17-MAR-1999 (first entry)

cDNA encoding an allelic varaint of human Zcytor5.

COYOCTS: Cytokinin-like receptor; down-regulation; growth factor;

maintenance factor; thyroid; heart; skeletal muscle; cardiotrophin-l;

cardiac pathology; heart enlargement; Zcytor5 ligand; allelic varaint;
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                                                                                                                                             New mammalian cytokinin-like down-regulating Zcytor5 natu
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natural ligands or detecting cardiotrophin-1
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Best Local Similarity 84.7%;
Matches 1095; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     comprising Zcytor5 DNA or RNA can be used to determine the presence and integrity of the Zcytor5 gene on chromosome 19. Antibodies and enti-idiotypic antibody could be used to purify Zcytor5 and therapeutically to modify Zcytor5 ligand effects.

Sequence 1813 BP: 415 A; 604 C; 519 G; 275 T;
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Query Match
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New nucleic acid encoding U4 haematopoietin receptor superfamily rechain - potentially useful, e.g. for modulating cell proliferation or immune response, for treating cancer and auto:immune disease SC laim 1; Page 28; 38pp; English.

This is the nucleotide sequence encoding the human U4 protein from the haematopoietin receptor superfamily, used in the method of the invention for the modulation of cell proliferation, or the immune response. Transformed mammalian cells are used to produce recombinant U4 protein. The U4 protein is used to screen for specific binding agents, raise antibodies. It is also used as reagents for assays and as tissue markers for isolation of cognate ligands and receptors, and in pharmaceutical compositions which may modulate cell proliferation, cell differentiation, and the immune system (e.g. for treating immune deficiency, inherited or the result of infection, autoimmune diseases, sequence 1579 BP; 304 A; 535 C; 473 G; 267 T;
                                                                                                                                                                                                                      16-JAN-1997; US-784863.
(GEMY) GENETICS INST IN
COLLINS M, DONALGSON DD,
WPI; 98-414109/35.
P-PSDB; W59805.
New nucleic acid encodin
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15-JAN-1998; 1
16-JAN-1997; 1
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Nucleotide sequence of the human U4
Human; U4 protein; haematopoletin re
cell proliferation; immune response;
autoimmune disease; cancer; allergy;
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Best Local Similarity
Matches 832; Conser
                                                                                                                                                                                                                                                                                                                                                           The nucleotide sequence was generated by a SN RACE of brain cDNA using NR6 specific primers. NR6 is a novel Haemopoletin receptor (HR). Interaction between the novel HR and a ligand facilitates proliferation, differentiation and survival of a wide variety of cells. The HR and it's derivatives can be used for modulating the activity of the receptors e.g. to regulate development, maintenance or regeneration in an array of different cells and tissues in vitro and in vivo. They can be present in therapeutics used for modulating neuronal proliferation, differentiation and survival. The products can also be used for detection and diagnosis, e.g. for cancers or predisposition to cancers, or for drug screening. Sequence 834 BP; 167 A; 274 C; 225 G; 168 T;
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29-SEP-1998 (first entry)
Nucleotide sequence of products generated by 5N race of brain cDI Haemopoletin receptor; cell proliferation; cell differentiation; cell survival; therapeutic; neuronal proliferation; drug screeni
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 New isolated haemopoletin receptor - used for for modulating proliferation, differentiation e.g. neuronal cells Claim 7; Page 93-95; 182pp; English.
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WPI; 98-260970/23.
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(AMRA-) AMRAD OPERATIONS PTY LTD.

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Alevander W. Fabril L, Farley A, F
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19-MAR-1998.
11-SEP-1997; G02479.
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Nicola NA, Rakar S, Willson
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Pred. No. 1.6e-163;
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W09811225-A2.
D 19-MAR-1998.
F 11-SEP-1997; G02479.
PA (AMRA-) AMRAD OPERATIONS PTY LTD.
PA (DZIE/) DZIEGLEWSKA H E.
PA (PARAMA MARAMA MARAMA MARAMA MARAMA MARAMA MARAMA MARAMA MARAMA MASA A, Micola NA, Ra)
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New isolated haemopoletin receptor - used for developing products for modulating proliferation, differentiation and survival of cells, e.g. neuronal cells.

Claim 7; Page 102-104; 182pp; English.

The NR6 gene encodes a novel Haemopoletin receptor (HR). Interaction between the novel HR and a ligand facilitates proliferation. The HR and it's differentiation and survival of a wide variety of cells. The HR and it's derivatives can be used for modulating the activity of the receptors e.g. to regulate development, maintenance or regeneration in an array of different cells and tissues in vitroe and in vivo. They can be present in therapeutics used for modulating neuronal proliferation, differentiation and diagnosis, and survival. The products can also be used for detection and diagnosis,
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Key
CDS
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Nucleotide sequence of clone HFK-66 encoding human NR6.
Haemopoletin receptor; cell proliferation; cell differentiation; cell survival; therapeutic; neuronal proliferation; drug screenia
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V27144;
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aagtcacacaagacccgaaaccaggtcctgccg
                                                     CGAGTGGAGGACAGTGTGGACTGGAAGGTGGTGGACGATGTGAGCAACCAGACCTCCTGC
                 CACGCGTACTGCTCCAACCTCAGCTTCCGCCTCTACGACCAGTGGCGAGCCTGGATGCAG
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Pred. No. 5.6e
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6.6e-157;
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Sequence 560 BP; 113 A; 182 C; 165 G; 100 T;
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11-SEP-1996; AU-002246.
(AMRA-) AMRAD OPERATIONS PTY LTD.
(DZIE/) DZIEGLEWSKA H E.
Alexander W, Fabri L, Farley A, Hilton DJ, Kikuchi Y,
Alexander W, Fabri L, Sarley A, Hilton DJ, Kikuchi Y,
Kojima T, Maeda M, Nash A, Nicola NA, Rakar S, Willson
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      New isolated haemopoietin receptor - used for modulating proliferation, differentiation
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PCR product for human NR6.
Haemopoletin receptor; cell
cell survival; therapeutic;
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neuronal proliferation; drug screening;
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Pred. No. 2.3e-85;
0; Mismatches 67;
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                                                                                                                                                                                 Query Match
Best Local S
Matches 305
                                                                                                                                                                                                                                                 Claim 5; Page 90-92; 182pp; English.

The haemopoletin receptor (HR) NR6.3 is a form of the novel HR NR6. Interaction between the novel HR and a ligand facilitates proliferation, differentiation and survival of a wide variety of cells. The HR and it's derivatives can be used for modulating the activity of the receptors e.g. to regulate development, maintenance or regeneration in an array of different cells and tissues in vitro and in vivo. They can be present in therapputics used for modulating neuronal proliferation, differentiation and survival. The products can also be used for detection and diagnosis, e.g. for cancers or predisposition to cancers, or for dring expections.
                      1222
                                                                   1162
                                                                                                                                                            1042
                                                                                                              1102
                                                                                                                                                                                                                                                                                                                                                        for modulating proliferation,
e.g. neuronal cells
e.g. neuronal cells
Claim 6; Page 90-92; 182pp; E
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Novel haemopoietin receptor NR6.3 gene. Haemopoietin receptor; cell proliferation; cell survival; therapeutic; neuronal proli
                                                                                                                                                                                                                                                                                                                                                                                                          P-PSDB; W55013.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mouse.
                                                                                                                                                                                                                                                                                                                                                                                              New isolated haemopoietin
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29-SEP-1998 (first entry)
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181
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                                                                                                                                                                                 h 18.7%;
Similarity 100.0%;
05; Conservative
                                                                                                                                                                                                                                            938
                                                                                                                                                                                                                                            BP;
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/product=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Location/Qualifiers
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                                                                                                                                                                                                                                        predisposition to cancers, or 243 A; 245 C; 272 G;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  938
                                                                                                                                                                                                                                                                                                                                                                                receptor - used for ion, differentiation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           560
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    "Haemopoietin receptor
                                                                                                                                                                                 Score 305; DB 1; ; Pred. No. 9.5e-55; 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                            Rakar
                                                                                                                                                                                                                                                                                                                                                                                                                                         DJ, Kikuchi
Rakar S, Will
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  cell differentiation;
                                                                                                                                                                                                                                                                                                                                                                                developing products and survival of cells,
                                                                                                                                                                                                     Length 938;
                                                                                                                                                                                                                                       for drug screening.
178 T;
                                                                                                                                                                                 Indels
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19-MAR-1998.

11-SEP-1997; G02479.

11-SEP-1996; AU-002246.

1 (AMRA-) AMRAD OPERATIONS PTY LTD.

A (DZIE/) DZIEGLEWSKA H E.

A (DZIE/) DZIEGLEWSKA H E.

Nash A, Nicola NA, Râj
                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local
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The NR6 protein is a novel Haemopoietin receptor (HR). Interaction between the novel HR and a ligand facilitates proliferation, differentiation and survival of a wide variety of cells. The HR and it's derivatives can be used for modulating the activity of the receptors e.g. to regulate development, maintenance or regeneration in an array of differentics used for modulating neuronal proliferation, differentiation and disquests in vitro and in vivo. They can be present in therapeutics used for modulating neuronal proliferation, differentiation and survival. The products can also be used for detection and diagnosis, e.g. for cancers or predisposition to cancers, or for drug screening. Sequence 11832 BP; 2447 A; 3367 C; 3298 G; 2720 T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               New isolated haemopoietin receptor - used for developing products for modulating proliferation, differentiation and survival of cells, e.g. neuronal cells Claim 9; Fig 3; 182nn: Franchist
                                                                                                                                                              6450
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Haemopoletin receptor; cell
cell survival; therapeutic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Kojima T, Maeda M, Nash
Zhang J;
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W09811225-A2.
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                                       atggtcgccgcctgccctctgagctgtcccgcctccttaacacctccaccctggccctgg
                                                                                                                                                                                                                  CCTGCTCTATACATGGAGACACACCTGGGGCCACCGCTGAGGGGGCTCTACTGGACCTTCA
                                                                                                                                                                                                                                 cctgctctatacatggagacacacctggggccaccgctgaggggctctactggaccctca
                                                                                                CCCTGGCTAACCTTAATGGGTCCAGGCAGCAGTCAGGAGACAATCTGGTGTCACGCCC
                                                                                                              ccctggctaaccttaatgggtccaggcagtcaggagacaatctggtgtgtcacgccc
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                                                                                                                                                                                                                                                                                                                                          281;
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                                                                                                                                                                                                                                                                                                                                                    Similarity
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99.6%;
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                                                                                                                                                                                                                                                                                                                                    Score 280.4; I
Pred. No. 1.9e
0; Mismatches
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Rakar S, Willson
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V27145

standard;

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Best Local
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  17-MAR-1999 (first entry)
Expressed sequence tag used to identify human Zcytor5.
Zcytor5; cytokinin-like receptor; down-regulation; growth factor; maintenance factor; thyroid; heart; skeletal muscle; cardiotrophi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The NR6 gene encodes a novel Haemopoletin receptor (HR). Interaction between the novel HR and a ligand facilitates proliferation, differentiation and survival of a wide variety of cells. The HR and it's products can be used for modulating the activity of the receptors e.g. to regulate development, maintenance or regeneration in an array of different cells and tissues in vitro and in vivo. They can be present in therapeutics used for modulating neuronal proliferation, differentiation and survival. The products can also be used for detection and diagnosis, e.g. for cancers or predisposition to cancers, or for drug screening. Sequence 6663 BP; 1462 A; 1852 C; 1715 G; 1634 T;
                                                                                                                                                    1399
                                                                                                                                                                                                                                                                                                                   1219
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for modulating proliferation,
e.g. neuronal cells
Claim 8; Page 108-114; 182pp;
The NR6 gene encodes a novel i
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                                                                               V70897
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Haemopoletin receptor; cell proliferation; cell differentiation; cancer; cell survival; therapeutic; neuronal proliferation; drug
                                                                                                   1.5
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P-PSDB; W55016.
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19-MAR-1998.
11-SEP-1997; G02479.
11-SEP-1996; AU-002246.
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02-OCT-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Zhang
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    screening;
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                                                                                                                                                                                                                                                                        atggtcgccgcctgcctctgagctgtcccgcctccttaacaccctccaccctggccctgg
                                                                                                                                               GAGACGGCAGCATTCTGGCTGGCTCCTGCCTCTATGTTGGCT 1440
                                                                                                                                                              gagacggcagcattctggctggctcctgcctctatgttggct
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                                                                                                                                                                                                     CCCTGGCTAACCTTAATGGGTCCAGGCAGCAGTCAGGAGACAATCTGGTGTGTCACGCCC
                                                                                                                                                                                                                                                        ATGGTCGCCGCCTGCCCTCTGAGCTGTCCCGCCTTCCTTAACACCTCCACCCTGGCCCTGG
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                                                                             standard;
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                                                                             cDNA;
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/note= "No start or sta
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Nash
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,, Farley A, Hilton [
Wash A, Nicola NA, R;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   receptor - used for ion, differentiation
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Pred. No. 1.7e-49;
0; Mismatches :
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Rakar S, Willson
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   eloping products survival of cells,
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        cardiotrophin-1;
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Best Local Similarity 81:
Matches 209; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                          The present sequence represents an expressed sequence tag (EST) used to identify cDNA encoding a protein designated Zcytor5, which is a cytokinin-like receptor. Soluble Zcytor5 may be administered to down-regulate the effects of a growth and/or maintenance factor in thyroid, heart, and skeletal muscle for example to lessen the effect of cardiotrophin-1 on cardiac pathologies, so preventing heart enlargement. Zcytor5 could be used to detect cardiotrophin-1 in the blood, and to discover other possible Zcytor5 ligands. A probe comprising Zcytor5 DNA or RNA can be used to determine the presence and integrity of the Zcytor5 gene on chromosome 19. Antibodies and the anti-idiotypic antibody could be used to purify Zcytor5 and therapeutically to modify Zcytor5 ligand effects.

Sequence 259 BP; 53 A; 64 C; 81 G; 46 T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-MAY-1998; UO8865.
13-FEB-1998; US-074721.
01-MAY-1997; US-045287.
01-MAY-1997; US-850030.
13-FEB-1998; US-023890.
                                                                                                                          1163 cgggcccgggcggcggg 1179
                                                                                  1103 cgggaatctggagcgagtggagccaccccaccgctgcctccacccctcgaagtgagcgcc 1162
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (ZYMO) ZYMOGENETICS INC.
Adams RL, Foster DC, Gilbert T, Jelmberg AC, Lehner JM,
Lok S, Presnell SR, Whitmore TE;
                                                                   180
                                                                                                                                                                                                                                                             Example 1; Page 77; 55pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                New mammalian cytokinin-like receptor Zcytor5 - useful for, e.g.
   240
                                                                                                                                                                                           NGGGCCCGGGNGGNGGG 256
                                                             CCGGGATCTNGAGTGAGTGAGCCANCCCACAGCCGGCTTCANTTCCCGCAGTGAGCGNC
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                                                                                                                                                                                                                                                                                                                                                 11.0%;
81.3%;
                                                                                                                                                                                                                                                                                                                                 Score 178.8; DB 1;
Pred. No. 9.4e-29;
0; Mismatches 47;
                                                                                                                                                                                                                                                                                                                                                               Length 259;
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Search completed: September 28, 1999, 16:44:42 Job time: 7267 sec

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Database :
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Perfect score:
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ALIGNMENTS

ACCESSION	RESULT 1 AA049280 LOCUS DEFINITION
RECEPTOR BETA CHAIN PRECURSOR ;, mRNA sequence. AA049280 g1755311	AA049280 464 bp mRNA EST 30-DEC-1996 mj45d02.rl Soares mouse embryo NbME13.5 14.5 Mus muscultus CDNA Clone IMAGE:479043 5' similar to SW-TIAR MOUSE CONGACO TURBUFULTUS.5

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This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
MGI:289787
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Washington University School of MedicineP
4444 Forest Park Parkway, Box 8501, St. L
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Geisel,S., Kucaba,T., Lacy,M., Le,M., Martin,J., Morris,M.,
Schellenberg,K., Steptoe,M., Tan,F., Underwood,K., Moore,B.,
Theising,B., Wylie,T., Lennon,G., Soares,B., Wilson,R. and
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On Dec 30, 1996 this sequence version
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/clone="IMAGE:479043"
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dev_stage="13.5-14.5dpc total fetus"
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                                                                                                                                                                                                                                                                                                                                                                                                          Tel: 314 286 1800
Fax: 314 286 1810
                                                                                                                                                                                                                                                                                                                                                                                                                                        Contact: Marra M/Mouse EST Project
WashU-HHMI Mouse EST Project
Washington University School of MedicineP
4444 Forest Park Parkway, Box 8501, St. Lo
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Marra,M., Hillier,L., Allen,M., Bowles,M., Dietrich,N., Dub. Geisel,S., Kucaba,T., Lacy,M., Le;M., Martin,J., Morris,M., Schellenberg,K., Steptoe,M., Tan,F., Underwood,K., Moore,B., Theising,B., Wylie,T., Lennon,G., Soares,B., Wilson,R. and
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The WashU-HHMI Mouse EST Project
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            /tissue_type="embryo"
/dev_stage="13.5-14.5dpc total fetus"
/lab_host="DH10B"
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/sex="unknown"
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/map="10 pter-cen"
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/strain="C57BL/6J"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             cgtggaggacagcgtggactggaaggtggtggatgacgtcagcaaccagacctcctgccg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AA866388 428 bp mRNA EST 05-FEB-1999 UI-R-AO-aj-f-04-0-UI.S3 UI-R-AO Rattus norvegicus cDNA clone UI-R-AO-aj-f-04-0-UI 3' similar to gbjAC003112|AC003112 Human from chromosome 19 specific cosmid R30292, genomic sequence,
                                              Genome Res. 6 (9),
97044477
On Mar 16, 1998 thi
                                                                                                                        Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
1 (bases 1 to 428)
Bonaldo, M. F., Lennon, G. and Soares, M.B.
                                                                                                                                                                                                                                                                        complete sequence [Homo AA866388
                                                                                              discovery
                                                                                                         Bonaldo, M.F., Lennon, G. and Soares, M.B. Normalization and subtraction: two appr
Contact: Soares,
Program for Rat
                                                                                                                                                                                            Rattus norvegicus
                                                                                                                                                                                                           Norway rat
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                                                                                                                                                                                                                                          GI:4230568
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                                                                                                                                                                                              gccgtctcgcgggcctgaagcccggcaccgtttacttcgtccaagtgcgttgtaaccccat 1078
                                                                                                                                                                                                                                                    ACCGCGTGGAGGACAGCGTGGACTGGAAGGTGGATGACGTCAGCAACCAGACCTCCT
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                                                                                                                                                                                                                                                                                                                               GCTGGGTCTCACCACCAGCTCTCAAGGATTTCCTCTTCCAAGCCAAATACCAGATTCGCT
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                                                                                                                                                                                                                                                                                                                                                                                                            ACCCTCCACCCGACGTGCACGTGAGCCGCGTTGGGGGCCCTGGAGGACCAGCTGAGTGTGC
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405; Conser
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Tel: 319 335 9565

Email: msoars@blue.weeg.ulowa.edu

Coligo-dT track not found, Not I site shown in beginning of sequence is likely internal to the message. cDNA Library Preparation: M. Fatima Bonaldo, Ph.D. Clone distribution: clones will be available through Research Genetics
  AI421423
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451 Eckstein Medic
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /lab_host="DH10B (Life Technologies)"
/note="Vector: p773D-Pac (Pharmacia) with a modified polylinker; Site_1: Not I; Site_2: Eco RI; This library consists of a mixture of individually tagged normalized libraries constructed from rat placenta, adult lung, brain, liver, kidney, heart, spleen, ovary, and muscle. The tag is a string of 3-5 nucleotides present between the Not I site and the oligo-dT track which allows identification of the library of origin of a clone within the mixture."
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /strain="sprague-Dawley"
/db_xref="taxon:10116"
/db_xref="taxon:10116"
/map="between D11S1765 and UGB"
/clone="UI-R-A0-aj-f-04-0-UI"
/clone_11b="UI-R-A0"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /organism="Rattus norvegicus"
/strain="Sprague-Dawley"
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                                                                                                           ccgcctgccctctgagctgtcccgcctccttaacacctccaccctggccctggccctggc 434
                                                                       tatacatggagacacacctggggccaccgctgaggggctctactggaccctcaatggtcg 374
                                                                                                                                             tgtaatcagcccccaggaccccacccttctcatcggctcctccctgcaagctacctgctc 314
                                                                                                                                                                                   GCCCCTGCTGCTGCTCTGCGTCCTCGGGGGCGCGCGAGCCGGATCAGGAGCCCACACAGC 60
                                                                                                                                                                                                                                                            405;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CDNA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome
Clone distribution: NCI-CGAP clone distribution
found through the I.M.A.G.E. Consortium/ILML at:
www-bio.llnl.gov/bbrp/image/image.html
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 (bases 1 to 474)
NCI/NINDS-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
NATIONAl Cancer Institute / National Institute of Neurological Disorders and Stroke, Brain Tumor Genome Anatomy Project (CGAP/BTGAP), Tumor Gene Index
Unpublished (1998)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Bonaldo,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Insert Length: 1664 Std E. Seq primer: -40UP from Gibco High quality sequence stop:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Contact: Robert Strausberg, Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                                                                                                                                                                                                                                            Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                          adaptors (Pharmacia), digested with Not I the Not I and Eco RI sites of the modified Library is normalized, and was constructed Soares and M.Fatima Bonaldo."

181 c 128 g 83 t 1 others
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/lab_host="DH10B"
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/clone_lib="NCI_CGAP_Brn23"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Contact: Robert Strausberg, Ph.D. Tel: (301) 496-1550 Email: Robert_Strausberg@nih.gov
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Unpublished (1997)
On Feb 17, 1998 this sequence version
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP).
Tumor Gene Index
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                                                                                                                                                                                                                                                                                                                                                                                           High quality sequence stop: 467.
                                                                                                                                                                                                                                                                                                                                                                                                            This clone is available royalty-free through LLNL; contact the IMAGE Consortium (info@image.lln1.gov) for further information. Insert Length: 1552 Std Error: 0.00 Seq primer: -40UP from Glbco
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                81
                                                             from the same fetus as the fetal heart library, fetal heart NbHH19W."
183 c 129 g 83 t 1 others
                                                                                                                                                                                                                                                                              /clone="IMAGE:1742408"
/clone_lib="Soares_fetal_lung_NbHL19W"
                                                                                                                                                                                                                                                                                                                     /organism="Homo sapiens"
/db_xref="taxon:9606"
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Query Match
Best Local Similarity
Matches 403; Conserv

Conservative

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Score 362.8; DB 43; Pred. No. 2.3e-60; 0; Mismatches 68;

Length

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Marra, M., Hillier, L., Allen, M., Bowles, M., Dietrich, N., Dubuque, Geisel, S., Kucaba, T., Lacy, M., Le, M., Martin, J., Morris, M., Schellenberg, K., Steptoe, M., Tan, F., Underwood, K., Moore, B., Theising, B., Wylie, T., Lennon, G., Soares, B., Wilson, R. and
                                                                                                              Contact: Marra M/Mouse EST Project
WashUrHHMI Mouse EST Project
WashIngton University School of Medicinep
4444 Forest Park Parkway, Box 8501, St. Louis,
Tel: 314 286 1800
                                                                                                                                                                                             The WashU-HHMI Mouse EST Project
Unpublished (1996)
On Dec 30, 1996 this sequence version
                                                                                                                                                                                                                                                                                                                                                                                                                                     mj45c04.rl Soares mouse embryo NbME13.5 14.5 Mus clone IMAGE:479046 5', mRNA sequence.
                                                              This clone is available royalty-free through LLNL;
                                                                                Email: mouseest@watson.wustl.edu
                                                                                                                                                                                                                                                                                                                               Eukaryota; Metazoa;
Eutheria; Rodentia;
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                                            MGI:289790
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primer: -28M13 rev2 from Amersham
h quality sequence stop: 486.
Location/Qualifiers
                                                                                                  314 286 1800
314 286 1810
                                                     Consortium (info@image.linl.gov)
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                                                                                                                                                                                                                                                                                                                                          ACGACCAGTGGCGTGCTTGGATGCAGAAGTCACAAGACCCGAAACCAGGACGAGGGGA 208
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                  AI394468 462 bp mRNA EST tf79d12 x1 NCI_CGAP_Brn23 Homo sapiens cDNA
mRNA sequence
AI394468
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14.5dpc embryos [total RNA provided by Minoru Ko, Wayne State Univ., from 2]; double-stranded cDNA was ligated Eco RI adaptors (pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of the modified pT7T3 vector. Library went through one round of normalization, and was constructed by Bento Soares and M.Fatima Bonaldo. "
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /note="Vector: pT7T3D-Pac (Pharmacia) with a modified
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /organism="Mus musculus"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="IMAGE:479046"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /dev_stage="13.5-14.5dpc
/lab_host="DH10B"
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                                                                   121
                                                                                                                                                        255 tgtaatcagcccccaggaccccacccttctcatcggctcctccctgcaagctacctgctc 314
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                                                                                   tatacatggagacacacctgggggccaccgctgaggggctctactggaccctcaatggtcg 374
                                                                   TGTGATCAGTCCCCAGGATCCCACGCTTCTCATCGGCTCCTCCCTGCTGGCCACCTGCTC
 CCGCCTGCCCCTGAGCTCTCCCGTGTACTCAACGCCTCCACCTTGGCTCTGGCCCTGGC
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1. (bases 1 to 462)

NCI/NINDS-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.

National Cancer Institute / National Institute of Neurological Disorders and Stroke, Brain Tumor Genome Anatomy Project (CGAP/BTGAP), Tumor Gene Index
Unpublished (1998)

On Feb 17, 1998 this sequence version replaced gi:2887603.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Seq F
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Contact: Robert Strausberg, Ph.D. Tel: (301) 496-1550
Email: Robert_Strausberg@nih.gov
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Tissue Procurement: David N. Louis, M.D., Myrna R. Rosenfeld M.D.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Insert Length: 1631
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CDNA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome
Clone distribution: NCI-CGAP clone distribution
found through the I.M.A.G.E. Consortium/LLNL at:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /ww-bio.llnl.gov/bbrp/image/image.html
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                                                                                                                                                                                                                                                                                               Similarity
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h quality sequence stop: 454.
Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                               /organism="Homo sapiens"
/db_xref="taxon:9606"
/map="10; 1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /clone="IMAGE: 2105495"
/clone_lib="NCI_CGAPE Brn23"
/tissue_type="glioblastoma (pooled)"
/lab_host="DH10B"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Contact: Novel 496-1550
Tel: (301) 496-1550
Email: Robert_Strausberg@nih.gov
Email: Robert_Strausberg@nih.gov
This clone is available royalty-free through LLNL; contact the
TMAGE Consortium (info@image.llnl.gov) for further information.

The rength: 1599 Std Error: 0.00
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Unpublished (1997)
On Jan 19, 1998 this sequence version
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High quality sequence stop: 454.
Location/Qualifiers '
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Eutheria; Primates;
1 (bases 1 to 466)
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National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
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                                                                                                                                /dev_stage="19 weeks"
//lab_host="DBHOB (ampicillin resistant)"
//lab_host="DBHOB (ampicillin resistant)
//lab_hos
                                                                            same fetus as the fetal lung NbHL19W."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /organism-"Homo sapiens"
/db_xxef-"taxon:9606"
/map-"839602; 821611; 4; 4p15.33-4p16.1;
/clone-"IMAGE:1705398"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /clone_lib="Soares_fetal_heart_NbHH19W"
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Query Match Best Local Similarity

21.7%;

Score Pred.

354; No. 1

DB 43;

Length 466

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REFERENCE
AUTHORS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            aatcagcccccaggaccccacccttctcatcggctcctccctgcaagctacctgctatat 317
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     gcetetgttgetetgtgteeteggggtgeeteggggeggategggageeeacacacgetgt 257
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GATCAGTCCCCAGGATCCCACGCTTCTCATCGGCTCCTCCCTGCTGGCCACCTGCTCAGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AI185780

Ge44h04.x1 Soa:

'IMAGE:1741879

AI185780
                                                                                                                                                                                                                            rel: (301) 496-1550
Email: Robert 7
                                                                                                                                                                                                         Email: Robert_Strausberg@nih.gov
This clone is available royalty-free through LLNL;
                                                                                                                                                                                   Contact: Robert Strausberg, Tel: (301) 496-1550
                                                                                                                                                                                                                                                                                            9
                                                                                                                                                                                                                                                                                                       Tumor Gene Index
Unpublished (1997)
                                                                                                                                                                                                                                                                                                                              NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy
                                                                                                                                                                                                                                                                                                                                                                 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 466)
                                                                                                                                                                                                                                                                                                                                                                                              Eukaryota;
                                                                                                                                                                                                                                                                                                                                                                                                             Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                          AI185780.1
                                                                                                                                                                                                                                                                                    Jan 19, 1998 this sequence version
                                                                                                                                   primer: -40UP from Gibco quality sequence stop: 466.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Conservative
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:1741879"
/clone="IMAGE:1741879"
/clone=lib="Soares_fetal_lung_NbHL19W"
/dev_stage="19 weeks"
/lab_host="DH10B (ampicillin resistant)"
/note="Organ: lung; Vector: pT7T3D (Pharmacia) with
modified polylinker; Site_1: Not I; Site_2: Eco RI;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              466 bp mRNA
Soares_fetal_lung_NbHL19W
.879 3', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mismatches
                                                                                                                                                                                                                                                          Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Homo sapiens
                                                                                                                                                                                                                                                                                    replaced
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   66;
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                                                                                                                                                                                                                                                                                                                              Project (CGAP),
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CDNA clone
                                                                                                                                                                                               information.
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                                                                                618
                    427
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CTGCTGGTCCAAGAACATGAAGGACTTGACCTGCCGCTGGACGCCAGGGGCCCACGGNGA
                                                                                                                                                                          ctgctggtcccggaacatgaaggatctcacgtgccgctggacaccgggtgcacacgggga
                                                                                                                                                                                                                                                                 CATCCTGGCTGGCTCCTGCCTCTATGTTGGCCTGCCCCAGAGAAACCCGTCAACATCAG
                                                                                                                                                                                                                                                                                                           cattotggctggctcctgcctctatgttggcttgcccctgagaagccctttaacatcag
                                                                                                                                                                                                                                                                                                                                                                                                      CCTCAATGGGTCCAGGCAGCGGTCGGGGGACAACCTCGTGTGCCACGCCCGTGACGGCAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                cctgccctctgagctgtcccgcctccttaacacctccaccctggccctggccctggctaa 437
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              acatggagacacacctggggccaccgctgaggggctctactggaccctcaatggtcgccg
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CCTGCCCCTGAGCTCTCCCGTGTACTCAACGCCTCCACCTTGGCTCTGGCCCTGGCCAA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    normalization to a Cot - 5. Library constructed by Bento Soares and M.Fatima Bonaldo. This library was constructed from the same fetus as the fetal heart library, Soares fetal heart NbHH19W."

183 C 123 g 80 t 1 others
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             double stranded cDNA was size selected, ligated to Eccadapters (Pharmacia), digested with Not I and cloned i the Not I and Ecc RI sites of a modified pT7T3 vector (Pharmacia). Library went through one round of the Not I and Eccade with the second control of the se
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            21.7%;
85.6%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 354; DB 43;
Pred. No. 1.1e-58;
0; Mismatches 66;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 466;
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cloned into
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REFERENCE
AUTHORS
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KEYWORDS
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                                                                                                                                                                                                                                      SOURCE
                                                                                                                                                                                                                                                                                                                       ACCESSION
                                                                                                                                                                                                                                                                                                                                                                 DEFINITION
                                                                                                                                                                                                                                                                                                                                                                                                                               RESULT
                                                                                                                                                                                                                  ORGANISM
                                                                                                                                                                                                                                                                                                                   AA039053 445 bp mRNA m199d07.rl Soares mouse embryo NbME13.5 clone IMAGE:474733 5', mRNA sequence. AA039053
The WashU-HHMI Mouse EST Project 
Unpublished (1996)
                                                  Geisel, S., Kucaba, T., Lacy, M., Bowles, M., Dietrich, N., Dub Geisel, S., Kucaba, T., Lacy, M., Le, M., Martin, J., Morris, M., Schellenberg, K., Steptoe, M., Tan, F., Underwood, K., Moore, B. Theising, B., Wylie, T., Lennon, G., Soares, B., Wilson, R. and Waterston, R.
                                                                                                                    Eutheria; Rodentia; Sciurognath
1 (bases 1 to 445)
Marra, M., Hillier, L., Allen, M.,
                                                                                                                                                                                        Eukaryota; Metazoa;
                                                                                                                                                                                                              Mus musculus
                                                                                                                                                                                                                                                                           AA039053.1
                                                                                                                                                                                                                                    house mouse.
                                                                                                                                                              Chordata; Craniata; Vertebrata;
Sciurognathi; Muridae; Murinae;
                                                                                                                                                                                                                                                                                                                                                        EST
14.5
                                                                                                                                                                                                                                                                                                                                                        Mus
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465

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BASE COUNT
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Best Local S
Matches 395
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                                                                                                                                                                                                                                1343
                                                                                                                                                                                                                                                                                    1326
                                                                                                                                                                                                                                                                                                                                        1266
                                                                                                                      1463
                                                                                                                                                            1403 tcacctgaattggagccctctgtaccatctgggcaacaaagaaacctaccagaggctgg 1462
                                                                                                                                                                                                                                                                                                                                                                  445
                                                                                                                                                                                                                                                           325
                                                                                                                                                                                                                                                                                                               385 ATACTGCTCGAACCTTAGTTTCCGCCTGTACGACCAGTGGCGTGCTTGGATGCAGAAGTC
                                                                                                                                                                                                      265
                                         85
                                                                                                                                                                                                                    aggtcctgccggctaaactctaaggataggccatcctcctgctggtcagacctggaggc 1402
                                                                                                                                                                                                                                                                                                                             atactgctcgaaccttagtttccgcctgtacgaccagtggcgtgcttggatgcagaagtc 1325
                                                                                                                                                                                                                                                                                 acacaagacccgaaacc------
                                                                                                                                                                                                                                                                                                                                                                  ACACAAGACCCGAAACCAGGACGAGGGGATCCTGCCCTCGGGCAGACGGGGTGCGGCGAG
aggagttgttcaggtaaaaaaaaaa 1607
                                                                                                          ggcacaatgagctcccacaaccacagctttggtccacatgatggtcacactttggatatac 1522
                                                      GGCACAATGAGCTCCCACAACCACAGCTTTGGTCCACATGATGGTCACACTTGGATATAC
                                                                                                                                                  TCACCTGAATTGGAGCCCCTCTGTACCATCTGGGCAACAAAGAAACCTACCAGAGGCTGG
                                                                                                                                                                                                      AGGTCCTGCCGGCTAAACTCTAAGGATAGGCCATCCTCCTGCTGGGTCAGACCTGGAGGC
                                         395;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Email: mouseest@watson.wustl.edu
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Contact: Marra M/Mouse EST project
washington University School of MedicineP
Washington University School of MedicineP
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MGI:285477
                                                                                                                                                                                                                                                                                                                                                                                                                                     Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              quality sequence stop: 441.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           314 286 1800
314 286 1810
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                                                                                                                                                                                                                                                                                                                                                                                                                         Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /tissue_type="embryo"
/dev_stage="13.5-14.5dpc total
/lab_host="DH10B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /clone_lib-"Soares mouse embryo NbME13.5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /db_xref="taxon:10090"
/clone="IMAGE:474733"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /organism="Mus musculus"
/strain="C57BL/6J"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /sex="unknown"
                                                                                                                                                                                                                                                                                                                                                                                                                                    20.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 337.8; DB 27; Pred. No. 1.4e-55;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              fetus"
                                                                                                                                                                                                                                                                                                                                                                                                                         Indels 43;
                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length
                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                              266
                                                                                                                                                                                                                                                                                       1343
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                                            26
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AUTHORS
TITLE
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AI187074
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   VERSION
KEYWORDS
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ORIGIN
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                                                                                                                          234
                                                                                                                                                                              174
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                                              121
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Matches 376;
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Best Local Similarity
354 ctactggaccctcaatggtcgccgcctgcctctgagctgtcccgcctccttaacacctc
                                                      ctccctgcaagctacctgctctatacatggagacacacctgggggccaccgctgaggggct 353
                                                                                                              cggatcgggagcccacacagctgtaatcagcccccaggaccccacccttctcatcggctc 293
                                                                                                                                                                       gcggccgctgtcctcgctgtggtcgcctctgttgctcttgtgtcctcgggggtgcctcgggg 233
                                         CTCCCTGCTGGCCACCTGCTCAGTGCACGGAGACCCACCAGGAGCCACCGCCGAGGGCCT
                                                                                                 CGGATCAGGAGCCCACACAGCTGTGATCAGTCCCCAGGATCCCACGCTTCTCATCGGCTC
                                                                                                                                                       GCGGCCGCCGTTGCTGCCCCCTGCTGCTGCTCCTCCGCGCGCGCGCCGAGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AI187074 447 bp mRNA
qe38a03.s1 Soares_fetal_lung_NbHL19W
IMAGE:1741228 3', mRNA sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Tumor Gene Index
Unpublished (1997)
On Aug 21, 1998 this sequence version replaced
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 447)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EST.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       National Cancer Institute,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ÃI187074.1 GI:3737712
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy
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                                                                                                                                                                                                                                                                                          Conservative
                                                                                                                                                                                                                                                                                                  69
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /db_xref="taxon:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                organism="Homo sapiens"
/db xref="taxon:9606"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ocation/Qualifiers
                                                                                                                                                                                                                            20.5%;
                                                                                                                                                                                                                 0
                                                                                                                                                                                                              Score 334; DB 43;
Pred. No. 7.4e-55;
0; Mismatches 71;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Homo
                                                                                                                                                                                                               71;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              sapiens cDNA clone
                                                                                                                                                                                                                                             Length 447
                                                                                                                                                                                                                  Indels
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                                                                                                                                                                                                                 0,:
                                                                                                                                                                                                                 Gaps
                 413
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                                                                                                    120
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Length

431;

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VERSION
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BASE COUNT
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AI333812
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CACCTTGGCTCTGGCCCAACCTCAATGGGTCCAGGCAGCGGTCGGGGGGACAACCT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        rel: (301) 496-1550
Email: Robert 7
                                                                                                                                                                                                                                                                                                                                                                                    High quality sequence stop: 407.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                       Email: Robert_Strausberg@nih.gov
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
Insert Length: 1615 Std Error: 0.00
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AI333812 431 bp mRNA EST 13-FEB-1999 qp93e12.x1 Soares_fetal_lung_NbHL19W Homo sapiens cDNA clone IMAGE:1930606 3' similar to TR:Q16354 Q16354 PROLACTIN RECEPTOR
                                                                                                                                                                                                                                                                                                                                                                                                                        Seq primer: -40UP from Gibco
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Contact: Robert Strausberg, Ph.D.
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National Cancer Institute, Cancer Genome Anatomy
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                89
                                                        from the same fetus as the fetal heart library, Soares fetal heart NbHH19W."
                                                                                                                                                                                                                                        /clone_lib="Soares_fetal_lung_NbHL19W"
/dev_stage="19 weeks"
/lab_host="DH10B (ampicillin resistant)"
                                                                                                                                                                                                                                                                                               /map="4p16.1-4pter"
/clone="IMAGE:1930606"
                                                                                                                                                                                                                                                                                                                                  /db_xref="taxon:9606"
                                                                                                                                                                                                                                                                                                                                                   organism="Homo sapiens"
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                                                                                                                                                                                                                                                                                                                                                                                                             q126b05.xl Soares_NhHMPu_S1
3', mRNA sequence.
A1269388
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                                                                                                                         Seq primer: -400P from Gibco High quality sequence stop: '
                                                                                                                                                                                                                           On Aug 21, 1998 this sequence version
                                                                                                                                                                                                                                          Tumor Gene Index
Unpublished (1997)
                                                                                                                                                                                                                                                                                                  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 417)
                                                                                                                                                                                                                                                                                                                                                                                                        g3888555
                                                                                                                                                                                                                                                                      NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anat
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                                                                                  quality sequence stop: 406.
Location/Qualifiers
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/tissue_type="Pooled human melanocyte,
                /clone_lib="Soares_NhHMPu_S1"
                             /clone="IMAGE:1857585"
                                         /organism="Homo sapiens"
/db_xref="taxon:9606"
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                                                                                                                                                                                                                                                                     Anatomy Project (CGAP),
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CDNA clone IMAGE:1857585
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1 UI-R-GO-ut-h-08-0-UI.s

UI-R-GO-ut-h-08-0-UI 3

AI579568
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    351;
Contact: Soares, MB Program for Rat Gene Discovery and Mapping University of Iowa
                                                                                                                                                                        Rattus norvegicus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
                                                                                             Genome Res. 6 (9),
                                                                                                              discovery
                                                                                                                         1 (bases 1 to 332)
Bonaldo, M.F., Lennon, G. and Soares, M.B.
Normalization and subtraction: two approaches
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                                                                 Mar 10,
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Pred. No. 1.6e-50;
0; Mismatches 66;
                                                                sequence version
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UI-R-GO-uc-b-11-0-UI
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Oligo-dT track not found, Not I site shown in beginning of sequence
is likely internal to the message. cDNA Library Preparation: M.B.
Soares Lab Clone distribution: clones will be available through
                                                                   EST.
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Seq primer: M13 Forward.
Eukaryota; Métazoa; Chordata; Craniata; Vej
Eutheria; Rodentia; Sciurognathi; Muridae;
                               Norway rat.
Rattus norvegicus
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/note="Vector: pT773D-Pac (Pharmacia) with a modified polylinker; Site_1: Not I; Site_2: Eco RI; The UI-R-G0 library is a normalized library constructed from a mixture of rat tissues (nodose ganglia, dorsal root ganglia, and trigeminal ganglia). The tag is a string of nucleotides present between the Not I site and the oligo-dT track. The library was constructed as described by Bonaldo, Lennon and Soares, Genome Research 6:
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3', mRNA sequence.
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Oligo-dT track not found, Not I site shown in beginning of sequence
is likely internal to the message. cDNA Library Preparation: M.B.
Soares Lab Clone distribution: clones will be available through
Research Genetics (www.resgen.com)
Seq primer: M13 Forward.
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Bonaldo,M.F., Lennon,G. and Soares,M.B.
Normalization and subtraction: two approaches to facilitate gene
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Program for Rat Gene Discovery and Mapping
University of Iowa
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791-806, 1996.
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/note="Vector: pT/T3D-Pac (Pharmacia) with a modified
polylinker; Site_1: Not I; Site_2: Eco RI; The UI-R-G0
library is a normalized library constructed from a
mixture of rat tissues (nodose ganglia, dorsal root
ganglia, and trigeminal ganglia). The tag is a string of
nucleotides present between the Not I site and the
oligo-dT track. The library was constructed as described
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BASE COUNT ORIGIN	FEATURES source	TITLE JOURNAL	REFERENCE AUTHORS	NID VERSION KEYWORDS SOURCE ORGANISM	RESULT 1 A70384 LOCUS DEFINITION ACCESSION
/organism="unidentified" /db_xref="taxon:32644" 344 a 550 c 474 g 305 t	NICOLA NICON (AU) COCATION/Qualifiers 11673	KIKUCHLY: MAEGA,M. and KIKUCH, M. AND A NOVEL HAEMOPOIETIN RECEPTOR AND GENETIC SEQUENCES ENCODING SAME PATENT WO 9811225-A 19-MAR-1998;	unclassified. 1 (bases 1 to 1673) Nicola, N.A., Fabri, L., Farley, A., Nash, A., Willson, T., Rakar, S., Zhang, J. Alexander W. Hilton D. T. Folias m. Modio V. Carlos M. Carl	94774664 A70384.1 GI:4774664 unidentified. unidentified	A70384 1673 bp DNA Sequence 14 from Patent WO9811225. A70384

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unidentified unidentified unclassified. 1 (bases 1 to 162 Nicola,N.A., Fabri Zhang,J., Alexande Kikuchi,Y. ANOVEL HAEMOPOIET Patent: WO 9811225 NICOLA NICOS ANTON LOCATION OF 1.1659 Ce //db_xref= T 336 a 541 c	### ##################################	atataccccagtgtgggtaaggttggggtattgcagggcctcccaacaatctctttaaat 1620 	99ct9999cacaatgagotocoacaaccacagotttggtocacatgatggtocacattgg 1560 	99a99ctcacctgaattggagcccctctgtaccatctgggcaacaaagaaacctaccaga 1500 	ggcgagaggtcctgccggttaaactctaaggataggccatcctcctgctggtcagacct 1440 	gaagtcacacaagacccgaaaccaggacgagggatcctgccttcgggcagacggggtgc 1380	gcacgcatactgctcgaaccttagtttccgcctgtacgaccagtggcgtgcttggatgca 1320 	cgagcccagctcgggcccggtgcggcgcgagctcaagcagttcctcggctggct	ctccacccctcgaagtgagcgcccgggcccgggcggcggggtgtgcgagccgcgggggcgg 1200 	cgggatctatgggtcgaaaaaggcgggaatctggagcgagtggagccaccccaccgctgc 1140 	CCGTCTCGCGGGCCTGAAGCCCGGCACCGTTTACTTCGTCCAAGTGCGTTGTAACCCATT 1080

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                                                      A NOVEL HAEMOPOIETIN RECEPTOR AND Patent: WO 9811225-A 19-MAR-1998; NICOLA NICOS ANTONY (AU)
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Patent: WO 9811225-A 19-MAR-1998;
NICOLA NICOS ANTONY (AU)
Location/Qualifiers
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Nicola, N.A., Fabri, L.
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1 (bases 1 to 834)

Nicola, N.A., Fabri, L., Farley, A., Nash, A., Willson, T., Rakar, Nicola, N.A., Alexander, W., Hilton, D.J., Kojima, T., Maeda, M. and
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Sequence 23
A70393
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Location/Qualifiers
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Nicola, N.A., Fabri, L., F
Zhang, J., Alexander, W.,
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                                                                                                                                                                                                                                                                                                                                   Patent
                                                                            Score 452.8; DB 5; Pred. No. 3.2e-85; 0; Mismatches 67;
                                                                                                                                                                                                                           Farley, A., Nash, A., Willson, T., Rakar, S., Hilton, D.J., Kojima, T., Maeda, M. and
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Sequence
A70386
                                                                                                                                                                                                                                                1 (bases 1 to 938)
Nicola,N.A., Fabri,L., Farley,A., Nash,A., Willson,T., R.
Zhang,J., Alexander,W., Hilton,D.J., Kojima,T., Maeda,M.
                                                                                                                                                                                                  A NOVEL HAEMOPOIETIN RECEPTOR AND GENETIC Patent: WO 9811225-A 19-MAR-1998; NICOLA NICOS ANTONY (AU)
                                                                                                                                                                                                                                                                                                          unidentified
                                                                                                                                                                                                                                                                                             unclassified
           243
  /translation="GTVYFYQVRCNPFGIYGSKKAGIWSEWSHPTAASTPRSERPGPGGVCEPRGGEPSSGPVRRELKQFLGWLKKHAYCSNLSFRLYDQWRAWMQKSHKTRNQVGKLGEACVGGKCAEEEENDPGEQPPQHRTLLSKHRTRGSCPRADGVRREVRGSG"

245 c 272 g 178 t
                                                                                                                                                                                                                                                                                                                                                                                    16
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/db_xref="PID:e1433693"
/db_xref="PID:g4774666"
/db_xref="GI:4774666"
                                                                                                                                               /organism-"unidentified'
/db_xref-"taxon:32644"
                                                                                                             /codon_start=1
                                                                                                                      /note="unnamed protein product"
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Query Match 18.2%; Best Local Similarity 100.0%; Matches 304; Conservative

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Score 304; DB 5; I Pred. No. 3.9e-54; 0; Mismatches 0;

Length

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BASE COUNT
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gagacggcagcattctggctggctcctgcctctatgttggct 530
                                                                                                              CCTGCTCTATACATGGAGACACACCTGGGGGCCACCGCTGAGGGGCTCTACTGGACCTTCA 1278
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Sequence
A70398
94774676
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Nicola, N.A., Fabri, L., Farley, A., Nash, A., Willson, T., Rakar, S., Zhang, J., Alexander, W., Hilton, D.J., Kojima, T., Maeda, M. and Kikuchi, Y.
                                                                                                                                                                                                                                                                                                                                    A NOVEL HAEMOPOIETIN RECEPTOR AND Patent: WO 9811225-A 19-MAR-1998; NICOLA NICOS ANTONY (AU)
                                                                                                                                                                                                                                                                                                                                                                                                                                  unidentified
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1852 c 1715 g 1
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Pred. No. 3.2e-49;
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Sequence
A70408
94774683
A70408.1
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AC003112.1
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Human DNA
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1 (bases 1 to 11832)

1 (bases 1 to 11832)

1 (bases 1 to 11832)

2 hang,J., Alexander,W., Hilton,D.J., Kojima,T., Maeda,M.
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 4068)

Lamerdin, J. E., McCready, P. M., Adamson, A. W., Burkhart-Schultz, K., Gordon; L., Christensen, M., Kyle, A., Ramirez, M., Stilwagen, S., Garnes, J., Danganan, L., Bruce, R., Quan, G., Montgomery, M., Ow, D., Kobayashi, A., Olsen, A.O. and Carrano, A.V.
                                                                               Homo sapiens
                                                                                            human.
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NICOLA NICOS ANTONY (AU)
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/db_xref="taxon:32644"
3367 c 3298 g 272
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M. and
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence analysis of an \mbox{-1} Mb region containing the MEF2B gene in 19p12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Direct Submission
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (bases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /note="predicted exon, program: grail2exons_human_1.3, frame: 1, quality: good, score: 63.000" complement(9529. 9672) /note="predicted exon, program: grail2exons_human_1.3, frame: 1, quality: excellent, score: 75.000" complement(928. .10123) /rpt_family="Alu" 10409. .10540
/note="predicted exon, program: grail2exons_human_1.3, frame: 1, quality: excellent, score: 100.000-DDS similarity to AA047548 zf15e02.rl Scares fetal heart NbH19W Homo sapiens cDNA clone 377018 5' (139. .221); 100% identity.--DDS similarity to AA136115 zk90b04.rl Scares pregnant uterus NbHFU Homo sapiens cDNA clone 490063 5' (111. .192); 99% identity.--DDS similarity to AA452628 zx33f04.rl Scares total fetus Nb2HF0 9W Homo sapiens cDNA clone 490063 5' (111. .192); 99% identity.--DDS similarity to AA452628 zx33f04.rl Scares total fetus Nb2HF0 9W Homo sapiens cDNA clone 788287 5' (83. .165); 100% identity.--DDS similarity
                                                                                                                                                                                                                                                                                                                     /note="DDS similarity to AA047548 zf15e02.rl Soares fetal heart NbHH19W Homo sapiens cDNA clone 377018 5' (1. 138); 96% identity.—Other overlapping matches:-(10435. 10548) DDS similarity to AA136115 zk900b4.rl Soares pregnant uterus NbHPU Homo sapiens cDNA clone 490063 5' (1. 110); 93% identity.—-(10466. 10548) DDS similarity to AA452628 zx33f04.rl Soares total fetus Nb2HFB 9w Homo sapiens cDNA clone 788287 5' (1. 82); 95% identity.—-(10486. 10548) DDS similarity to AA009412 ze82h02.rl Soares fetal heart NbHH19W Homo sapiens cDNA clone 365523 5' (1. 61); 97%
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      complement(571. .640)
/note="predicted exon, program: grail2exons_human_1.3,
frame: 1, quality: good, score: 71.000"
complement(1383. .1444)
/note="predicted exon, program: grail2exons_human_1.3,
/note="predicted exon, program: grail2exons_human_1.3,
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/rpt_family="Alu"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /note="HERV9 retroviral
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /organism="Homo sapiens"
/db_xref="taxon:9606"
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ement(7500
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_line="5HL2-B"
                                                                                                                                                                                                                                                                           .10725
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NV9 retroviral sequence"
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d, score: 62.000"
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                                                                                                                                                                                                                                                                                                                                                                    Inote-PDS similarity to AA406406 zvile07.sl Soares NhHMPu Sl Homo sapiens cDNA clone 753348 3' (1.433); Score: 858 Identity: 431/433 (99%).---(14884.1523) DDS similarity to W37175 zb21a02.rl Soares fetal lung NbHL19W Homo sapiens cDNA clone 302666 5' (1.355); 94% Identity.--(15227.14885) DDS similarity to AA121532 zk89c11.sl Soares pregnant uterus NbHPU Homo sapiens cDNA clone 49004 3' (342.1); 99% Identity.--(15227.14885) DDS similarity to AA127694 zk89c11.rl Soares pregnant uterus NbHPU Homo sapiens cDNA clone 490004 5' (126.467); 99% Identity.--(15227.14897) DDS similarity to W46603 zc32h10.rl Soares senescent fibroblasts NbHSF Homo sapiens cDNA clone 324067 5 (328.1); 98% Identity.--(15227.15088) DDS similarity to W46604 zc32h10.sl Soares senescent fibroblasts NbHSF Homo sapiens cDNA clone 324067 5 (328.1); 98% Identity.--(15227.15088) DDS similarity to W46604 zc32h10.sl Soares senescent fibroblasts NbHSF Homo sapiens cDNA clone 324067 3' (322.465); 96% Identity."
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pregnant uterus NbHPŪ Homo sapiens cDNA clone 490004 3' (389...343); 99% identity.--DDS similarity to AA127694 zk890:11.r1 Soares pregnant uterus NbHPŪ Homo sapiens cDNA clone 490004 5' (77...125); 90% identity.--(15735...15713) DDS similarity to W46603 zc32h10.r1 Soares senescent fibroblasts NbHSF Homo sapiens cDNA clone 324067.5'
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/rpt_family="Alu"
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/rpt_family="Alu"
                                                                                                                                                                                                                                                                                          'note-"DDS similarity to AA121532 zk89c11.s1 Soares
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DEFINITION
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HTG; НТ
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Caenorhabditis elegans
                                                                                                                                                SEQUENCE, in unordered
       HTGS_PHASE1.
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//note="predicted exon, program: grail2exons_human_1.3,
//n
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//note="predicted exon, program: grail2exons_human_1.3,
/rote="predicted exon, program: grail2exons_human_1.3,
/rote="predicted exon, program: grail2exons_human_1.3,
/rote="predicted exon, program: grail2exons_human_1.3,
/rote="predicted exon: 81.000-other overlapping matches:"(15936. 15895) DDS similarity toAn127694
zk89c11.rl Soares pregnant uterus NDHPU Homo sapiens cDNA
clone 490004 5' (1. .76); 100% identity."
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17926. .18190
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Sequence
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92724471
166494.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Submitted (09 JUN-1999) Nematode Sequencing Project, Sanger Centre, Hinxton, Cambridge CB10 1RQ, UK and Department of Genetics, Washington University, St. Louis, MO 53110, USA. E-mail: jes@sanger.ac.uk or rw@nematode.wustl.edu
On Jun 11, 1999 this sequence version replaced gi:4725958.
Order of segments is not known: 800 n's separate segments.
IMPORTANT: This sequence is unfinished and does not necessarily represent the correct sequence. Work on the sequence is in progress and the release of this data is based on the understanding that the sequence may change as work continues. The sequence may be contaminated with foreign sequence from E.coli, yeast, vector,
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Caenorhabditis elegans
Eukaryota; Metazoa; Nematoda; Secernentea; Rhabditia; Rhabditida;
Rhabditina; Rhabditoidea; Rhabditidae; Peloderinae; Caenorhabditis.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    be preserved
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/db_xref="taxon:6239"
/chromosome="v"
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                                                                                                                                                                                                                                                                                                     Gl gene; glycoprotein; Gs gene; membrane protein; nucleocapsid protein; ORF1a; ORF1a; ORF4; replicase; replicase polyprotein; ribosomal frameshift signal. Equine arteritis virus.
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Plasmid pEAV030 conta
                                                                    An infectious arterivirus cDNA clone: identification of a replicase point mutation that abolishes discontinuous mRNA transcription Proc. Natl. Acad. Sci. U.S.A. 94 (3), 991-996 (1997).
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                                                                                                                                                                                                                       Viruses; ssRNA positive-strand viruses, no DNA stage; Nidovirales; Arteriviridae; Arterivirus.

[ bases 1 to 15528)
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8; Conser
                       (bases 1 to 15528)
                                                                                                                                                                                         Dinten, L.C., den Boon, J.A., Wassenaar, A.L.,
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1491 c 1486 g
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      containing cDNA of Equine arteritis virus,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Pred. No. 0.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       mRNA
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                                                                                                                                                                                         Spaan, W.J. and
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                                                                                                                                                                                                      VTASVTRAYGKPITQESLTATLAALTDDDFQFLSDVLDCRAVRSAMNLRAALTSFQVA
QYRNILNASLQVDRDAARSRRLMAKLADFAVEQEVTAGDRVVVIDGLDRMAHFKDDLV
                                                                                                                                                                                                                                                                                      PQATLVTMGYWACVAALAVYSLMGLRVKVNVPMCVTPAHFILLARSÄGGSREGNILRVS
AAAPTNISLIGVAROCYVTGTTRLYIPKEGGMVFEGLFRSPKARGNVGFVAGSSYGTGS
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LHFAQPTTGPÄSWCTATGDEEGLLSGEVCLAWTTSGDSGSAVVGGDAVGVHTGSNTS
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GLSNRESSLSGPQLLLIACFMWSYLNOPAYLPYVLGFFAANFFLPKSVGRPVVTGLLM
CCCLFTPLSMRLCLFHLVCATVTGNVISLWFYITAAGTSYLSEMWFGGYPTMLFVPRF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GSALQCLNVMWKRPIGSTVLGEQTGAVVTAVKSISFSPPCCVSTTLPTRPGVTVVDHA
codon_start=1
                                 'note="ORF1ab;
                                                             oin (225
                                                                                                                                         VPLTTKVVGGSRCTICDVVKEEANDTPVKPMPSRRRRKGLPKGAQLEWDRHQEEKRN
GDDDFAVSNDYVKRVPKYMDPSDTRGTTVKIAGTTYQKVYDYSGNVHYVEHQEDLLD
                                                                                                                                                                                                                                        /TASVTRAYGKPITQESLTATLAALTDDDFQFLSD1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DHFSKPTIDVVGMATGWSGCYTGTAAMERQCASTVDPHSFDQKKAGATVYLTPPVNS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /product="replicase 0
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                                                                                                                                                                                                                                                       VYQFPGWAIGTVLAVCSITMLAAALGHTLLLDVFSASGRFDRTFMMKYFLEGGVKES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             YNRLTASGVDPALLRVGQGDFLKLNPGFRLIGGWIYGICYFVLVVVSTFTCLPIKCG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /organism="Equine arteritis virus"
/db_xref="taxon:11047"
                                                                                                              VLGKGSYEGLDQDKVLDLTNMLKVDPTELSSKDKAKARHVAHLLLDLANPVEAVNQL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           translation-"MATFSATGFGGSFVRDWSLDLPDACEHGAGLCCEVDGSTLCAEC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      db_xref="SPTREMBL:P89938"
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db_xref="taxon:57026"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   'organism="Plasmid pEAV030"
'db_xref="taxon:57026"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               _xref="taxon:5702
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     host="Escerichia coli strain K12-PC2495"
                                                             .5405,5405.
                           slippery
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                                                       .9751)
                           sequence causes
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                           Ļ
                           frameshift"
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/translation="matfsatgfggsfyrdwsldlpdacehgagicceydgstlcaec frgcegmegcpglfmglkklaspypyghkfligwyraakytgrynfleilohpafagl ryvdarlaieeasyfistdhasakrffgarfaltpyyanawyyspaansliyttdoeo

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/product="replicase ORF1b polyprotein"
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/db_xref="pID:e280872"

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misc_feature
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VTSALAAVSKLIKVPANEPVSFHVASGYRTNALVAPQAKISIGAYAAEWALSTEPPPA
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Fdhlesssyappinayroailsgypoeloleainckilavvapalyhnyhlanltgpa
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VTASYTRAYGKPITQESLTATLAALTDDDFQFLSDYLDCRAYRSAMNLRAALTSFQYA
QYRNILNASLQYDRDAARSRRLMAKLADFAYEQEYTAGDRYYVIDGLDRMAHFKDDLY
                                                                                                                                                                                                                                 GTLPRRKIL"
                                                                                                                                                                                                                                                                  TWVVPTVGQLHYYASSSIFASSVEVLAAIILLFACIPLVTRVYISFTRLMSPSRRTSS
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/protein id="CAM69188,1"
/db_xref="PID:e265651"
/db_xref="PID:g1835172"
/db_xref="GI:1835172"
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9824. .10507
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AVVADVGGNIVFGCGPGSHIAVPLQDTLKGVVVNKALKNAAASEYVEGPPGSGKTFHL
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AASFDRWVFHLQALLGFKVDPKKTVNTSSPSFLGCRFKQVDGKCYLASLQDRVTRSLL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AGDDDFAVSNDYVKRYPKYNDPSDTRGTTVKIAGTTYGKVVDYSGNVHYVEHGEDLLD
YVLGKGSYEGLDQDKVLDLTNMLKVDETELSSKDKAKAHVAHLLDLANPVEAVNQL
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TLLGYVRACPGYWFIFRRTHRSLIDAYWDSMECVYALFTISDFDVSPGDVAVTGERWD
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GLSNRESSLSGPQLLLIACFMMSYLNQPAYLPYVLGFFAANFFLPKSVGRPVVTGLLM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             VKDVLAVVGSATLVVPTHASMLDCINKLKQAGADPYFVVPKYTVLDFPRPGSGNITVR
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                                                                                                                                                         /note="ORF3"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /gene="Gs"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     gene-"Gs"
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                                                                                                                codon_start=1
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TLQQVCELSKPCSAGYNVGQSVFVQTPGVTSYWLTEWVDGKARALPDSLFSSGRFET
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                KEAEAODLIHGPPTACHLGQEIDLWSNEGLEYYKEVNLLYTHVPIKDGVIHSYPNC
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AUTHORS
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Best Local S
Matches 88
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Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 248287)
Bruce,D., Mundt,M., Doggett,N., Munk,C., Saunders,E., Robinso
Jones,M., Buckingham,J., Chasteen,L., Thompson,S., Goodwin,L.,
Druger, T., Buckingham,J., Chasteen,L., Thompson,S., Goodwin,L.
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FYAANVTFPSHFQRHFAAAQDFVVHTGYEYAGVTMLVHLFANLVLTFPSLVNCSRPVN
VFAAASCVQVVCSHINSTTGLGQLSFSFVDEDLRLHIRPTLICWFALLLVHFLPMPRC
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Alamos, NM 87545, USA
* NOTE: This is a 'working draft' sequence. It currently
* consists of 38 contigs. The true order of the pieces
* is not known and their order in this sequence record is
* arbitrary. Gaps between the contigs are represented as
* runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence
* as soon as it is available and the accession number will
* be preserved.
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New nucleic acid encoding U4 haematopoietin receptor superfamily PT chain - potentially useful, e.g. for modulating cell proliferation PT or immune response, for treating cancer and auto:immune disease PS Claim 1; Pages 25-26; 38pp; English.

CC This is the nucleotide sequence encoding the murine U4 protein from CC the haematopoietin receptor superfamily used in the method of the CC invention for the modulation of cell proliferation, or the immune CC response. Transformed mammalian cells are used to produce recombinant CC U4 protein. The U4 protein is used to screen for specific binding CC agents, raise antibodies. It is also used as reagents for assays and CC as tissue markers for isolation of cognate ligands and receptors, and CC cell differentiation, and the immune system (e.g. for treating immune CC deficiency, inherited or the result of infection, autoimmune diseases, CC cancer, and allergy).

So Sequence 1656 BP; 318 A; 552 C; 478 G; 308 T;
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23-UUI-1998; U00334
15-JAN-1999; U00334
16-JAN-1997; US-784863
(GEWY) GENETICS INST INC.
COLLINS M, Donaldson DD, N
WPI, 98-444109/35
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V41688;
V41688;
26-OCT-1998 (first entry)
Nucleotide sequence of the murine U4 gene.
Murine; U4 protein; haematopoietin receptor superfamily;
murine; U4 protein; immune response; antibody; cell difference; cancer; allergy; ds.
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122. .1399
/*tag= a
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19-MAR-1998.
11-SEP-1996; G02479.
11-SEP-1996; AU-002246.
(AMRA) AMRAD OPERATIONS P
(DZIE/) DZIEGLEWSKA H E.
for modulating proliferation, differentiation and survival of cells, e.g. neuronal cells
Claim 4; Page 77-81; 182pp; English.
The haempoletin receptor (HR) NR6.1 is a form of the novel HR NR6.
Interaction between the novel HR and a ligand facilitates proliferation, differentiation and survival of a wide variety of cells. The HR and it's derivatives can be used for modulating the activity of the receptors e.g. to regulate development, maintenance or regeneration in an array of different cells and tissues in vitro and in vivo. They can be present in therapeutics used for modulating neuronal proliferation, differentiation and survival. The products can also be used for detection and diagnosis, e.g. for cancers or predisposition to cancers, or for drug screening.
Sequence 1629 BP; 336 A; 541 C; 453 G; 299 T;
                                                                                                                                                                                                                                                                                                                             Zhang J;
WPI; 98-260970/2
P-PSDB; W55011.
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V27140;
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L, Farley A, Hilton I
Nash A, Nicola NA, R
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WO9849307-A1.
05-NOV-1998:
01-MAY-1998: U08865.
13-FEB-1998: US-074721.
01-MAY-1997: US-850030.
13-FEB-1998: US-023890.
(ZYMO) ZYMOGENETICS INC.
Adams RL, FOSTET DC, Gilbert T
LOK S, Presnell SR, Whitmore T
WPI; 99-034662/03. New mammalian cytokinin-like receptor Zcytor5 - useful for, e.g. down-regulating Zcytor5 natural ligands or detecting cardiotrophin-l in blood Disclosure; Page 72-75; 55pp; English. The present sequence encodes a protein designated Zcytor5, which is V70896 standard; cDNA; 1724 BP.

Y70896;

17-MAR-1999 (first entry)

CDNA encoding rat Zcytor5.

Zcytor5; cytokinin-like receptor; down-regulation; growth maintenance factor; thyroid; heart; skeletal muscle; cardicac pathology; heart enlargement; Zcytor5 ligand; ss.

Rattus sp. Location/Qualifiers 159. 1436 /*tag= a /product= Zcytor5 TE; Jelmberg Lehner cardiotrophin-1;

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Sequence 1724 BP; 350 A; 550 C; 500 G; 324 T;
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                                                                   GGGGCTGGGGCACAATGAGCTCCCACAACCACAGCTTTGG-CCACATGATGGTCAACTTT
                                                                                                    CTCGCGGGCTTGAAGCCCGGCACCGTTTACTTCGTCCAAGTTCGTTGTAACCCATTCGGG
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V27158; V27158; standard; 1930 8

PPR PPU OKKE DAC

19-MAR-1998. 11-SEP-1997; GO2479. 11-SEP-1996; AU-002246. (AMRA-) AWRAD OPERATIONS I (DZIE/) DZIEGLEWSKA H E. 29-SEP-1998 (first entry)
Unspliced murine NR6 nucleotide sequence.
Haemopoletin receptor; cell proliferation;
cell survival; therapeutic; neuronal proli Mus sp. W09811225-A2. Mouse proliferation;

cell differentiation;

drug

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Pr Example 8; Page 99-100; 182pp; English.

CC NR6 is a novel haemopoletin receptor (HR). Interaction between the novel CC and a ligand facilitates proliferation, differentiation and survival CC of a wide variety of cells. The HR and it's derivatives can be used for CC modulating the activity of the receptors e.g. to regulate development, CC maintenance or regeneration in an array of different cells and tissues in CC vitro and in vivo. They can be present in therapeutics used for vitro and in vivo. They can be present in therapeutics used for CC modulating neuronal proliferation, differentiation and survival. The products can also be used for detection and diagnosis, e.g. for cancers CC or predisposition to cancers, or for drug screening.

SQ Sequence 1930 BP; 375 A; 623 C; 561 G; 371 T;
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Best Local Similarity
Matches 1346; Conser
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Kojima T,
Zhang J;
WPI; 98-26
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Maeda M,
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01-MAY-1998; US-0474721.
13-EBB-1998; US-045287.
01-MAY-1997; US-045287.
01-MAY-1997; US-05030.
13-EBB-1998; US-023890.
(ZYMO) ZYMOGENETICS INC.
Adams RL, Foster DC, Gilbert T.
LOK S, Presnell SR, Whitmore TI
WPI; 99-034662/03.
arew mammalian cytokinin-like redown-regulating Zcytor5 natural in blood
                                                                                                                                                                                              CDNA encoding human Zcytor5.
Zcytor5; Cytokinin-like receptor; down-regulation; growth factor; maintenance factor; thyroid; heart; skeletal muscle; cardiotrophicardiac pathology; heart enlargement; Zcytor5 ligand; ss.
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ligands or detec
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So Sequence 1690 BP; 319 A; 592 C; 505 G; 274 T;
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Best Local Sir
Matches 1132;
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Pred. No. 6.3e-201;
D; Mismatches 168;
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2 13-FEB-1998; US-074721.
2 01-MAY-1997; US-045287.
3 -FEB-1998; US-023890.
3 -FEB-1998; US-023890.
(ZYMO) ZYMOGENETICS INC.
Adams RL, Foster DC, Gilbert T.
Lok S, Presnell SR, Whitmore Ti
in blood
Disclosure; Page 68-70; 55pp; English.
The present sequence encodes an allelic variant of protein design Zcytor5, which is a cytokinin-like receptor. Soluble Zcytor5 may administered to down-regulate the effects of a growth and/or mainfactor in thyroid, heart, and skeletal muscle for example to les effect of cardiotrophin-1 on cardiac pathologies, so preventing enlargement. Zcytor5 could be used to detect cardiotrophin-1 in the country and to discover other possible Zcytor5 ligands. A probe
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17-MAR-1999 (first entry)
cDNA encoding an allelic varaint of human 2cytor5.
2cytor5; cytokinin-11ke receptor; down-regulation; growth factor;
2cytor5; cytokinin-11ke receptor; skeletal muscle; cardiotrophin-1;
maintenance factor; thyroid; heart; skeletal muscle; cardiotrophin-1;
                                                                                                                                                                                                                                                              New mammalian cytokinin-like receptor 2 down-regulating Zcytor5 natural ligands
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Proceeding U4 haematopoietin receptor superfamily procedure and auto:immune disease procedure response, for treating cancer and auto:immune disease procedure 1; Page 28; 38pp; English.

CC This is the nucleotide sequence encoding the human U4 protein from the haematopoietin receptor superfamily, used in the method of the convention for the modulation of cell proliferation, or the immune convention for the U4 protein is used to screen for specific binding agents, raise antibodies. It is also used as reagents for assays and cas tissue markers for isolation of coll grants and receptors, and coll differentiation, and the immune system (e.g. for treating immune coll differentiation, and the immune system (e.g. for treating immune coll differentiation, and the immune system (e.g. for treating immune coll coll differentiation and the immune system (e.g. for treating immune coll coll differentiation).
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15-JAN-1998; U00334.
16-JAN-1997; US-784863.
(GEMY) GENETICS INST INC.
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Query Match Best Local :

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Matches 926;
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                                                                                                                                                                                                                                                                                                                                                                                                                          New isolated haemopoletin receptor - used for for modulating proliferation, differentiation e.g. neuronal cells claim 7; Page 102-104; 182pp; English. The NR6 gene encodes a novel Haemopoletin rece
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (AMRA-) AMRAD OPERATIONS (DZIE/) DZIEGLEWSKA H E. Alexander W, Fabri L, Fa
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Nucleotide sequence of clone HFK-66 encoding human Haemopoletin receptor; cell proliferation; cell dif cell survival; therapeutic; neuronal proliferation;
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11-SEP-1997; G02479.
11-SEP-1996; AU-002246.
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sh A, Nicola NA, Rakar S, Willson
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V27143
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Nucleotide sequence of products generated
Haemopoletin receptor; cell proliferation;
cell survival; therapeutic; neuronal proliferation.
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"Haemopoietin
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19-MAR-1998.
11-SEP-1997; G02479.
11-SEP-1996; AU-002246.
(AMRA-) AMRAD OPERATIONS P
(DZIE/) DZIEGLEWSKA H E.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The nucleotide sequence was generated by a 5N RACE of brain cDNA using NR6 specific primers. NR6 is a novel Haemopoietin receptor (HR). Interaction between the novel HR and a ligand facilitates proliferation, differentiation and survival of a wide variety of cells. The HR and it's derivatives can be used for modulating the activity of the receptors e.g. to regulate development, maintenance or regeneration in an array of different cells and tissues in vitro and in vivo. They can be present in therapeutics used for modulating neuronal proliferation, differentiation and survival. The products can also be used for detection and diagnosis, e.g. for cancers or predisposition to cancers, or for drug screening. Sequence 834 BP; 167 A; 274 C; 225 G; 168 T;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     New isolated haemopoletin receptor - used for for modulating proliferation, differentiation e.g. neuronal cells Claim 7; Page 93-95; 182pp; English.
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P-PSDB; W55014.
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                                                                                     cacactgtgggccctcactcatgccatatccccaaggacctggccctcttcactccctat
                                                                                                                                   aactactccctcaagtacaagctgaggtggtacggtcaggataacacatgtgaggagtac
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                                          TGCCTCTATGTTGGCTTGCCCCCTGAGAAGCCCTTTAACATCAGCTGCTGGTCCCGGAAC
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Matches 493
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Disclosure; Page 101; 182pp; English.
NR6 is a novel haemopoletin receptor (HR). Interaction between the novel had a ligand facilitates proliferation, differentiation and survival of a wide variety of cells. The HR and it's derivatives can be used for modulating the activity of the receptors e.g. to regulate development, maintenance or regeneration in an array of different cells and tissues vitro and in vivo. They can be present in therapeutics used for modulating neuronal proliferation, differentiation and survival. The
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        products can also be used for detection and diagnosis, e.g. or predisposition to cancers, or for drug screening. Sequence 560 BP; 113 A; 182 C; 165 G; 100 T;
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11-SEP-1996; AU-002246.
(AMRA-) AMRAD OPERATIONS PTY LTD.
(DZIEK) DZIEGLEWSKA H E.
Alexander W, Fabri L, Farley A, Hilton
KOjima T, Maeda M, Nash A, Nicola NA, R
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W09811225-A2.
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                                                   CACACCAACTACTCCCTCAAGTACAAGCTTAGGTGGGTATGGCCAGGACAACACATGTGAG
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gagtaccacactgtgggccctcactcatgccatatccccaaggacctggccctcttcact
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Pred. No. 2.4e-85;
0; Mismatches 67
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Rakar S, Willson
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Query Match Best Local S Matches 304

Similarity

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P-PSDB; W55013.

P-PSDB; W55013.

Provided haemopoletin receptor - used for developing products for modulating proiferation, differentiation and survival of cells.

Provided Hambooletin Foreign Formation and Survival of cells.

Claim 6; Page 90-92; 182pp; English.

Chaim 6; Page 90-92; 182pp; Page 90-92; 182pp; English.

Chaim 6; Page
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19-MAR-1998.
11-SEP-1997; G02479.
11-SEP-1996; AU-002246.
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receptor; cell proliferation; cell differentiation; car
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Best Local Similarity
Matches 281; Conser
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29-55P-1998 (first entry)
Nucleotide sequence for murine NR6 containing additional 5N sequence.
Nucleotide sequence for murine NR6 containing additional 5N sequence.
Haemopoietin receptor; cell proliferation; cell differentiation; cancell survival; therapeutic; neuronal proliferation; drug screening; seell survival;
                                                                                                                                                                                                                                            Claim 9; Fig 3; 182pp; English.

The NR6 protein is a novel Haemopoletin receptor (HR). Interaction between the novel HR and a ligand facilitates proliferation, differentiation and survival of a wide variety of cells. The HR and it's derivatives can be used for modulating the activity of the receptors e.g. to regulate development, maintenance or regeneration in an array of different cells and tissues in vitro and in vivo. They can be present in therapeutics used for modulating neuronal proliferation, differentiation and survival. The products can also be used for detection and diagnosis, e.g. for cancers or predisposition to cancers, or for drug screening.

Sequence 11832 BP; 2447 A; 3367 C; 3298 G; 2720 T;
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11-SEP-1996; AU-002246.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Alexander W,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (AMRA-) AMRAD OPERATIONS PTY LTD (DZIE/) DZIEGLEWSKA H E.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   241
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                                                                                                                                                                                                                                                                                                                                                                                                         modulating proliferation, neuronal cells
                                                                                                                                                                                                                                                                                                                                                                                                                                       isolated haemopoletin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CAGG
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                                                                                                                                acacagctgtaatcagcccccaggaccccacccttctcatcggctcctccctgcaagcta 308
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                                                                      cctgctctatacatggagacacacctggggccaccgctgaggggctctactggaccctca
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          cggcgcgagctcaagcagttcctcggctggctcaagaagcacgcatactgctcgaacctt
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ATGGTCGCCGCCTGCCCTCTGAGCTGTCCCGCCTCCTTAACACCTCCACCCTGGCCCTGG
                                                       CCTGCTCTATACATGGAGACACCCTGGGGGCCACCGCTGAGGGGCTCTACTGGACCTTCA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                der W, Fabri L, Fa
T, Maeda M, Nash
                                                                                                                                                                          Conservative
                                                                                                                                                                                      99
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Farley A, Hilton
sh A, Nicola NA, F
                                                                                                                                                                                      receptor - used for ion, differentiation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ВP
                                                                                                                                                                          0
                                                                                                                                                                       Score 280.4; DB Pred. No. 2e-49; D; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Rakar
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DJ, Kikuchi Y,
Rakar S, Willson
                                                                                                                                                                                                                                                                                                                                                                                                                        and survival of cells,
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VALUE OF THE PART 
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11-SEP-1997; G02479.
11-SEP-1997; AU-002246.
11-SEP-1996; AU-002246.
(AMRA-) AMRAD OPERATIONS PTY LTD.,
(AMRA-) BZIEGLEWSKA H E.
(DZIE/) DZIEGLEWSKA H E.
(DZIE/) My Fabri L, Farley A, Hilton DJ, Kikuchi Y,
Nash A, Nicola NA, Rakar S, Willson
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      V27145 stand
V27145;
02-OCT-1998
e.g. for
Sequence
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                                             The NR6 gene encodes a novel Haemopoietin receptor (HR). Interaction between the novel HR and a ligand facilitates proliferation, differentiation and survival of a wide variety of cells. The HR and it's products can be used for modulating the activity of the receptors e.g. to regulate development, maintenance or regeneration in an array of different cells and tissues in vitro and in vivo. They can be present in therapeutics used for modulating neuronal proliferation, differentiation and diagnosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           02-ocr-1998 (first entry)
Nucleotide sequence of Murine NR6.
Haemopoletin receptor; cell prolif
cancer; cell survival; therapeutic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   screening; ss; Mouse
                                                                                                                                                                                                                                                                                                 Claim
                                                                                                                                                                                                                                                                                                                         for modulating proliferation,
e.g. neuronal cells
                                                                                                                                                                                                                                                                                                                                                                                   New isolated haemopoietin
                                                                                                                                                                                                                                                                                                                                                                                                                 P-PSDB; W55016.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WO9811225-A2.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          8; Page 108-114; 182pp;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                standard;
   cancers or predisposition 6663 BP; 1462 A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /product= "
/note= "No
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Location/Qualifiers
1182. .1744
/*tag= a
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                                                                                                                                                                                                                                                                                                                                                  receptor - used for developing products ion, differentiation and survival of cel
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          "Murine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              start
                                                                                                                                                                                                                                                                                              English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        e NR6"
   1852 C; 1715
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        stop
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proliferation; drug
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for drug screening.
G; 1634 T;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 drug;
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Best Local S
Matches 281
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            489
                              ccctggctaaccttaatgggtccaggcagtcaggagacaatctggtgtgtcacgccc
                                                                                                                                                                     acacagctgtaatcagcccccaggaccccacccttctcatcggctccttccctgcaagcta
                                                                                 atggtcgccctccctccaccctggccttccctcacaccctccaccctggccctgg
                                                                                                                             ACACAGCTGTAATCAGCCCCCAGGACCCCACCCTTCTCATCGGCTCCTCCCTGCAAGCTA
gagacggcagcattctggctggctcctgcctctatgttggct
                                                                                                                  CCTGCTCTATACATGGAGACACACCTGGGGGCCACCGCTGAGGGGGCTCTACTGGACCTTCA
                                                                         ATGGTCGCCGCCTGCCCTCTGAGCTGTCCCGCCTCCTTAACACCTCCACCCTGGCCCTGG
                                                                                                                                                                                                              Similarity
                                                                                                                                                                                                    Conservative
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94
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                                                                                                                                                                                                              Score
Pred.
                                                                                                                                                                                                    Mismatches
                                                                                                                                                                                                            280.4; DB 1
No. 1.8e-49;
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                                                                                                                                                                                                                         6663;
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                                                                                                                                                                                                    Gaps
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                                                                         1338
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                                                                                                                                      368
                                                                                                                                                                               308
                                                                                                                   1278
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1399 GAGACGGCAGCATTCTGGCTGGCTCCTGCCTCTATGTTGGCT 1440

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Query Match
Best Local S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Best Local Similarity Matches 209; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            of cardiotrophin-1 on cardiac pathologies, so preventing heart enlargement. Zcytor5 could be used to detect cardiotrophin-1 in the blood, and to discover other possible Zcytor5 ligands. A probe comprising Zcytor5 DNA or RNA can be used to determine the presence and integrity of the Zcytor5 gene on chromosome 19. Antibodies and the anti-idiotypic antibody could be used to purify Zcytor5 and therapeutically to modify Zcytor5 ligand effects.

Sequence 259 BP; 53 A; 64 C; 81 G;
                                                                                                                                                                       1104
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           thyroid, heart, and skeletal muscle for example to lessen the effect of cardiotrophin-1 on cardiac pathologies, so preventing heart
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The present sequence represents an expressed sequence tag (EST) used to identify cDNA encoding a protein designated Zcytor5, which a cytokinin-like receptor. Soluble Zcytor5 may be administered to down-regulate the effects of a growth and/or maintenance factor in
                          1164 cgggcccgggcggcggg 1180
                                                                                                                                                                                                                                                   1044 gcaccgtttacttcgtccaagtgcgttgtaacccattcgggatctatgggtcgaaaaagg 1103
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Example 1; Page 77; 55pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       New mammalian cytokinin-like receptor Zcytor5 - useful for, e.g.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (2YMO) ZYMOGENETICS INC.
Adams RL, Foster DC, Gilbert T, Jelmberg AC, Lehner JM,
LOK S, Presnell SR, Whitmore TE;
WPI; 99-034662/03.
                                                                                                                                                                                                                                                                                                                                                                                                                                            01-MAY-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 V70897 standard; cDNA; 259 BP
V70897;
                                                                                                                                                                                                                   120 GCANCGTGTACTTCGTGCAAGTGCGCTGCAANCCCTTTGGCATCTATGGCTNCAAGAAAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            n blood.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        .3-FEB-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Expressed sequence tag used to identify human 2cytors.cytor5; cytokinin-like receptor; down-regulation; groaintenance factor; thyroid; heart; skeletal muscle; c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 aintenance factor; thyroid; heart; skeletal muscle; cardiotrophin-1; ardiac pathology; heart enlargement; 2cytor5 ligand; EST; ss.
                                                                                                                                                                                                                                                                                                                                            61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          -MAY-1998;
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                                                                                                                                                                                                                                                                                                                                                                   ggaaggtggtggatgacgtcagcaaccagacctcctgccgtctcgcggggcctgaagcccg 1043
                                                                                                                                       GGAAGGTGGTGGANGATGTGAGCAACCAGACCTTCTGCCG-CTGGNCGGCCTGAAACCCG
                                                                                                   CCGGGATCINGAGTGAGTGAGCCANCCCACAGCCGGCTTCANTICCCGCAGTGAGCGNC 239
NGGGCCCGGGNGGNGGG 256
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Conservative
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US-045287.
US-850030.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               10.7%; Score 178.8; DB 1; 81.3%; Pred. No. 9.7e-29; tive 0; Mismatches 47;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 259;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Zcytor5, which is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ۲,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                      179
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Search completed: September 28, 1999, 16:45:17 Job time: 7302 sec

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GenCore version 4.5
Copyright (c) 1993 - 1998 Compugen Ltd.
OM nucleic - nucleic search, using sw model
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ng table: IDENTITY_NUC

176461 segs, 45838279 residues

Issued_Patents_NA:

1: /cgn2_6/ptodata/2/ina/5A_COMB.seq:*
2: /cgn2_6/ptodata/2/ina/5B_COMB.seq:*
3: /cgn2_6/ptodata/2/ina/5C_COMB.seq:*
4: /cgn2_6/ptodata/2/ina/5C_COMB.seq:*
5: /cgn2_6/ptodata/2/ina/DCTUS9_COMB.seq:*
6: /cgn2_6/ptodata/2/ina/backfiles1.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result	Score	Query Match	èn	DB	ID	Description
—	53	3.2	21	2	-08-232-463-	Sequence 14, Appl
c 2	45.4	2.7	8	w	S-08-458-568A-	quence 11, Ap
- ω	Ü	2.7	4257	4	S-08-690-473-1	equence 1, Ap
4	44		66	4	S-08-267-803B	equence 8, App
ı Ut		2.6	40	4	S-08-284-941-1	equence 1, App
1 O			58	4	S-08-738-349	equence 1, App
7	43.4		40	Çī	CT-US93-02147	equenc
. ~		٠	74	Ģ	T-US94-037	equence 3, App
9	ω	٠	17	N	08-242-677-	equence 1, App
10	43		55	w	S-08-467-607-	equence 2, App
1	. 4.	•	55	4	S-08-469-362	equence 2, Ap
12	4	٠	55	4	-08-850-392-	equence 2, App
i ji	N	•	œ	N	S-08-341-568-	e 3, Ap
14	N	•	28	4	S-08-911-020-	equence 3, App
, L		•	62	N	S-08-143-219-	equence 1, Ap
		•	23	U	CT-US94-10080-	equence 5,
 		•	88	Ç	CT-US96-10521-	∍ 14, Ap
, i	42.6	٠	٠,	· U	-US96-10521-1	equence 1
) <u> </u>		٠	3 5	٠.	S-08-728-259A-	equence 10, Ap
2 0	4.		0 5		S-08-056-051-5	equence 5, App
2 2	4.2		80	بر.	07-928-61	equence 12,
) K	4.2		Ē	بر.	-07-928-611-21	Sequence 21, Appl
23	42	-	Ö	4	S-08-487-811A-1	ce 12,
24	42		, –	4	S-08-487-811A-2	equence 21,
25			80	U	S	equence 12,
) N	٠,		, ,	G	CT-US93-07370-2	equence 21,
27		•	30	ω	S-08-614-801A-	equence 5,
C 28	سو ،		27	4	08-520-678A-	equence 30,
29	۲.		290	G	CT-US96-00419-	equence 4, A
30	٠.		00	w	S-08-458-568A	equence 11, Ap
3 H	۲		4	4	08-623-471-8	equence 8, Ap
32	۳	٠	45	_	S-07-923-692C	quence 5, App
i (u	41.2		1400		S-08-085-122-1	equence
. J.	۲.	٠	45	-ر	S-08-184-237-	equence 5, App
. υ	۲		22	2	S-08-296-624-	uence 1, App
36	41.2		45	4	-08-482-920-	equence 5, App
37	41	2.5	88	Н	8-148-2	equenc

STAININE

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; IMMEDIATE SOURCE:
; CLONE: pTZgpt-F1s
US-08-232-463-14
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US-08-232-463-14
                                                                                                                                      INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GENERAL INFORMATION:
                                                                                                                                                                                      REFERENCE/DOCKET NUMBER: 30472/114 IMMU TELECOMMUNICATION INFORMATION: TELEPHONE: (703)836-9300
                                                                                                                                                                                                                                        APPLICATION NUMBER: .EP 91 114 300.6 FILING DATE: .26-AUG-1991 ATTORNEY/AGENT INFORMATION: NAME: BENT, Stephen A REGISTRATION NUMBER: 29,768
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                  SEQUENCE CHARACTERISTICS:
LENGTH: 7218 base pair
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                                                                                                                                                                                                                                                                                                                                                                PRIOR APPLICATION DATA:
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                                                                LENGTH: 7218 base pairs TYPE: nucleic acid STRANDEDNESS: single
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CLASSIFICATION: 435
                                                                                                                                                                      TELEFAX:
                                                                                                                                                                                                                                                                                                                                 FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                              APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                      SOFTWARE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                E OF INVENTION:
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1800 Diagonal Road,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SCHEIFLINGER,
                                                                                                                                                                        (703)683-4109
                                                                                                                                                                                                                                                                                                                                                                                                                                                  PatentIn Release #1.0, Version #1.25
                                                  linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RECOMBINANT FOWLPOX VIRUS
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Length 12001;

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US-08-458-568A-11/c
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·08-458-568A-11
                                                                                                                                                                                                                                                 CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: LEATY Ph.D., Kathry R.
REGISTRATION NUMBER: 36,317
REFERENCE/DOCKET NUMBER: DECI-00
TELECOMMUNICATION INFORMATION:
TELEPHONE: (215) 568-3100
                                                                                                                                                                                              TELEFAX: (215) 568-343
NFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                    MOLECULE TYPE:
HYPOTHETICAL: N
ANTI-SENSE: NO
             ORIGINAL SOURCE:
ORGANISM: Herpes
STRAIN: Herpes
                                                                                                                                                                                                                                                                                                                                                                                CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: U
FILING DATE: 05-MAY-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SOFTWARE: WORDPERFECT 5.:
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDIUM TYPE: Floppy
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                273 accccacccttctcatcggctcctccctgcaagctacctgctctatacatggagacacac 332
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              393 tgtcccgcctccttaacacctcc 415
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COUNTRY: U
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CITY: Philadelphia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TLE OF INVENTION: Composition Infections
                                                                                                                                          STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                            FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER: US/08/458,568A FILING DATE: 02-JUNE-1995
                                                                                                                           OPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ADDRESSEE:
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                                                                                                                                                             nucleic acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Schaffer, Priscilla A
           Herpes simplex virus
erpes Simplex Virus Type 1
                                                                                                                         linear
                                                                                                                                                                                                                                                                                                                                                                                  05-MAY-1993
                                                                                                    DNA (genomic)
                                                                                                                                          double
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     Matches
                                    Query Match
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Best Local :
                                                                                                                                                           TELEFAX: 512/474-7577
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 4257 base pair
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GENERAL INFORMATION:
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          3856 GGGCCCAGCCACACGGCGCGCGCCGCGCGCCGCCCTGGAGG 3814
                                                                                                                                                                                                                                                 TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                     ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          3916 GTGTCGCGCCGGCCCGAGGGCCCCGACCCCTGGGCGGCTGGCCGCCGCCAGCCCCCG
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ZIP: 77210
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Local Similarity
hes 112; Conserv
   Local Similarity
les 112; Conserv
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REFERENCE/DOCKET NUMBER: ARCD:239
                                                                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER: US/08/690,473 FILING DATE: 26-JUL-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TLE OF INVENTION:
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                                                                                                                            STRANDEDNESS:
                                                                                                                                                                                                                                                                                    NAME: Highlander, Steven REGISTRATION NUMBER: 37,6
                                                                                                                                                                                                                                                                                                                                           CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2 gcacgagcttcgctgtccgcgcccagtgacgcgcgtgcggacccgaagccccaatctgcac
                                                                                                                                                                                                                                 ELEPHONE:
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                                                                                                                                         : 4257 base pairs
nucleic acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        P.O. Box 4433
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                                                                                                           linear
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                  2.7%;
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HERPES SIMPLEX VIRUS ICP4 AS
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Score 45.4; DB 4; pred. No. 0.11; 0; Mismatches 111;
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                                  Length 4257;
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Conservative

Mismatches 111;

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                                                                                                                Query Match
Best Local Similarity
Matches 80; Conserv
                                                              10498
                                                                                                                                                                                                                                                                                                                                                    TELEFAX: 612-305-1228 INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             equence 8, Application US/08267803B atent No. 5834183
ENERAL INFORMATION
                          1534 tttggtccacatgatggtcacacttggatataccccagtgtgggtaaggttggggtattg 1593
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ZIP: 55458-1415
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                    SEQUENCE CHARACTERISTICS:
LENGTH: 10660 base pai
                                                                                                                                                                                                                                                                                                                                                                                TELEPHONE: 612-305-1217
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2818 GGCCCAGCCACACGCGGCGGCGCCGGCCGCCCCTGGAGG 2860
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                                                                                                                                                                                                                                                          OLECULE TYPE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      122 ccaatgcccgcgggtcgcccgggccccgtcgccaatccgcgcggcggccgccgcgggccg
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                                                                                                                                                                                                             NAME/KEY:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TLE OF
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OPERATING SYSTEM:
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                                                                                                                                                                                                                                                                                                                                                                                                              REGISTRATION NUMBER: 36,602
REFERENCE/DOCKET NUMBER: 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER: US/08/267,803B FILING DATE: 28-JUN-1994
                                                                                                                                                                                                                                                                            TOPOLOGY:
                                                                                                                                                                                                                                                                                        STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ADDRESSEE:
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                                                          TTTGATTCAAAATTTGAACAAAATTGTTTTAAATAAATTGTCTGTATACCAGTACAAGTT 10557
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WARE:
                                                                                                                                                                                                                                                                                   nucleic acid
DEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       5834183
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Minneapolis
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                USA
                                                                                                                        Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PatentIn Release #1.0,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                IBM PC compatible
SYSTEM: PC-DOS/MS-DOS
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936..3384
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                                                                                                                                     2.6%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gene Sequence for Spinocerebellar Ataxia
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                                                                                                                                   Score 44; DB 4; Length 10660; Pred. No. 0.29;
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                                                                                                                       Mismatches
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                                                                                                                                                                                                                                       Query Match 2.6%;
Best Local Similarity 51.9%;
Matches 98; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                          INFORMATION FOR SEQ ID NO:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SOFTWARE: Patentin Rel
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE CHARACTERISTICS:
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                                                                                                                                                                                                                                                                                                                                                                            MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ATTORNEY/AGENT INFORMATION:
                                                                                  140 ccgggccccgtcgcccaatccgcgcggcggccgccgcggcggctgtcctcgctgtggtcg 199
                                                                                                                                                                             UMBER OF SEQUENCES:
                             200 cctctgttg
                                                                                                                   NAME/KEY:
LOCATION:
                                                                                                                                            80 ccccataccggcgttgcagtcaccgccgttgcgcgccacccccaatgcccgcgggtcgc 139
                                                                                                                                                                                                        20 gcgcccagtgacgcgcgtgcggacccgagccccaatctgcaccccgcagactcgcccccg 79
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NAME: NEELEY PH.D., RICHARD L. REGISTRATION NUMBER: 30092
REFERENCE/DOCKET NUMBER: CHIR-
                                                                                                                                                                                                                                                                                                                                                                                             TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                           STRANDEDNESS:
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CIGCIGCIG
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                                                                                                                                                                                                                                                                                                                                                                                                                         nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     415) 857-0663
380816 COOLEY PA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      E: COOLEY GODWARD CASTRO HUDDLESON & TATUM
FIVE PALO ALTO SQUARE
                                                                                                                                                                                                                                                                                                                                                                                                                                       4403 base pairs
                                                                                                                                                                                                                                                                                                                                  CDS
170..3077
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334
                             208
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                                                                                                                                                                                                                                                                                                                                                                                                           double
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                                                                                                                                                                                                                                                    Score 43.4; DB 4;
Pred. No. 0.31;
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US-08-738-349-1
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Best Local
                                                                                                             Matches
3529
                                                                      1665 aaaaaaaaa 1673
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CURRENT APPLICATION DATA:
                                                     3469 ААССААССТТТСААЛТАЛАЛАЛАЛАСТТСТТТТТАЛЛАЛАЛЛАЛЛАЛЛАЛЛАЛЛАЛЛАЛЛАЛ
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                                                                                                                                                                                                                                                                                                                         SEQUENCE CHARACTERISTICS:
LENGTH: 3581 base pairs
TYPE: nucleic acid
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                                                                                                                                                                                                                                                                                                           TRANDEDNESS:
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AAAAAAAAA 3537
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                                                                                                              53; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Application US/08738349
                                                                                                                                                                                                                                        : Mus musculus osteoblastic cell line MC3T3E1
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                                                                                                              Conservative
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E: BM PC compatible
SYSTEM: PC-DOS/MS-DOS
Patentin Release #1.0, Version #1.25
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Tsujimura, Atsushi
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                                                                                                          Score 43.4; DB 4;
Pred. No. 0.3;
0; Mismatches 16,
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                                                                                                                                      Length 3581;
                                                                                                           Indels
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RESULT

Sequence 3, Application PC/TUS9403705 GENERAL INFORMATION:

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PCT-US94-03705-3
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Matches
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TELEX: 380816 COOLEY PA
INFORMATION FOR SEQ ID NO: 1
SEQUENCE CHARACTERISTICS:
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APPLICATION NUMBER: PC'
FILING DATE: 19930309
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APPLICATION NUMBER: US 07/848,
ETLING DATE: 09-MAR-1992
ATTORNEY/AGENT INFORMATION:
NAME: NEELEY PH.D., RICHARD L
REGISTRATION NUMBER: 30092
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
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                                                                       326 CTGCTGCTG 334
                                                                                                          200 cctctgttg 208
                                                                                                                                              266 GCGGGGGGCGCCGGGCTCCGGGTTCCGGCCGCCGCGCGCGCTCCCTGGCGCTGGCTG 325
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CITY: PALO ALTO
STATE. COLLEY GODWARD CASTRO HUDDLESON & TATUM
                                                                                                                                                                                                                                                    80 ccccataccggcgttgcagtcaccgccgttgcgcgccacccccaatgcccgcgggtcgc 139
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les 98; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SOFTWARE: PatentIn Release #1.0,
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ilarity 51.9%;
Conservative
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Pred. No. 0.31;
0; Mismatches 91;
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Query Match
Best Local Similarity
Matches 68; Conserv
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Patent No. 5677143
                                                                                                                                                                                                                     -08-242-677-1
                                                                             APPLICANT: Gaynor, Rich
APPLICANT: Wu, Foon W.
TITLE OF INVENTION: Cold
TITLE OF INVENTION: and
TITLE OF INVENTION: Tre
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TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 542-5070
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE CHARACTERISTICS:
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CURRENT APPLICATION DATA:
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                                                                                                                                                                                                                                                                               855 GGCTGCGGCTGCTGCTGCTACCGCTGCTGTGGCTACTGGTGCT 903
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ADDRESSEE: Fish & Richardson
STREET: 225 Franklin Street
                                               RRESPONDENCE ADDRESS
                                                                MBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: nucleic acid
STRANDEDNESS: double
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SOFTWARE: WordPer
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                                 ADDRESSEE:
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                                                                                                                                                                    INFORMATION:
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Houston
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               P.O. Box 4433
                                                                                                                                              Gaynor, Richard B
                                                                                                                                                                                                                                                                                                                                                                                                                          Conservative
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IBM PS/2 Model 50Z or 55SX
SYSTEM: MS-DOS (Version 5.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              linear
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                                                                              Cellular Nucleic Acid and Uses Thereof in reTreatment of AIDS
                                                                                                                                                                                                                                                                                                                                                                                                                                      2.6%;
                             White & Durkee
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ER: 05433/007001
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Pred. NO. 0.28;
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US-08-242-677-1
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Best Local Similarity
Matches 51; Conserv
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                                      COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CURRENT APPLICATION DATA:
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                                                                                                                                                                                                                    CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                              ent No.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELECOMMUNICATION INFORMATION:
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MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                  TITLE OF INVENTION:
TITLE OF INVENTION:
UMBER OF SEQUENCES:
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                                                                                                                                                                   ADDRESSEE: ATHENA NEUROSCIENCES
STREET: 800 F. Gateway Blvd.
CITY: South San Francisco
      FILING DATE:
                                                                                                                            COUNTRY: U
                 APPLICATION NUMBER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NAME/KEY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LOCATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                REGISTRATION NUMBER: 33
REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COUNTRY:
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                                                                                                                                                                                                                                                                                                                                                                               INFORMATION:
                                                                                                                                                         CA.
                                                                                                                                                                                                                                                                                                                                                                                                          Application US/08467607
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  5173 base pairs
                                                                                                                                           USA
                                                                                                                                                                                                                                                                               ANDERSON, JOHN
CHRYSLER, SUSANNA
                                                                                                                                                                                                                                                                                                                              MCCONLOGUE,
                                                                                                                                                                                                                                                                                                                TATSUNO, GWEN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PatentIn Release #1.0, Version #1.25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     IBM PC compatible
MBER: US/08/467,607
06-JUN-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ID NO:
                                                                                                                                                                                                                                                                                                                                           SUKANTO
                                                                                                                                                                                                                                               NOVEL CATHEPSIN AND METHODS AND COMPOSITIONS FOR INHIBITION THEREOF
                                                                                                                                                                                                                                                                                                                              LISA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 43.2; DB 2;
Pred. No. 0.36;
0; Mismatches 13;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 5173;
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REGISTRATION NUMBER: 32, REFERENCE/DOCKET NUMBER:

002010-007

CLASSIFICATION:

ORNEY/AGENT INFORMATION:

DUVALL,

JEAN M.

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; NAME/KEY:
; LOCATION:
US-08-467-607-2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    08-469-362-2
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                                                                                                                                                                                      COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TELEPHONE: (415) 877-0900
                                                                                                                           SOFTWARE: Patentin Rel
                                                               ATTORNEY/AGENT INFORMATION:
ELECOMMUNICATION INFORMATION
                                                                                                                                                                                                                                         STREET: 800 r. Garantisco
CITY: South San Francisco
STATE: CA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                          COUNTRY: UZIP: 94080
                                                                  CLASSIFICATION: 514
                                                                                                                                                         OPERATING SYSTEM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           OPOLOGY:
                REGISTRATION NUMBER: 32,73:
                                                                                                            APPLICATION NUMBER:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                      , Application US/08469362 5849711
                                              DUVALL,
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103..1011
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           linear
                                                                                                                                                           E: Floppy disk
IBM PC compatible
SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                    ATHENA NEUROSCIENCES
                                                                                                                                                                                                                                                                                                                        ADDRESS
                                                JEAN M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          877-8370
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2.6%; Score 43; 49.6%; Pred. No.
                                                                                                                                          Release #1.0, Version #1.30
                                                                                                            US/08/469,362
                                                                                                                                                                                                                                                                                                                                                        CATHEPSIN AND METHODS AND SITIONS FOR INHIBITION THEREOF
                  002010-005
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DB 3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 1558;
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US-08-469-362-2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             08-850-392-2
                             NEORMATION FOR SEQ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1373 TCMCCATTCTTATTTCACYTTAGRATCMAGGGTGGGRGGGGGGGGGGGGGGAATTGTCART 1432
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                                                                                                                                                                PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                           COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                               CURRENT APPLICATION DATA:
                                                           TELEPHONE: (415) 877-0900
                                                                                                                                                                                                                                                            OPERATING SYSTEM:
SOFTWARE: PatentT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NAME/KEY:
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                                                                                                                                                                                                                                  APPLICATION NUMBER: US/08/850,392
                                                                                                                                                                                                                                                                                                                                                       COUNTRY:
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                                                                                          REFERENCE/DOCKET NUMBER:
                                                                                                          REGISTRATION NUMBER:
                                                                                                                                      ORNEY/AGENT INFORMATION:
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ENGTH:
                                                                                                                                                                                                   ASSIFICATION:
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                                                                                                                                                                                                                                                                                                                                             94080
                                                                                                                                                                                                                                                                                                                                                                                       South San
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                                                                                                                                                                                                                                                                                                                                                          USA
                                          (415)
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103..1011
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linear
                                                                                                                                                                                                                                                                            IBM PC compatible
SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TUNG, JAY S
                                                                                                                                                                                                                                                                 PatentIn
                                                                                                                                                                                                                                                                                                                                                                                                                         ATHENA NEUROSCIENCES
                                                                                                                                                                                                                                                                                                           Floppy disk
                                                                                                                                                        06-JUN-1995
                                                                                                                         JEAN M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CHRIST
                                                                                                                                                                                                                                                                                                                                                                                          Francisco
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49.6%; Pred. No. 0.29;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPOSITIONS FOR INHIBITION
                                                                                                                                                                                                                                                               Release #1.0, Version #1.30
                                                                                                                                                                   US 08/469,362
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     OPHER M.F
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   13;
                                                                                            002010-005
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 2.6%; Score 43; DB 4; Length 1558; Best Local Similarity 49.6%; Pred. No. 0.29; Matches 67; Conservative 13; Mismatches 55; Indels
                                                                                                                                               NFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                ZIP: 22040-0747
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                          COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
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                                                                                                             SEQUENCE CHARACTERISTICS:
LENGTH: 289 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1539 tccacatgatggtcacacttggatataccccagtgtgggtaaggttggggtattgcaggg 1598
                             ORIGINAL SOURCE:
                                              MOLECULE TYPE:
                                                                                                                                                                                                TELEPHONE: (703) 205-8000
                                                                                                                                                                                                                                                                                   ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Marjatta, FITLE OF INVENTION: FITLE OF INVENTION: FITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STREET: PO Box / ...
                 ORGANISM:
                                                                                                                                                                  TELEFAX: (70)
                                                                                                                                                                                                                                 NAME: Murphy Jr, Gerald M
REGISTRATION NUMBER: 28,9:
REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER: FILING DATE: 22-NO
                                                                               STRANDEDNESS:
                                                                                                                                                                                                                                                                                                    CLASSIFICATION:
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                                                                                                  nucleic acid
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QM9414
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PO Box 747
                                                                                                                                                                               : (703) 205-80
(703) 205-8050
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Siika-aho, Matti
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                                                              linear
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103..1011
             Trichoderma reesei
                                                CDNA
                                                                                                                                                                                                                                                                                                                  22-NOV-1994
                                                                             single
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                                                                                                                                                                                                                                                                                                                                US/08/341,568
                                                                                                                                                                                                                                               28,977
                                                                                                                                                 <u>س</u>
                                                                                                                                                                                                                                  365-262P
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RESULT 14
US-08-911-020-3
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                                                                                                                TELEFAX: (703) 205-805
TELEX: 248345
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ent No.
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                           MOLECULE TYPE: ORIGINAL SOURCE:
                                                                                                                                                                                                                                           FILING DATE: 22-NOV-1994
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                          PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                     CURRENT APPLICATION DATA
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                                                                                                                                                                                        FELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               132 GATTIGATGAAGAATATGACATTGCATGCCTGCTACATACGTAGATTATGATTGGGGGAG 191
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        252 AAAAAAAAAAAAAAAAAAAA 273
                                                                                                                                                                                                                                                                                                                                                                             COMPUTER: IBM PC
OPERATING SYSTEM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STREET: PO Box /4/
CITY: Falls Church
                                                                                                                                                                                                                                                              APPLICATION NUMBER: U
                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER: US/08/911,020 FILING DATE: 13-AUG-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                           COUNTRY: US
ZIP: 22040-0747
               ORGANISM:
                                                                     STRANDEDNESS:
                                                                                                                                                                                                      REGISTRATION NUMBER: 28,977
REFERENCE/DOCKET NUMBER: 365-262P
                                                                                                                                                                                                                    REGISTRATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                     SOFTWARE:
                                                                                                                                                                                                                                                                                                                                                                                                              MEDIUM TYPE:
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                                                                                                                                                                           TELEPHONE:
                                                                                                                                                                                                                                                                                                             CLASSIFICATION:
                                                                                                    ENGTH:
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LE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Similarity 56.3%;
80; Conservative
                                                                                    nucleic acid
                                                                                                                                                                                                                                 Murphy Jr, Geral
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ٧A
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1: Trichoderma reesei
QM9414
                                                                                                 289 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     E: Birch, Stewart, Kolasch and Birch
PO Box 747
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Siika-aho, Matti
Viikari, Liisa
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                                                           linear
                                                                                                                                                                                                                                                                                                                                                                     PatentIn
                                                                                                                                                                                                                                                                                                                                                                                 IBM PC compatible SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                           (703)
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Query Match
Best Local Similarity

2.6%;

Score 42.8; DB 4; Pred. No. 0.21; 0; Mismatches 62;

62;

0

Gaps

0

Length 289; Indels

Matches

Conservative

1532 gctttggtccacatgatggtcacacttggatataccccagtgtgggtaaggttggggtat 1591

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3-143-219-1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
                                                         MOLECULE TYPE: DI
HYPOTHETICAL: NO
DRIGINAL SOURCE:
                                                                                                                                                                                                                                                                                         TILING DATE: September 29, ITTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                              CURRENT APPLICATION DATA
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NAME/KEY:
                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER: FILING DATE: Octobe
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                                                                                                                                                                                                         (213) 955-0440
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                                                                        linear
3: DNA (genomic)
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Katze, Michael G.
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1 West Sixth Street
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                                         HUMAN PKR GENE, FIGURE 5
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US-08-143-219-1

Matches Query Match Best Local Similarity Conservative 84.2%; Score 42.6; DB Pred. No. 0.41; Mismatches Length 2628; 0, Gaps

0

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Search completed: September 28, 1999, 16:39:36
Job time: 6962 sec

GenCore version 4.5 Copyright (c) 1993 - 1998 Com Compugen Ltd

OM nucleic nucleic search, using sw model

91: September 28, 1999, 16:44:42; (without alignments)
1377.741 Million cell updates/sec Search time 303.81 Seconds

Title: Perfect score: Sequence: US-09-037-657-14 1673 1 ggcacgagdttcqct

ggcacgagcttcgctgtccg aaaaaaaaaaaaaaaaa 1673

Scoring table: IDENTITY_NUC

seqs, 125096042 residues

Database N_Geneseq_36:*

score Pred. No. S, No. is the number of results predicted by chance to have a greater than or equal to the score of the result being printed, serived by analysis of the total score distribution.

SUMMARIES

Result

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44433333332284332118 280.4 280.4 178.8 120.2 51.2 Score 1673 Query Match 1934 114955 Length 11629 1724 1930 .1690 .1690 .1813 1579 1391 834 560 938 11832 6663 210 210 210 15827 985 DB T61347 T61348 T61332 T61339 T613 T613 T6133 T613 T613 T613 N90929 V0903 H X5349: Batten disease patten Human 3' fra Clone Batten Batten Batten OR-1 orphan recept Human adenosine Al Batten Batten Batten Batten disease Batten disease Equine arteritis v Polydeoxyribonucle Expressed sequence Equine arteritis v Nucleotide sequenc Nucleotide sequenc Nucleotide sequenc PCR product for hu Nucleotide cDNA encoding an cDNA encoding huma Unspliced murine Expressed Novel Nucleotide sequenc cDNA encoding Novel haemopoietin Description Nucleotide Novel haemopoietin disease disease disease disease disease n disease n disease n disease secreted disease disease secreted haemopoietin sequence sequenc

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Human adenosine HSV L/ST region. . A

ALIGNMENTS

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19-MAR-1998.
11-SEP-1997; G02479.
11-SEP-1996; AU-002246.
(AMRA-) AMRAD OPERATIONS P.
(DZIE/) DZIEGLEWSKA H E.
The haemopoletin receptor (HR) NR6.2 is a form of the novel HR NR6. Interaction between the novel HR and a ligand facilitates proliferation, differentiation and survival of a wide variety of cells. The HR and it's derivatives can be used for modulating the activity of the receptors e.g. to regulate development, maintenance or regeneration in an array of different cells and tissues in vitro and in vivo. They can be present in therapeutics used for modulating neuronal proliferation, differentiation and survival. The products can also be used for detection and diagnosis, e.g. for cancers or predisposition to cancers, or for drug screening. Sequence 1673 BP; 344 A; 550 C; 474 G; 305 T;
                                                                                                                                                                                                                                                                                               New isolated haemopoietin receptor - used for for modulating proliferation, differentiation e.g. neuronal cells Claim 5; Page 84-87; 182pp; English.

The haemopoietin receptor (HR) NRG. 2 is a form the haemopoietin recepto
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WPI; 9
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P-PSDB; W55012.
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Rakar S, Willson
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and survival of cells,
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301 gcaagetacetgetetatacatggagacacacetggggecacegetgaggggetetactg

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REFECENCE
AUTHORS
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AI233311/c
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                    Eutharyota; Metazoa; Chordata; Craniata; Vertebrata; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; 1 (bases 1 to 470)
Lee, N.H., Glodek, A., Chandra, I., Mason, T.M., Quackel
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62; Conservative
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                                                                              464 bp mRNA
UI-R-C2-nb-d-08-0-UI-S1 UI-R-C2 Rattus norvegicus
UI-R-C2-nb-d-08-0-UI 3', mRNA sequence
 Rattus norvegicus
Eukaryota; Metazor
                            Norway rat.
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Tel: (301)-838-3529
Fax: (301)-838-0208
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Unpublished (1998)
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Seq primer: M13-21
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Contact: Lee,
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/db_xref="taxon:10118"
/clone="RxIDD49"
/clone_lib="Normalized rat kidney, Bento Soares"
/note="Organ: kidney; Vector: pT7r3Pac; Site_1:
Site_2: NotI"
site_2: 124 g 115 t
  Metazoa;
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Pred. No. 1.2e-52;
0; Mismatches 41
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Craniata;
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Vertebrata;
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ge38a03.s1 Soares_fetal_lung_NbHL19W Homo
IMAGE:1741228 3', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Tel: (301) 496-1550
Email: Robert Stranger
                                                                                                                                                                                                                                                                                                                                                                                         Seq primer: -40ml3 fwd. ET from Amersham
High quality sequence stop: 431.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    This clone is available royalty-free through LLNL IMAGE Consortium (info@image.llnl.gov) for further
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Unpublished (1997)
On Aug 21, 1998 this sequence version replaced.
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National Cancer Institute, Cancer Genome Anat
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                   69
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Robert_Strausberg@nih.gov
                                                                       double-stranded cDNA was size selected, ligated to Eco RI adapters (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of a modified PT7T3 vector (Pharmacia). Library went through one round of normalization to a Cot = 5. Library constructed by Bento Soares and M.Fatima Bonaldo. This library was constructed
                 from the same fetus as the fetal heart library, fetal heart NDHH19W."
175 c 128 g 74 t 1 others
                                                                                                                                                                                /organism-"Homo sapiens"
/db_xref-"taxon:9606"
/clone-"IMAGE:1741228"
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Best Local Similarity 84.3
Matches 376; Conservative
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qp93e12.x1 Soares fetal_lung_NbHL19W Homo sapiens cDNA clone
qMAGE:1930606 3' similar to TR:Q16354 Q16354 PROLACTIN RECEPTOR
                                                                                                                             Contact: Robert Strausberg, Ph.D. Tel: (301) 496-1550
Email: Robert_Strausberg@nih.gov
                                                                                Tumor Gene Index
Unpublished (1997)
On Jan 14, 1998 this sequence version
                                                                                                                                                                                                                                     NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy
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Eutheria; Primates; Catarrhini
1 (bases 1 to 431)
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                                        High quality sequence stop: 407.
Location/Qualifiers
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/organism="Homo sapiens"
/db_xref="taxon:9606"
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Pred. No. 1.1e-54;
0; Mismatches 71;
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gacattottacataccaactactcoctcaagtacaagct 657
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                                                                                                    CATCCTGGCTGGCTCCTGCCTATGTTGGCCTGCCCCCAGAGAAACCCGTCAACATCAG
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                                                                                                                                                                                                                                           cotgocototgagotgtocogoctcottaacacottocacoctggocottggocotggotaa 438
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                                            CTGCTGGTCCAAGAACATGAAGGACTTGACCTGCCGCTGGACGCCAGGGGGCCCACGGNGA
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NCI-CGAP http://www.ncbi.nlm.nlh.goy/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
Unpublished (1997)
On Jan 19, 1998 this sequence version replaced g1:2151491.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Seq primer: -40UP from Gibco
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            This clone is available royalty-free through LLNL; contact the IMAGE Consortium (info@image.llnl.gov) for further information. Insert Length: 1622 Std Error: 0.00
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Email: Robert_Strausberg@nih.gov
This clone is available royalty-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Contact: Robert Strausberg, Ph.D
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Conservative
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Location/Qualifiers
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/clone="IMAGE:1741879"
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/dev_stage="19 weeks"
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85.6%;
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Pred. No. 1.8e-58;
0; Mismatches 66;
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                                                                G
                                                        GCACGAGGAGTTCCTCGGCTGGCTCAAGAAGCACGCATACTGCTCGAACCTTAGTTTCCG 64
Email: mouseest@watson.wustl.edu
This clone is available royalty-free through LLNL; contact the IMAGE Consortium (info@image.llnl.gov) for further information.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Tel: 314 286 1800
Fax: 314 286 1810
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Contact: Marra M/Mouse EST Project
WashIngton University School of Medicinep
4444 Forest Park Parkway, Box 8501, St. Louis,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Unpublished (1996)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Marra,M., Hillier,L., Allen,M., Bowles,M., Dietrich,N., Dubuque,T., Geisel,S., Kucaba,T., Lacy,M., Le,M., Martin,J., Morris,M., Schellenberg,K., Steptoe,M., Tan,F., Underwood,K., Moore,B., Theising,B., Wylie,T., Lennon,G., Soares,B., Wilson,R. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                W17583 390 bp mRNA mb75b01.rl Soares mouse p3NMF19.5 IMAGE:335209 5', mRNA sequence.
                                                                                                                                      Similarity
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The WashU-HHMI Mouse EST Project
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Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
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Pred. No. 1.8e-56;
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NCI-GGAP http://www.ncbi.nlm.nih.gov/ncicgap.

National Cancer Institute, Cancer Genome Anatomy Pro
                                                                                                                                                                                                                                                                                                                   AI161002 466 bp mRNA ES; qb69g04.x1 Soares_fetal_heart_NbHH19W Homo IMAGE:1705398 3', mRNA sequence.
                                                                                           Contact: Robert Strausberg, Ph.D. Tel: (301) 496-1550
Email: Robert_Strausberg@nih anv
                                                                                                                                                                                                                                                                       EST
                   Unpublished (1997)
On Jan 19, 1998 this sequence version
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g3736418
                                                                                               AI185780 466 bp mRNA ES qe44h04.x1 Soares_fetal_lung_NbHL19W Homo IMAGE:1741879 3', mRNA sequence.
Homo sapiens
Eukaryota; Metazoa;
Eutheria; Primates;
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183 c 123 g 80 t 1 others
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/map="839C02; 821G11; 4;
/clone="IMAGE:1705398"
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Chordata; Craniata; Vertebrata; Catarrhini; Hominidae; Homo.
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Pred. No. 1.8e-58;
D; Mismatches 66
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              Mammalia;
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Best Local Similarity
Matches 403; Conserv
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Email: Robert_Strausberg@nih.gov
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project
Tumor Gene Index
Unpublished (1997)
On Feb 17, 1998 this sequence version replaced g1:2150926
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               High quality sequence stop: 467.
Location/Qualifiers
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1 (bases 1 to 477)
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//lab_host="Dbi0B (ampicillin resistant)"
//lab_host="Dbi0B (ampicillin resistant)"
//lab_host="Dbi0B (ampicillin resistant)"
//lab_host="Display the provided 
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/dev_stage="19 weeks"
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/clone="IMAGE:1742408"
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Pred. No. 3.7e-60;
0; Mismatches 68;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 rel: (301) 496-1550
Email: Robert
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1 (bases 1 to 462)

NCI/NINDS-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute / National Institute of Neurola Disorders and Stroke, Brain Tumor Genome Anatomy Project (CGAP/BTGAP), Tumor Gene Index
                                                                                                                                                                                                                                                                                                                                                                         www-bio.llnl.gov/bbrp/image/image.html
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Email: Robert_Strausberg@nih.gov
Tissue Procurement: David N. Lou
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          tf79d12.xl NCI_CGAP_Brn23 Homo sapiens cDNA clone IMAGE:2105495 3',
                                                                                                                                                                                                                                                                                                                                       Insert Length: 1631
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Unpublished (1998)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Contact: Robert Strausberg, Ph.D.
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DNA Sequencing by: Washington University Genome
Clone distribution: NCI-CGAP clone distribution
cound through the I.M.A.G.E. Consortium/LLNL at:
                                                                                                                                                                                                                                                                                                                                                                                                                                                              cDNA Library Preparation: M. Bento Soares, Ph.D.,
ionaldo, Ph.D.
                                                                                                                                                                                                                                                                                                                       primer: -40UP from Gibco
                                                                                                                                                                                                                                                                                   quality sequence stop: Location/Qualifiers
/clone_lib="NCI_CGAP_Brn23"
/tissue_type="glioblastoma (pooled)"
/lab_host="DH10B"
                                                                                                                                                                                                                    /map-"10; 1"
                                                                                                                                                                                                  /clone="IMAGE:2105495"
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/db_xref="taxon:9606"
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BASE CO
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                                                                                                                                                                                                                                                                           AI421423 474 bp mRNA EST 30-MAR-1999 tf25h01.x1 NCI_CGAP_Brn23 Homo sapiens cDNA clone IMAGE:2097265 3' similar to SW:IL6B_MOUSE Q00560 INTERLEUKIN-6 RECEPTOR BETA CHAIN PRECURSOR; mRNA sequence.
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 474)

NCI/NINDS-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.

National Cancer Institute / National Institute of Neurological Disorders and Stroke, Brain Tumor Genome Anatomy Project (CGAP/BTGAP), Tumor Gene Index

Unpublished (1998)

On Apr 7, 1998 this sequence version replaced g1:3034955.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /lab_host="DH10B (Life Technologies)"
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Pred. No. 1.1e-65;
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                                                              cagctgctggtcccggaacatgaaggatctcacgtgccgctggacaccggggtgcacacgg
                                                                                                             cagcattctggctggctcctgcctctatgttggcttgccccctgagaagccctttaacat
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              | ggagacattcttacataccaactactccctcaagtacaagctgaggtggtacgg
                                                CAGCTGCTGGTCCAAGAACATGAAGGACTTGACCTGCCGCTGGACGCCCAGGGGCCCACGG
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NGAGACCTTCCTCCACACCACCTACTCCCTCAAGTACAAGCTTAGGTGGTATGG
                                                                                                                                                                                                                                                                                                                                                                                                       405;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Tel: (301) 496-1550
Email: Robert_Strausberg@nih.gov
Tissue Procurement: David N. Lou
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Contact: Robert Strausberg,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Insert Length: 1664
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /organism="Homo sapiens"
/db_xref="taxon:9606"
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/lab_host="DH10B"
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                                                                                  436;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Email: mouseest@watson.wustl.edu
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Contact: Marra M/Mouse EST Project
WashU-HHMI Mouse EST Project
Washington University School of MedicineP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia
Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 445)
Marra, M., Hillier, L., Allen, M., Bowles, M., Dietrich, N., Dubl
Geisel, S., Kucaba, T., Lacy, M., Le, M., Martin, J., Morris, M.,
Schellenberg, K., Steptoe, M., Tan, F., Underwood, K., Moore, B.,
Theising, B., Wylie, T., Lennon, G., Soares, B., Wilson, R. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AA039053 445 bp mRNA m199d07.rl Soares mouse embryo NbME13.5 clone iMAGE:474733 5', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Tel:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             4444 Forest Park Parkway, Box 8501,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The WashU-HHMI Mouse EST Project Unpublished (1996)
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Location/Qualifiers
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314 286 1810
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14.5dpc embryos [total RNA provided by Minoru Ko, Wayne
State Univ., from 2 ]; double-stranded cDNA was ligated t
Eco RI adaptors (Pharmacia), digested with Not I and
Cloned into the Not I and Eco RI sites of the modified
pT773 vector. Library went through one round of
normalization, and was constructed by Bento Soares and
M.Fatima Bonaldo.

M.Fatima Bonaldo.

129 c 124 g 107 t
                                                                                                                                                                                                                                                                                                                                                     /tissue_type="embryo"
/dev_stage="13.5-14.5dpc total fetus"
/lab_host="DHIOB"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /organism="Mus musculus"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="IMAGE:474733"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /sex="unknown"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               clone_lib="Soares mouse embryo NbME13.5
                                                                                               25.7%;
98.0%;
                                                                        Score 430.6; DB 27; Pred. No. 4.3e-73; 0; Mismatches 9;
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                                                                                                                          Email: msoares@blue.weeg.uiowa.edu
Oligo-dT track not found, Not I site shown in beginning of sequence
is likely internal to the message. cDNA Library Preparation: M.
Fatima Bonaldo, Ph.D. Clone distribution: clones will be available
                                                                                                                                                                                          Program for Rat Gene Discovery and Mapping University of Iowa 451 Eckstein Medical Research Building Iow Tel: 319 335 8250 Fax: 319 335 9565
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AA866388 428 bp mRNA EST 05-FEB-1999 UI-R-A0-aj-f-04-0-UI-S3 UI-R-A0 Rattus norvegicus cDNA clone UI-R-A0-aj-f-04-0-UI-S3 UI-R-A0-aj-k-04-0-UI-S similar to gb|Ac003112|AC003112 Human from chromosome 19 specific cosmid R30292, genomic sequence,
                                                                                                                                                                                                                                                                  Contact: Soares,
                                                                                                                                                                                                                                                                                          On Mar 16, 1998 this sequence version replaced
                                                                                                                                                                                                                                                                                                              Genome Res. 6 (9), 791-806 (1996)
97044477
                                                                                                                                                                                                                                                                                                                                                                                              Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
                                                                                                                                                                                                                                                                                                                                         discovery
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                                                                                                                                                                                                                                                                                                                                                     Normalization and subtraction:
                                                                                                                                                                                                                                                                                                                                                                                  (bases 1 to 428)
                                                                                                      ough Research Genetics primer: M13 Forward.
/organism="Rattus norvegicus"
/strain="Sprague-Dawley"
/db_xref="taxon.10116"
/map="between D1151765 and UGB"
/clone="UI-R-A0-a1-f-04-0-UI"
                                                                                         Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GI:4230568
                                                                                                                                                                                                                                                                                                                                                                      Lennon, G.
                                                                                                                                                                                                                                                                                                                                                                   and Soares, M.B
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                                                                                         Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 503)
1 (bases 1 to 503)
Marra,M., Hillier,L., Allen,M., Bowles,M., Dietrich,N., Dubuque,T., Geisel,S., Kucaba,T., Lacy,M., Le,M., Martin,J., Morris,M., Schellenberg,K., Steptoe,M., Tan,F., Underwood,K., Moore,B., Theising,B., Wylie,T., Lennon,G., Soares,B., Wilson,R. and
                                                                                                                                                                                                                                                                           AA049278 503 bp mRNA EST mj45c04.rl Soares mouse embryo NbME13.5 14.5 clone IMAGE:479046 5', mRNA sequence. AA049278 g1755309
Contact: Marra M/Mouse EST Project WashU-HHMI Mouse EST Project
                                            The WashU-HHMI Mouse EST Project
Unpublished (1996)
On Dec 30, 1996 this sequence ve
                                                                                                                                                                                                                                                                AA049278.1
                                                                                                                                                                                                                                    house mouse.
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                                                                                                                                                                                                                                                                GI:1755309
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     This clone is available royalty-free through LLNL; contact the IMAGE Consortium (info@image.llnl.gov) for further information.
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Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        mouseest@watson.wustl.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /note="Vector:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /db_xref="taxon:10090"
/clone="IMAGE:479046"
/clone_lib="Soares mouse
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /organism="Mus musculus"
/strain="C57BL/6J"
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/dev_stage="13.5-14.5dpc
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      'lab_host-"DH10B"
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Pred. No. 1.1e
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                                             gctgctggtcccggaacatgaaggatctcacgtgccgctggacaccgggtgcacacgggg
agacattcttacataccaactactccctcaagtacaagctgaggtggtacggtcaggata 677
                                                                                                                                                                  GCTGCTGGTCCCGGAACATGAAGGATCTCACGTGCCGCTGGACACCGGGTGCACACGGGG
                                                                                                       AGACATTCTTACATACCAACTACTCCCTCAAGTACAAGCTGAGGTGGTACGGTCAGGATA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WashU-HHMI Mouse EST Project
Washington University School of MedicineP
4444 Forest Park Parkway, Box 8501, St. La
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The WashU-HHMI Mouse EST Project Unpublished (1996)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 (bases 1 to 464)
Marra, M., Hillier, L., Allen, M., Bowles, M., Dietrich, N., Dubuque, T.,
Geissel, S., Kucaba, T., Lacy, M., Le, M., Martin, J., Morris, M.,
Schellenberg, K., Steptoe, M., Tan, F., Underwood, K., Moore, B.,
Theising, B., Wylie, T., Lennon, G., Soares, B., Wilson, R. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  This clone is available royalty-free through LLNL; contact the IMAGE Consortium (info@image.llnl.gov) for further information
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Tel: 314 286 1800
Fax: 314 286 1810
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Email: mouseest@watson.wustl.edu
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         nouse mouse
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                                                                                                                                                                                                                                   Conservative
                                                                                                                                                                                                                                                                                                              30, 1996 this sequence version
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Marra M/Mouse EST Project
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /organism="Mus musculus"
/strain="C57BL/6J"
/db_xref="taxon:10090"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /tissue_type="embryo"
/dev_stage="13.5-14.5dpc total fetus"
/lab_host="DH10B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /sex≖"unknown"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /clone-"IMAGE:479043"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /clone_lib="Soares mouse embryo NbME13.5 14.5"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           location/Qualifiers
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                                                                                                                                                                                                                              Score 464; DB 29;
Pred. No. 1.9e-79;
0; Mismatches 0;
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                                                                                                                                                                                                                                                     Length 464;
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REFERENCE
AUTHORS
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W66776/c
LOCUS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CTCTCAAGGATTTCCTCTTCCAAGCCAAGTACCAGATCCGCTACCGCGTGGAGGACAGCG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    acgtgagccgcgttgggggcctggaggaccagctgagtgtgcgctggggtctcaccaccag
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ACGTGAGCCGCGTTGGGGGCCTGGAGGACCAGCTGAGTGTGCGCTGGGGTCTCACCACCAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CTGATGTCCTCACACTGGATGTCCTGGACGTGGTGACCACGGACCCCCCCACCCGACGTGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         W66776 482 bp mRNA EST 14-JUN-1 mel7b11.rl Soares mouse embryo NbMEl3.5 14.5 Mus musculus clone IMAGE:887741 5' similar to PIR:B38252 B38252 granulo colony-stimulating factor receptor precursor ;, mRNA seque
                                                                                                                                                                                                                                                                                                                                                                                                                      WashIngton University School of MedicineP
4444 Forest Park Parkway, Box 8501, St. L/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   g1375694
W66776.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      W66776
                                                                                                                                                                                                                                                                                                                                     This clone is available royalty-free through LLNL; contact the LMAGE Consortium (info@image.llnl.gov) for further information.
                                                                                                                                                                                                                                                                                                                                                                                            Tel: 314 286 1800
Fax: 314 286 1810
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          On Apr 14, 1993 this sequence version
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The WashU-HHMI Mouse EST Project Unpublished (1996)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Marra,M., Hiller,L., Allen,M., Bowles,M., Dietrich,N., Dubuque, Geisel,S., Kucaba,T., Lacy,M., Le,M., Martin,J., Morris,M., Schellenberg,K., Steptoe,M., Tan,F., Underwood,K., Moore,B., Theising,B., Wylie,T., Lennon,G., Soares,B., Wilson,R. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mus musculus
                                                                                                                                                                                                                                                                                                     Possible reversed clone: similarity on wrong strand
                                                                                                                                                                                                                                                                                                                                                                         Email: mouseest@watson.wustl.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Contact: Marra M/Mouse EST Project
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Waterston, R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota; Metazoa;
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                                                                                                                                                                                                                                                                        quality sequence stop: 359
/db_xref="taxon:10090"
/map="10 pter-cen"
/clone="IMAGE:387741"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GI:1375694
                                                                                                                                                                                                           /organism="Mus musculus"
/strain="C57BL/6J"
                                                                                                                           /sex="unknown"
                                                                                                                                    clone_lib="Soares mouse embryo NbME13.5"
                                                                                                                                                                                                                                                          ocation/Qualifiers
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GenCore version 4.5 Copyright (c) 1993 - 1998 Compugen Ltd.
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Run OM nucleic - nucleic search, using sw model 음 ::

September 28, 1999, 15:38:03; 3; Search time 2095.87 Seconds (without alignments) 1574.548 Million cell updates/sec

US-09-037-657-14 1673

Title: Perfect score: Sequence:

IDENTITY_NUC

Searched: Scoring table:

Database : 2546578 seqs, 986266752 residues

em_est1:*

em_est3

em_est22:*
em_est23:*
em_est24:*
em_est25:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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.849564 EST1923	2205 mc69e09.r	57868 qv13b02.	417616 tg80c02.	264328 q109c05.	14965 mh23e02.	374006 SWOVAFCA	121532 zk89c11.	27378 om27a08.	27694 zk89c11.	22128 om45e12	35068 UI-R-C3-	873 zb17h05.s	009 EST00035	77893 EST9055	25924 UI-R-A1-	74921 c	11309 AV01130	10798 AV01079	407 vm88d09.s	604 zc32h10.s1	43001 zk56f01	75060 UI-R-GO-	70365 va63h12	32198 AV032198	42914 zk56f01	70108 we65f03.	74687 UI-R-GO-	79568 ŪI-R-GO-	69388 qi26	71408 HT-R-C2-	AT233311 EST229999	33913 ge30a03.	583 mb/5b01.rl	85780 ge44h04.	51002 gb69g04.	94468 tf79d12	85924 qe50c05.	21423 tf25h01.	56388 UI-R-AO-	39053 m199d0	19278 mj45c04	76 me17b11.	049280 mj45d02	Description

ALIGNMENTS

RESULT 1
AA049280
LOCUS
DEFINITION

ACCESSION NID my49280 464 bp mRNA EST 30-DEC-1996 my45602.rl Soares mouse embryo NbMEl3.5 14.5 Mus musculus cDNA clone IMAGE:479043 5' similar to SW:IL6B_MOUSE Q00560 INTERLEUKIN-6 RECEPTOR BETA CHAIN PRECURSOR ;, mRNA sequence.
AA049280 g1755311

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REFERENCE
AUTHORS
TITLE
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ORIGIN
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MEDLINE
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Best Local Similarity
                                                                                                                                                                                                                                                                        Matches 403;
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                                                                                  463
                                                                                                                                                                              Eutheria;
1 (bases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Contact: Soares, MB
Program for Rat Gene Discovery and Mapping
University of Iowa
451:EDCkstein Medical Research Building Iowa City, IA 52242, USA
Tel? 319 335 8250
Fax: 319 335 9565
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Genome Res. 6 (9), 791-806 (1996)
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                                                                                                                                                                                                                                                                                                                                                                                                                    86
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CCGAAACCAGGACGAGGGGATCCTGCCCTCGGGCAGACGGGGTGCGGCGAGA 284
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Rodentia; Sciurognathi; Muridae; Murinae; Rattus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        into DH10B bacteria (Life Technologies) to generate the UI-R-C2 library. This procedure has been received.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ocation/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                used as a driver in a hybridization with the UI-R-Cl
library in the form of single-stranded circles. The
remaining single-stranded circles (subtracted library) was
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    purified by hydroxyapatite column chromatography, converted to double-stranded circles and electroporated
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  organism="Rattus norvegicus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ixture of individually tagged normalized libraries onstructed from rat placenta, adult lung, brain, liver, of index, heart, spleen, ovary, muscle, 8, 12 and 18-day mbryo. The tag is a string of 3-5 nucleotides present etween the Not I site and the oligo-dT track which allows dentification of the library of origin of a clone within he mixture. The subtracted library (UTR-C2) was onstructed as follows; PCR amplified cDNA inserts from I-R-C1 clones from which 3, ESTs had been derived was
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              to 464)
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                                                                                                                                                                                                                                                                          Score 318.8; DB 41; Length 464;
Pred. No. 9.1e-52;
0; Mismatches 42; Indels 19;
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	1610 tetetttaaataaataaaggagttgtteaggtaaaaaaaa	Qγ
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105	163 GCTGGGGCACAATGAGCTCCCACAACCACAGCTTTGG-CCACATGATGGTCAACTTTGGA 105	당
1561	1502 gctggggcacaatgagctcccacaaccacagctttggtccacatgatggtcacacttgga 1561	Qy
164	223 TCACCTGAACTGGAGACCATCTGTACTGTCACTTTGGGGCAATGAAGAAACAAAC	₽
1501	1447 tcacctgaattggagcccctctgtaccatctgggcaacaaagaaacctaccagag 1501	Qy
224	283 GGTCCTGCCGGCTAAACTCTGAGGATAGGCCATCCTCCTGCTGGATGCAGACCTGGAGGC 224	В
1446	1388 ggtcctgccggttaaactctaaggataggccatcctccttgctgggt-cagacctggaggc 1446	¥Q.

Search completed: September 28, 1999, 15:38:09 Job time: 3277 sec

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Result
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/cgn2_6/ptodata/2/ina/5E_COMB.seq:*
/cgn2_6/ptodata/2/ina/5D_COMB.seq:*
/cgn2_6/ptodata/2/ina/Dackfiles1.seq:*
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Query Match Best Local S Matches 8

Match 3.2%;
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	SOURCE:	•
	TOPOLOGY: linear	٠
	LENGTH: 7218 base pairs	٠
	TELEFAX: (703)683-4109	
	HABTEL	
	: REFERENCE/DOCKET NUMBER: 30472/114 IMMU : TELECOMMUNICATION INFORMATION:	
	ION NUMBER: 29,7	٠
	AGENT INFORMAT	
	; APPLICATION NUMBER: EP 91 114 300.6 ; FILING DATE: 26-AUG-1991	·· ··
	FILING DATE:	
	TION DATA:	
	CLASSIFICATION: 435	
	APPLICATION NUMBER: US/08/232,463	٠
٠	CATION DATA:	٠.
	SOFTWARE: Patentin Release #	••.
	COMPUTER: IBM PC COMPUTIBLE	
	PE: Flop	· ·
	COMPUTER READABLE FORM:	٠
	COUNTRY: USA	
	STATE: VA	٠.
	CITY: Alexandria	٠
	3: Foley & Lardner	
	PONDENCE ADDRESS	••
	; HITLE OF INVENTION: RECOMBINANT FOWLPOX VIRUS ; NUMBER OF SEQUENCES: 52	·. ·.
	CANT: FALKNER, F. G.	٠.
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	ALIGNMENTS	
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                                                                                                                                                                                 TELEFAX: (215) 568-343 INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            equence 11, Application US/08458568A
                                                                                                                                                                                                                                                                                                                                                                                PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                  SOFTWARE: WordPerfect
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US
FILING DATE: 02-JUNE-1
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                                                                              MOLECULE TYPE: DI
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDIUM TYPE: Floppy disk
COMPUTER: IEM PC compatible
OPERATING SYSTEM: PC DOS/MS DOS
                                                                                                                                                                                                                                                                                NAME: Leary Ph.D., Kathryn R. REGISTRATION NUMBER: 36,317
                                                                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER: US 0 FILING DATE: 05-MAY-1993
                                                                                                                                                                                                                                                                                                                                                                                                        CLASSIFICATION:
                                                                                                                                STRANDEDNESS:
                                                                                                                                                                                                                                                                    REFERENCE/DOCKET NUMBER:
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pedness: double
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erpes Simplex Virus Type
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NO: 11:
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Place, 46th
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Best Local :
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  2638
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                                                                                                                                                                                               SEQUENCE CHARACTERISTICS:
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                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER: US/08/690,473 FILING DATE: 26-JUL-1996 CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER: IBM PC
OPERATING SYSTEM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TLE OF INVENTION:
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                                                                                                                                                       STRANDEDNESS:
                                                                                                                                                                                                                                                                              NAME: Highlander, Steven REGISTRATION NUMBER: 37,6
                                                                                                                                                                                                                                                                                                                                                                                                                                                              COUNTRY: USA
                 2 gcacgagcttcgctgtccgcgcccagtgacgcgcgtgcggacccgagccccaatctgcac 61
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SYSTEM: PC-DOS/MS-DOS
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HERPES SIMPLEX VIRUS ICP4
INHIBITOR OF APOPTOSIS
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                                                                  Score 45.4; DB Pred. No. 0.11;
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JS-08-267-803B-8
                                                                                                                         Query Match
Best Local Similarity
Matches 80; Conserv
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                                                                10498
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1534 tttggtccacatgatggtcacacttggatataccccagtgtggggtaaggttgggggtattg 1593
                                                                                                                                                                                                                                                                                                                                SEQUENCE CHARACTERISTICS:
LENGTH: 10660 base pai
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2818 GGGCCCAGCCACACGCGGCGGCGGCGGGCGGCCGCCTGGAGG 2860
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                                                                                                                                                                                                                                                                                                                                                                                            TELEPHONE: 612-305-1217
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SOFTWARE: Patentin Release #1.0, Version CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ATTORNEY/AGENT INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COUNTRY:
                                                                                                                                                                                                                                       NAME/KEY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER: US/0 FILING DATE: 28-JUN-1994 CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            62
                                                                                                                                                                                                                                                                                                                                                                                                             REFERENCE/DOCKET NUMBER: 110
                                                                                                                                                                                                                                                                                OPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DDRESSEE
                                                                                                                                                                                                                                                                   ECULE TYPE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TTTGATTCAAAATTTGAACAAAATTGTTTTAAATAAATTGTCTGTATACCAGTACAAGTT 10557
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                                                                                                                                                                                                                                                                                                NDEDNESS:
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                                                                                                                                                                                                                                                                                                             : 10660 base pairs nucleic acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    USA
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936..3384
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                                                                                                                                         2.6%;
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                                                                                                                       Score 44; DB 4; Length 10660;
Pred. No. 0.29;
0; Mismatches 60; Indels
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US-08-284-941-1
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Best Local s
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                                                                                                                                                                                                                                                                                                                                                          FEATURE
                                                                                                                                                                                                                                                                                                                                                                      MOLECULE TYPE: DNA (genomic)
                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE CHARACTERISTICS:
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MEDIUM TYPE: Floppy disk
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                                                          266
                                                                              140 ccgggccccgtcgcccaatccgcgcggcggccgccgcggcggctgtcctcgctgtggtcg 199
                                                                                                                                                                          200 cctctgttg 208
                                                                                                                ELECOMMUNICATION INFORMATION:
                                                                                                                                       80 ccccataccggcgttgcagtcaccgccgttgcgcgccacccccaatgcccgcgggtcgc 139
                                                                                                                                                                                                                                   Y Match 2.6%;
Local Similarity 51.9%;
hes 98; Conservative
                                                                                                                                                                                                20 gcgcccagtgacgcgcgtgcggacccgagccccaatctgcaccccgcagactcgccccg 79
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0,
                                                                                                                                                                                                                                                                                                                                                                                       TOPOLOGY:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME: NEELEY PH.D., RICHARD L. REGISTRATION NUMBER: 30092
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TLASSIFICATION: 435
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICATION NUMBER: FILING DATE: 2 Aug
CIGCIGCIG 334
                                                       GCGGGGGGCCCGGCCCGGCTTCCGGCCCCCCCGCGTCCCTGGCGCTGGCTG
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                                                                                                                                                                                                                                                                                                                                                                                                           nucleic acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           E: COOLEY GODWARD CASTRO HUDDLESON & TATUM FIVE PALO ALTO SQUARE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 USA
                                                                                                                                                                                                                                                                                                                         CDS
170..3077
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                                                                                                                                                                                                                                  Score 43.4; DB 4; Length 4403; Pred. No. 0.31; 0; Mismatches 91; Indels 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CHIR-009/01US
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US-08-738-349-1
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                          NFORMATION FOR SEQ ID NO:
                          1665 aaaaaaaaa 1673
                                                        SEQUENCE CHARACTERISTICS:
LENGTH: 3581 base pairs
TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0.
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CLASSIFICATION: 435
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                          DRIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FILING DATE: 26-AUG-1993
ATTORNEY/AGENT INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                  ELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                 NAME/KEY:
                                                                                                                                                                                                                                                                                                                                                                                                                                 REGISTRATION NUMBER: 32, REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FILING DATE:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FILING DATE:
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                                                                                                                                                                                                                                                           ORGANISM:
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                                                                                                                                                                                                                                                                                                                RANDEDNESS: single
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AAAAAAAAA 3537
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                                                                                                                                                                                                                                                                                                                                                                                           202-408-4400
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Kawai, Shinj
                                                                                                               Conservative
                                                                                                                                                                                                                                                         Mus musculus
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                                                                                                                                                                                                                                                                                                      Linear
                                                                                                                                                                                                                                                                                                                                                                                                      202-408-4000
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                                                                                                                                                                                                                                                                                     CDNA to mRNA
                                                                                                                           76.8%;
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                                                                                                            Score 43.4; D: Pred. No. 0.3; 0; Mismatches
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                                                                                                                                       Length 3581;
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RESULT

PCT-US94-03705-3

Sequence 3, Application PC/TUS9403705 GENERAL INFORMATION:

RESULT

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LOCATION:
PCT-US93-02147A-1
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                                                                                                                                                                                                                                                                               Query Match
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                                                                                                                                                                                                                                                                                                                                                                           FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                          MOLECULE TYPE:
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326 CIGCIGCIG
                         200 cctctgttg 208
                                                          266 GCGGGGGGCCGGGCCCGGGTTCCGGCCGCTCGCGCGTCCCTGGCGCTGGCTG
                                                                                                                      80 ccccataccggcgttgcagtcaccgccgttgcgcgccacccccaatgcccgcgggtcgc 139
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                                                                                                                                                                                                                                                                Local
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NAME: NEELEY PH.D., RICHARD L
REGISTRATION NUMBER: 30092
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LECOMMUNICATION INFORMATION: TELEPHONE: (415) 494-7622
                                                                                                                                                                                                                                                                                                                                                                                                            OPOLOGY:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PPLICATION NUMBER: US 0
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1 Similarity 51.9%;
98; Conserva+'...
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CALIFORNIA
                                                                                                                                                                                                                                                                                                                                                                                                                                      nucleic acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                        4403 base pairs
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170..3077
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334
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                                                                                                                                                                                                                                                             Score 43.4; DB Pred. No. 0.31;
                                                                                                                                                                                                                                                Mismatches
                                                                                                                                                                                                                                                                             DB 5;
                                                                                                                                                                                                                                                                               Length 4403;
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                                                          325
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US-08-242-677-1
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Best Local Similarity
Matches 68; Conserv
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ZIP: 02110-2804

COMPUTER READABLE FORM:

MEDIUM TYPE: 3.5" Diskette, 1.44 MARINETER: IBM PS/2 Model 502 or 555X

""""FMEM: MS-DOS (Version 5.0)

""" (Version 5.1)
                                                                                                                                                                                         equence 1, Applic
atent No. 5677143
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                            CORRESPONDENCE ADDRESS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson
                                                                                                                                          APPLICANT:
                                                                                                                                                                                                                                                                                                             162 cgcggcggccgcggcgctgtcctcgctgtggtcgcctctgttgct 210
                                                                                                                                                                                                                                                                                                                                            795 CAGCCCTGTTCGCGCTCTCGGCAGTGCCGGGGGGGGGCGCCTCCCCCCATGCCGCCCTCCG 854
                                                                                                                                                                                                                                                                                                                                                                        102 ccqcccqttqcqcqccacccccaatqcccqcqqqqtcqccqggqccccqtcqccaatccq 161
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ELECOMMUNICATION INFORMATION: TELEPHONE: (617) 542-5070
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TTORNEY/AGENT INFORMATION:
                                                                                            ITLE OF INVENTION:
ITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     REGISTRATION NUMBER: Reg
                                               \DDRESSEE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICATION NUMBER: 5 Apr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ELEFAX:
                                                                                                                                                                                                                                                                               GGCTGCGGCTGCCGCTGCTGCTACCGCTGCTGGCTACTGGTGCT 903
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Houston
TX
                                                                                                                                                                                                       Application US/08242677
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                             P.O. Box 4433
                                                                                                                                           Wu, Foon W
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                                                                                                                                                                                                                                                                                                                                                                                                                 Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (617) 542-8906
                                                                                                                                                       Gaynor, Richard B
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                                              Arnold
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5 April 1994
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                                                                                     Cellular Nucleic Acid Binding Protein and Uses Thereof in regulating Gene E. Treatment of AIDS
                                            White & Durkee
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Pred. No. 0.28;
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INFORMATION FOR SEQ ID NO: 1:
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                             CURRENT APPLICATION DATA:
                                                                                          COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      5133 AAAA 5136
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NAME: Mayfield, Denise L
REGISTRATION NUMBER: 33,
                                                                                                                                                                                                                                                                                                                                                                  APPLICANT:
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                                                                                                                                                                                                                                                                                                                                   PPLICANT:
                                                                                                                                                                                       STREET:
                                                                                                                                                                                                                                                 PHICANT: ANDERSON, JOHN
PPHICANT: CHRYSLER, SUSANNA
TITLE OF INVENTION: NOVEL CATHEPSIN AND METHODS AND
TITLE OF INVENTION: COMPOSITIONS FOR INHIBITION THEREOF
                                            MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Local Similarity
APPLICATION NUMBER: US/0
FILING DATE: 06-JUN-1995
                                                                                                                                           COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME/KEY:
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CLASSIFICATION: 435
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South San Francisco
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MCCONLOGUE, LISA
                                                                                                                                                                                                                                                                                                                  TATSUNO, GWEN
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             US/08/467,607
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                                             Version #1.30
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CLASSIFICATION:

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; LOCATION:
US-08-467-607-2
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Best Local Similarity
Matches 67; Conser
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                                                                                                                                             SOFTWARE: PatentIn Release #1.0, Version #1.30
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                                                                                                                                                                                                                MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELEPHONE: (415) 877-0900
REGISTRATION NUMBER: 32,731
REFERENCE/DOCKET NUMBER: 00
ELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 877-0900
                                                             NAME: DUVALL, JEAN M.
                                                                                                                                                                                                                                                                                                                                                 ORRESPONDENCE ADDRESS
                                                                                                                                                                               MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                 APPLICATION NUMBER: US/08/469,362 FILING DATE: 06-JUN-1995 CLASSIFICATION: 514
                                                                                                                                                                                                                                                ZIP: 94080
                                                                                                                                                                                                                                                                 COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                REGISTRATION NUMBER: 32,731 REFERENCE/DOCKET NUMBER: 00
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                                                                                                                                                                                                                                                                                 South San Francisco
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49.6%; Pred. No.
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US-08-469-362-2
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Best Local
TELEFAX: (415) 877-837
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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                                                               REFERENCE/DOCKET NUMBER: 00
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                      PRIOR APPLICATION DATA: APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                        COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
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                                                                                                                                                                                                                                                         SOFTWARE: PatentIn Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                CORRESPONDENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LENGTH: 1558 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                         APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                        OPERATING SYSTEM:
                                                                                                    REGISTRATION NUMBER:
                                                                                                                                  FILING DATE: 06-JUN-1995
TORNEY/AGENT INFORMATION:
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                                                   ELEPHONE:
                                                                                                                                                                                                           LASSIFICATION:
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l Similarity 49.6%;
67; Conservative 1
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                                                                                                                                                                                                                                                                                                                                                                           USA
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                                                                                                                                                                                                                                                                                       E: Floppy disk
IBM PC compatible
SYSTEM: PC-DOS/MS-DOS
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                                                 (415)
                                                                                                                  JEAN M.
                                 877-8370
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Pred. No. 0.29;
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12ymes, genes coding for them, isolating the genes, and methods for bleaching
                                                                                                          1532 gotttggtocacatgatggtcacacttggatataccccagtgtgggtaaggttggggtat 1591
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                                 Score 42.8; DB 2; Length 289;
Pred. No. 0.21;
0; Mismatches 62; Indels
                                                                        Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CORRESPONDENCE ADDRESS:
ADDRESSEE: Birch, Stewart, Kolasch and Birch
STREET: PO Box 747
CITY: Falls Church
STATE: VA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 0S 08/341,568
FILING DATE: 22-NOV-1994
ATTORNEY/AGENT INFORMATION:
NAME: MUMBIN MUMBER: 28,977
REFERENCE/DOCKET NUMBER: 365-262P
                                                                                                                                                                                                                                                                      1652 аааааааааааааааааааа 1673
                                                                                                                                                                                                                                                                                                                                                                                                                 Application US/08911020
                                                                                                                                                                                                                                                                                                              252 AAAAAAAAAAAAAAAAAA 273
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ORGANISM: Trichoderma reese
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ELECOMMUNICATION INFORMATION
                                 Query Match 2.6%;
Best Local Similarity 56.3%;
Matches 80; Conservative
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Saloheimo, Anu
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(703) 205-8050
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STATE: VA
COUNTY: US
21P: 22040-0747
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy di
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS
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STRANDEDNESS: single
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TITLE OF INVENTION: M
TITLE OF INVENTION: M
TITLE OF INVENTION: INVINIBER OF SEQUENCES:
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                                                                                                 2.6%; Score 43; DB 4; Length 1558;
49.6%; Pred. No. 0.29;
tive 13; Mismatches 55; Indels
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
SURREMT APPLICATION DATA:
APPLICATION NUMBER: US/08/341,568
FILING DATE: 22-NOV-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEE: Birch, Stewart, Kolasch and Birch
: PO Box 747
Falls Church
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 3, Application US/08341568 Patent No. 5661021
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ATTORNEY/AGENT INFORMATION:
NAME: Murphy Jr, Gerald M
REGISTRATION NUMBER: 28,977
REFERENCE/DOCKET NUMBER: 365-
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 205-8000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               : Trichoderma reesei
QM9414
                                                                                             Query Match
Best Local Similarity 49.68
Matches 67; Conservative
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ITLE OF INVENTION: methor
ITLE OF INVENTION: pulps
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FORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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TYPE: nucleic acid
STRANDEDNESS: single
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
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ADDRESSEE: Birch, St
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ORIGINAL SOURCE:
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; NAME/KEY:
; LOCATION:
US-08-850-392-2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             JS-08-341-568-3
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                                                                                                                                                               132 GATTTGATGAAGAATATGACATTGCATGCCTGCTACATACGTAGATTATGATTGGGGGAG 191
                                                                                                                                                                                                        Query Match 2.6%; Score 42.8; DB 4; Length 289; Best Local Similarity 56.3%; Pred. No. 0.21; Matches 80; Conservative 0; Mismatches 62; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Barber, Glen N.
TITLE OF INVENTION: TUMOR-CELL ASSAY METHOD AND KIT NUMBER OF SEQUENCES: 27
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ORIGINAL SOURCE:
INDIVIDUAL ISOLATE: HUMAN PKR GENE, FIGURE 5
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MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
COMPUTER: IBM compatible
OPERATING SYSTEM: PC-DOS (Version. 5.0)
SOFTWARE: WordPerfect (Version. 5.1)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    UMBER: US/08/143,219
October 25, 1993
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APPLICATION NUMBER: 07/953,681
FILING DATE: September 29, 1997
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Roy, Sophie
Koromilas, Antonis E.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ADDRESSEE: Lyon & Lyon
STREET: 611 West Sixth Street
CITY: Los Angeles
STATE: CA
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Patent No. 5670330
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MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: NO
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nucleic acid
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FILING DATE: October 22
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                                                  Score 42.6; DB 2; Length 2628; Pred. No. 0.41; 0; Mismatches 9; Indels 0
                         Indels
Query Match
Best Local Similarity 84.2%;
Matches 48; Conservative
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Search completed: September 28, 1999, 16:39:36 Job time: 6962 sec

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GenCore version 4.5
Copyright (c) 1993 - 1998 Compugen Ltd
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- nucleic search, using sw model nucleic

September 28, 1999, 16:44:42 Run on:

2; Search time 303.81 Seconds (without alignments)
1377.741 Million cell updates/sec

US-09-037-657-14 Title: Perfect score: Sequence:

IDENTITY_NUC Scoring table: 311585 seqs, 125096042 residues

Searched:

N_Geneseq_36:*

Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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	Description	Noted because of	otide sequen	haemo		~	cDNA encoding huma	ဌ	Nucleotide sequenc		Nucleotide sequenc	PCR product for hu	Novel haemopoietin	Nucleotide sequenc	O)	ß		Equine arteritis v	Equine arteritis v	deoxyr1bon	OR-1 orphan recept	adenos	secreted	disease	disease	disea	disease	disease	atten disease	disease	disease	disease	disease	disease	atten disease	atten disease	Batten disease gen	atten disease	atten disease	tten disease q	disease	secreted	fragment	H905 107.
SUMMARIES	ID	. 4	168	$\overline{}$	089	715	680	V70895	V41689	V27144	V27143		V2/142	V2/148	V27145	V70897	V70899	V09036	V09039		T13229	X53491	V43617	T61334	T61335	T61336	T61337	161338	T61339	T61340	T61341	T61342	T61343	3.4	₹.	34	34	34	23	33	8	ñ	V00418	043
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A.		V27141 standard; cDNA; 1673	dard;	CDNA;	1673	BP.							
Y I		V2/141;											
3 1	-67	29-5EP-1998	#	(first entry)	ry)								
Ö	No.	Novel haemopoietin receptor	ooiet.	in rece	ptor		NR6.2 gene.						
KW	Hae	Haemopoietin receptor; cell	rec	eptor;	cell		proliferation;	ion; ce	cell di	differentiation;	iation	; cancer	; H
ΚW	cel	cell survival; therapeutic;	1), 七	herapeu	tic;		ronal p	rolife	ratior	neuronal proliferation; drug screening;	screen	ing; ss;	
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PN	WO9	WO9811225-A2) ;			7	7		7.04			
DD.	19-	MAR-1998.					•						
PF	11-	SEP-1997;	G02479.	179.									
PR	11	11-SEP-1996;	AU-(AU-002246.	•								
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Ы	Ko.	Kojima T, Maeda M, Nash A, Nicola NA. Rakar	leda 1	f, Nash	Ä	Nico	la NA.	Sakar .	S. Wil				
ΡΙ	2ha	Zhang J:											
DR	WPI	WPI; 98-260970/23	170/2	~									
DR	P-P	P-PSDB; W55012.	12.										
ΡŢ	Nev	New isolated haemopoletin receptor - used for	haen	nopolet	in re	ecep.	tor - us	sed for	dovo.	developing products	Cubout	0	
F	for	for modulating proliferation, differentiation	rd bu	colifer	tion	ď	1fferent	tiation	and	and survival of		7. Land	
Ę	9	. neurona	1, ce]	118								()	
bS	Cla	Claim 5; Page 84-87; 182pp; English.	Te 84	-87; 18;	:daz	Eng	lish.						
ပ္ပ	The	haemopol	etin	recept	120	HRY	NR6.2 14	a for	7 OF	the now	du la	NDA	
ខ្ល	Int	Interaction between the novel HR and a ligand facilitates proliferation	betwe	en the	nove	e1, H	R and a	ligano	faci	litates	proli	feratio	
ပ္ပ	dif	ferentiat	ion :	and sur	rival	l of	a wide	Variet	, O	Cells.	170	The HR and 4	4 ,
ប្ល	der	derivatives can be used for modulating the activity of the recentors	can 1	be used	for	modi	ulating	the ac	111011	v of the	1001		, 6
ပ္ပ	ដ	regulate	deve]	Lopment	maj	inter	nance or	reger	erati	on in a	9 11 2		n
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S	Sed	Sequence 1673 BP; 344 A; 550 C; 474 G; 305 T	673 E	3P;	344 7	Α.	550 C;	4	74 G;	305	••	. 611411)	
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                                                                                                                   GGCCCTGGCCTAACCTTAATGGGTCCAGGCAGCAGTCAGGAGAAATCTGGTGTG
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V41688 standard; cDNA; 1656 BP.
V41688;
26-007-1998 (first entry)
Nucleotide sequence of the murine U4 gene.
Murine; U4 protein; haematopoietin receptor superfamily;
cell proliferation; immune response; antibody; cell differentiation;
autolmmune disease; cancer; allergy; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                64
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                                                                                                                                                                                                                                                                                                                                                                                                         DB 1;
                                                                                                                                                                                                                                                                                                                                                                                                      Score 1614.6;
Pred. No. 0;
0; Mismatches
                                                                                                                    "U4 protein'
                                                                                    Location/Qualifiers 122. .1399
                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity 99.1%;
Matches 1634; Conservative
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/product=
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                                                                                                                                                                                                                                                                   acatggagacacacctggggccaccgctgaggggctctactggaccctcaatggtcgccg 378
                                                                                                                                                                                                                                                                                                         aatcagcccccaggaccccaccttctcatcggctcctccctgcaagctacctgctctat 318
                                                                                                                                                                                                                                                                                                                                                                          ccttaatgggtccaggcagcagtcaggagacaatctggtgtgtcacgcccgagacggcag 498
                                                                                                                                                                                                                                                                                                                                                                                    cattctggctggctcctgcctctatgttggcttgccccctgagaagccctttaacatcag 558
                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                               Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
1 (bases 1 to 470)
Lee N.H. Glodek, A., Chandra, I., Mason, T.M., Quackenbush, J., Kerlavage, A.R. and Adams, M.D.
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                                                                                                                                                                              19.4%; Score 324.2; DB 45; Length 431; 85.2%; Pred. No. 8.4e-53; 1.ve 0; Mismatches 63; Indels 0;
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Rattus sp.
Eukaryota: Metazoa; Chordata; Craniata; Vertebrata;
                                                                                                                                                                                                  63; Indels
    /dev_stage="19 weeks"
/lab_host="DH10B (ampicillin resistant)"
/lab_host="DH10B (ampicillin resistant)"
clone_lib="Soares_fetal_lung_NbHL19W
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EST229999 Normalized rat kidne
RKIDD49 3' end, mRNA sequence.
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AI233311.1 GI:3817191
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Best Local Similarity 85.2
Matches 362; Conservative
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/db_xref="texon:10118"
/clone="RKIDD49"
/clone="RKIDD49"
/clone=Lb="Normalized rat kidney, Bento Soares"
/note="Organ: kidney; Vector: pT/T3Pac; Site_1: EcoRI;
1 143 c 124 g 115 t
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               411
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CDNA clone
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Rattus norvegicus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       470 AACCGCGGGGGGGGGGAGATAGCTCGGGCCCGGTGCGGCGCGAGCTCAAGCAGTTCCTCG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1368 gcagacggggtgcggcgaggtcctgccggttaaactctaaggataggccatcctcctg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gene Index
Unpublished (1998)
On May 8, 1995 this sequence version replaced gi:801255.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              19;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 470;
                                                                                                                  The Institute for Genomic Research 9712, Medical Center Drive, Rockville, MD 20850, USA Tel: (301)-838-3529 Fax: (301)-838-0208 Email: nhee@tigr.org Seq primer: M13-21.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 323.4; DB 43; Length
Pred. No. 1.2e-52;
0; Mismatches 41; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     UI-R-C2-nb-d-08-0-UI.sl UI-R-C2 Rattus norvegicus UI-R-C2-nb-d-08-0-UI.sl UI-R-C2 Rattus norvegicus UI-R-C2-nb-d-08-0-UI 3', mRNA sequence. 93397623 AA071408.1 GI:33976>>> EST
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                                                                                                                                                                                                                                           location/Qualifiers
                                                                                                                                                                                                                                                                                /organism="Rattus
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Best Local Similarity 87.2%;
Matches 407; Conservative
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AI333812 431 bp mRNA EST 13-FEB-1999
qp93e12.x1 Soares_fetal_lung_NbHL19W Homo sapiens cDNA clone
IMAGE:1930606 3' similar to TR:Q16354 Q16354 PROLACTIN RECEPTOR ;;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 431)
NCI-GGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Tel: (301) 496-1550
Email: Robert_Strausbergenih.gov
This clone is available royalty-free through LLNL; contact the IMAGE Consortium (info@image.llnl.gov) for further information. Insert Length: 1615 Std Error: 0.00 Seq primer: -400p from Gibco
High quality sequence stop: 407.
Location/Qualifiers
                                                                                                                                                                                                                                                61 CGGATCAGGAGCCCACACAGCTGTGATCAGTCCCCAGGATCCCACGCTTCTCATCGGCTC 120
                                                                                                                                                                                                                              ctccctgcaagctacctgctctatacatggagacacacctggggccaccgctgaggggct 354
                                                                                175 geggeegetgteetegetgtggtegeetetgttgetetgtgteetegggggtgeeteggggg 234
                                                                                                                ctactggacceteaatggtcgccgcctgccetetgagctgtcccgcctcaacacete
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          535 ccctgagaagccctttaacatcagctgctggtcccggaacatgaaggatctcacgtgccg
                                                                                                                                                          cggatcggggagcccacacagctgtaatcagcccccaggaccccacccttctcatcggctc
                                                                                                                                                                                                                                                                                                                                                                                                                  241 CACCTTGGCTCTGGCCTTGGCCAACCTCAATGGGTCCAGGCGGTCGGGGGGACAACCT
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           Score 334; DB 43; Length 4
Pred. No. 1.1e-54;
0; Mismatches 71; Indels
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/map="4p16.1-4pter"
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           20.0%;
       Query Match 20.0
Best Local Similarity 84.1
Matches 376; Conservative
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Eukaryota: Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 447)
NCI-CGAP http://www.ncbi.nlm.nih.gov/nclogap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
1351 ggggatcctgccttcgggcagacggggtgcggcgagaggtcctgccggttaaactctaag 1410
                                                                          gataggccatcctcctgctgggtcagacctggaggctcacctgaattggagcccctctgt 1470
                                                                                                                                           1471 accatctgggcaacaaagaaacctaccagaggctggggcacaatgagctcccacaacac 1530
                                                                                                                                                                                                                         agctttggtccacatgatggtcacacttggatataccccaqtg--tgggtaaggttgggg 1588
                                  125 GGGGATCCTGCCCTC-GGCAGACGGGGTGCGGCGAGGGTCCTGCCGGCTAAACTCTAAG 183
                                                                                         mRNA EST 29-OCT-1998
lung_NbHL19W Homo saptens cDNA clone
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Tel: (301) 456-1550
Email: Robert_Strausberg@ih.gov
This clone is available royalty-free through LLNL
IMAGE Consortium (info@image.lini.gov) for further
Insert Length: 1667 8td Error: 0.00
Seq primer: -40mi3 fwd. ET from Amersham
High quality sequence stop: 431.
Location/Qualifiers
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Unpublished (1997)
On Aug 21, 1998 this sequence version replaced
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:1741228"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Contact: Robert Strausberg, Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                            qe38a03.s1 Soares_fetal_lung_NDF
IMAGE:1741228 3', mRNA sequence
                                                                                                                                                                                                                                                                                             1589 tattgcagggcctcccaacaatctctt 1615
                                                                                                                                                                                                                                                                                                                      11111111111111111 | 111111 | 390 | 364 TATTGCAGGCCTCCCAAGAGTCTCTT 390
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AI187074 LOCUS DEFINITION

ACCESSION

RESULT 12

VERSION KEYWORDS SOURCE ORGANISM

REFERENCE AUTHORS TITLE

JOURNAL

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source

FEATURES

BASE COUNT

ORIGIN

427 GACCTTCCTCCACACCAACTACTCCCTCAAGTACAAGCT 465

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1 (bases 1 to 466)
NCT-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
                                                                                                                       This clone is available royalty-free through LLNL; contact the IMAGE Consortium (info@image.llnl.gov) for further information. Insert Length: 1622 std Error: 0.00 Seq primer: -400P from Glbco
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                                  Tumor Gene Index
Unpublished (1997)
On Jan 19, 1998 this sequence version replaced gi:2151491
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ö
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                                                                                                                                                                                                                                                 /clone_lib="Soares_fetal_lung_NbHL19W"
/dev_stage="19 weeks"
/lab_host="DH10B (ampicillin resistant)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 66; Indels
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Pred. No. 1.8e-58;
0; Mismatches 66;
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Tel: (301) 496-1550
Email: Robert_Strausberg@nlh.gov
                                                                                                                                                                                                             /organism="Homo sapiens"
                                                                                                                                                                       High quality sequence stop: 466.
Location/Qualifiers
                                                                                                                                                                                                                          /db_xref="taxon:9606"
/clone="IMAGE:1741879"
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Best Local Similarity 85.6%;
Matches 393; Conservative
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AUTHORS
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Ettheria; wetazoa; Chordata; Craniata; Vertebrata; Mammalia; Ettheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. I (bases 1 to 390).

Marra,M., Hillier,L., Allen,M., Bowles,M., Dietrich,N., Dubuque,T., Geisel,S., Kucaba,T., Lacy,M., Le,M., Martin,J., Morris,M., Theising,B., Wylie,T., Lennon,G., Soares,B., Wilson,R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ä
                                                                                                                                                                                                                                                                                                                                                                                                                                                           This clone is available royalty-free through LLNL; contact the IMAGE Consortium (info@image.llnl.gov) for further information.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1291 cctgtacgaccagtggcgtgcttggatgcagaagtcacacaagacccgaaaccaggacga 1350
                                  mRNA EST 10-SEP-1996
P3NMF19.5 Mus musculus cDNA clone
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Unpublished (1996)
On May 9, 1995 this sequence version replaced gi:804170
                                                                                                                                                                                                                                                                                                                                                    Contact: Marra M/Mouse EST Project
WashU-HHMI Mouse EST Project
Washington University School of Medicinep
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llarity 96.4%; Pred. No. 1.8e-56;
Conservative 0; Mismatches 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /organism-"Mus musculus"
                                                                                                                                                                                                                                                                                                                                                                                                             Tel: 314 286 1800
Fax: 314 286 1810
Email: mouseest@watson.wustl.edu
                                                                                                                                                                                                                                                                                          The WashU-HHMI Mouse EST Project
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Seq primer: mob.REGA+ET
High quality sequence stop: 384.
Location/Qualifiers
1.390
                                                               , mRNA sequence
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                      390 bp
mb75b01.r1 Soares mouse,
IMAGE:335209 5', mPWN -
W1758?
                                                                                                        W17583.1 GI:1291995
                                                                                                                                                     Mus musculus
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Best Local Sim Matches 395; Query Match

196

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256 61 31,6 121 376 181 436

BASE COUNT ORIGIN

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/db_xref="taxon:9606"
/map="839C02; 821G11; 4; 4p15.33-4p16.1; 4p15.33-4p16.1"
/clone="IMAGE:1705398"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CTGCCCCTGAGGTCTCCCGTGTACTCAACGCCTCCACCTTGGCTCTGGCTCTGGCCGCAA 246
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qe44h04.xl Soares_fetal_lung_NbHL19W Homo sapiens
IMAGE:1741879 3', mRNA sequence.
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Catarrhini; Hominidae; Homo
                                                                             /clone_llb="Soares_fetal_heart_NbHH19W"
/sex="unknown"
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Pred. No. 1.8e-58;
0; Mismatches 66;
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Eutherla; Primates;
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Matches 393; Conserv
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1 (bases 1 to 466)

NCT-CASP http://www.ncbi.nlm.nih.gov/nciegap.
NAT-CASP http://www.ncbi.nlm.nih.gov/nciegap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          552
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qb69g04.x1 Soares_fetal_heart_NbHH19W Homo sapiens cDNA clone
IMAGE:1705398 3', mRNA sequence.
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Unpublished (1997)
On Jan 19, 1998 this sequence version replaced g1:2287379.
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                                                                                                                                           462;
                                                                                                                                           Length
                                  others
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                                                                                                                                        Score 355.4; DB 4
Pred. No. 9.5e-59;
0; Mismatches 67
             Soares and M.Fatima Bonaldo."
181 c 122 g 79 t
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Tel: (301) 496-1550
Email: Robert_Strausberg@nih.gov
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ilarity 85.5%;
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Gaps

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Indels

us-09-037-657-14.rst

VERSION KEYWORDS SOURCE ORGANISM

REFERENCE AUTHORS TITLE

JOURNAL

COMMENT

DEFINITION

ACCESSION

RESULT AI185924 LOCUS

558

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CDNA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
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tf79d12.xl NCI_CGAP_Brn23 Homo sapiens cDNA clone IMAGE:2105495 3',
187 CCTGCCCCTGAGCTCTCCCGTGTACTCAACGCCTCCACCTTGGCTCTGGCCCTGGCCAA 246
                                                            Homozota, Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 462)

NCI/NINDS-CGAP http://www.ncbi.nlm.nih.gov/ncicgap,
NTAINDS-CGAP http://www.ncbi.nlm.nih.gov/ncicgap,
NTAIONAL Cancer Institute / National Institute of Neurological Disorders and Stroke, Brain Tumor Genome Anatomy Project (CGAP/BFGAP), Tumor Gene Index
Unpublished (1998)

On Feb 17, 1998 this sequence version replaced gi:2887603.
                                                                                                                   cattotggctggctcctgcctctatgttggcttgcccctgagaagcccttaacatcag
                                                                                                                                                     307 CATCTGGCTGCTCCTGCTCTATGTTGGCCTGCCCCAGAGAAACCGGTCAACATCAG
                                                                                                                                                                                            559 ctgctggtcccggaacatgaaggatctcacgtgccgctggacaccgggtgcacacggggga
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                                          ccttaatgggtccaggcagcagtcaggagacaatctggtgtgtcacgcccgagacggcag
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Bonaldo, Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Tel: (301) 496-1550
Email: Robert_Strausbergenih.gov
Tissue Procurement: David N. Louis, M.D., Myrna
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /clone_lib="NCI_CGAP_Brn23"
/tissue_type="glioblastoma (pooled)"
/lab_host="DH10B"
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/db_xref="taxon:9606"
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Seq primer: -400P from Gibco
High quality sequence stop: 454.
Location/Qualifiers
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IMAGE:1742408 3' similar to TR:Q16354 Q16354 PROLACTIN RECEPTOR;;
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                                                                                                                                                                                                                                                                                                                                                                                                                                   Contact: Robert Strausberg, Ph.D.
Tel: (301) 496-1550
Email: Robert_Strausberg@iih.gov
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
Insert Length: 1552 Std Error: 0.00
Seg primer: -400P from Gibco
High quality sequence stop: 467.
Location/Qualifiers
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National Cancer Institute, Cancer Genome Anatomy Project (CGAP)
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Eutheria; Primates; Catarrhini; Hominidae; Homo.
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On Feb 17, 1998 this sequence version replaced g1:2150926
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Pred. No. 3.7e-60;
0; Mismatches 68; Indels
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/db_xref="taxon:9606"
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AI185924.1 GI:3736562
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R. Rosenfeld M.D.,

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/dev_stage="adult"

/dev_stage="adult"
/lab_nost="bhilds (Life Technologies)" with a modified
/note="vector: pT73D-Pac (Pharmacia) with a modified
polylinker; Site_1: Not I: Site_2: Eco RI: This library
consists of a mixture of individually tagged normalized
libraries constructed from rat placenta, adult lung,
brain, liver, kidney, heart, spleen, ovary, and muscle.
The tag is a string of 3-5 nucleotides present between the
Not I site and the oligo-dr track which allows
identification of the library of origin of a clone within
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1 (bases 1 to 474)

NCI/NINDS-GAP http://www.ncbi.nlm.nih.gov/ncicgap.
NCI/NINDS-GAP http://www.ncbi.nlm.nih.gov/ncicgap.
Disorders and Stroke, Brain Tumor Genome Anatomy Project (CGAP/BEGAP), Tumor Gene Index
Unpublished (1998)
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                                                                                                                                                                                  Length 428;
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                                         Rosenfeld
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                           Email: Robert_Strausberg@nih.gov
Tissue Procurement: David N. Louis, M.D., Myrna R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Indels
                                                                                                 cDNA Library Arrayed by: Greg Lennon, Ph.D. DNA Sequencing by: Washington University Genome Clone distribution: NOI-CGAP clone distribution cound through the I.M.A.G.E. Consortium/LLNL at:
                                                                      Soares, Ph.
                                                                                                                                                                                                                                                                                                    /clone_lib="NOI_CGAP_Brn23"
/tissue_type="glioblastoma (pooled)"
/lab_host="DH10B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 364.2; DB 46;
Pred. No. 2e-60;
0; Mismatches 69;
                                                                                                                                                            www-bio.llni.gov/bbrp/image/image.html
                                                                                                                                                                                        Std Error: 0.00
                                                                 cDNA Library Preparation: M. Bento
Bonaldo, Ph.D.

    474
/organism="Homo sapiens"

Contact: Robert Strausberg, Ph.D.
                                                                                                                                                                                      Insert Length: 1664 Std Error:
Seq primer: -400P from Gibco
High quality sequence stop: 450.
Location/Qualifiers
                                                                                                                                                                                                                                                                            /db_xref="taxon:9606"
/clone="IMAGE:2097265"
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larity 85.4%;
Conservative
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             Tel: (301)
Email: Robe
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us-09-037-657-14.rst

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Rattus norvegicus
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                                                                                                                                                                                                                                                                                                                                                                   WashUrthMI Mouse EST Project
WashIngton University School of MedicineP
444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
7e1: 314 286 1810
Fax: 314 286 1810
Email: mousestewatson.wustl.edu
Email: mousestewatson.wustl.edu
InAGE Consortium (info@image.llnl.gov) for further information.
MGI:285477
Seq primer: -28M13 rev2 from Amersham
High quality sequence stop: 441.
                                                                                      AA039053 445 bp mRNA EST 29-AUG-1996 mi999d07.rl Soares mouse embryo NbME13.5 14.5 Mus musculus CDNA clone IMAGE:474733 5', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
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Pred. No. 4.3e-73;
0: Mismatches 9; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /tissue_type="embryo"
/dev_stage="13.5-14.5dpc total fetus"
/lab_host="DH10B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0; Mismatches
                                                                                                                                                                                                                                                                                                                                                           Contact: Marra M/Mouse EST Project

    445
    /organism="Mus musculus"
    /strain="C57BL/6J"

                                                                                                                                                                                                                                                                                                                  The WashU-HHMI Mouse EST Project
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /db_xref="taxon:10090"
/clone="IMAGE:474733"
91514788
AA039053.1 GI:1514788
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /sex="unknown"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    25.7%;
                                                                                                                                                                                                                                                                                                                                    Unpublished (1996)
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Best Local Similarity 98.0
Matches 436; Conservative
                                                                                                                                                                                                                                                                                                         Waterston, R.
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                                                                                                                                                                                      house mouse.
                                                              RESULT 4
AA039053/c
LOCUS
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KEYWORDS
SOURCE
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Program for Rat Gene Discovery and Mapping
Program for Rat Gene Discovery and Mapping
University of Iowa
451 Eckstein Medical Research Building Iowa City, IA 52242, USA
Tel: 319 335 8250
Fax: 319 335 8260
Email: msoarces@blue.weeg.uiowa.edu
Oligo-dT track not found, Not I site shown in beginning of sequence is likely internal to the message. cDNA Library Preparation: M.
Fatima Bonaldo, Ph.D. Clone distribution: clones will be available through Research Genetics
Seq primer: M13 Forward.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AA866388 428 bp mRNA EST 05-FEB-1999 UI-R-A0-aj-f-04-0-UI.83 UI-R-A0 Rattus norvegicus cDNA clone UI-R-A0-aj-f-04-0-UI 3' similar to gb|AC003112|AC003112 Human DNA from chromosome 19 specific cosmid R30292, genomic sequence, complete sequence [Homo sapiens], mRNA sequence.
1567 cccagtgtgggtaaggttggggtattgcagggcctcccaacaatctcttaaataa 1626
                                                                                                                                                                                                                              On Mar 16, 1998 this sequence version replaced gi:2961849
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota; Metazoa; Chordata; Craniata; Jebuharia; Metazoa; Chordata; Craniata; Muridae; Murinae; 1 (bases 1 to 428)
Bonaldo,M.F., Lennon,G. and Soares,M.B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /strain="Sprague-Dawley"
/db_xref="taxon:10116"
/map="between D11S1765 and UGB"
/clone="UT-R-AO-aj-f-04-0-UI"
/clone="UT-R-AO"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /organism="Rattus norvegicus"
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97044477
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AA866388.1 GI:4230568
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. (Dasea; 1 to 503)
Marra, M., Hillier, L., Allen, M., Bowles, M., Dietrich, N., Dubuque, T. Geisel, S., Kucaba, T., Lacy, M., Le, M., Martin, J., Morris, M., Schellenberg, K., Steptoe, M., Tan, F., Underwood, K., Moore, B., Theising, B., Wylle, T., Lennon, G., Soares, B., Wilson, R. and Waterston, R.
14.5dpc embryos [total RNA provided by Minoru Ko, Wayne State Univ., from 2 ]; double-stranded cDNA was ligated 15 Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of the modified pT7T3 vector. Library went through one round of normalization, and was constructed by Bento Soares and M.Failma Bonaldo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAU49278 503 bp mRNA EST 30-DEC-1996 m/45c04.rl Soares mouse embryo NbME13.5 14.5 Mus musculus CDNA clone IMAGE:479046 5', mRNA sequence.
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                                                                                                                                                                                                                                                           904
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                                                                                                                                                                          Length 482;
                                                                                                                                                                         Score 457.8; DB 26; Length
Pred. No. 2.8e-78;
0; Mismatches 2; Indels
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                                                                                                                101
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WashU-HHMI Mouse EST Project
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                                                                                                                                                                          Query Match 27.4%;
Best Local Similarity 99.4%;
Matches 470; Conservative
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AA049278.1
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AA049278/c
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1056 tegtecaagtgegttgtaacecattegggatetatgggtegaaaaggegggaatetgga 1115
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    267 ACGACCAGIGGCGIGCTIGGAIGCAGAAGICCACAAGACCCGGAAACCAGGACGAGGGGA
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             MO 63108
                                                                                                                                                                                                              embryo NDME13.5 14.5"
Washington University School of MedicineP
4444 Forest Park Parkway, Box 8501, St. Louis,
Tel: 314 286 1800
Fat: 314 286 1810
                                                       This clone is available royalty-free through ITHSE Consortium (info@image.llnl.gov) for fun MGI:289790
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Pred. No. 1.1e-76;
0; Mismatches 6;
                                                                                                        Seq primer: -28M13 rev2 from Amersham High quality sequence stop: 486. Location/Qualiflers 1.503
                                                                                                                                                                          /db_xref="taxon:10090"
/clone="IMAGE:479046"
/clone_lib="Soares mouse er
                                                                                                                                                             /organism="Mus musculus'
                                                     Email: mouseest@watson.wustl.edu
                                                                                                                                                                        /strain="C57BL/6J
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98.0%;
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Best Local Similarity 98.0
Matches 497; Conservative
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Mus musculus
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AUTHORS
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Marrah. Hiller,L., Allen,M., Bowles,M., Dietrich,N., Dubuque,T.,
Gelsel,S., Kucaba,T., Lacy,M., Le,M., Martin,J., Morris,M.,
Schellenberg,K., Steptoe,M., Tan,F., Underwood,K., Moore,B.,
Theising,B., Wylie,T., Lennon,G., Soares,B., Wilson,R. and
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                                                                                                                                                                                                                                                                                                                                            This clone is available royalty-free through LLNL; contact the IMAGE Consortium (info@image.llnl.gov) for further information. MGI:289787
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                                                         Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalla;
Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 GCTGCTGGTCCCGGAACATGAAGGATCTCACGTGCCGCTGGACACCGGGTGCACACGGGG
                                                                                                                                                                                           Unpublished (1996)
On Dec 30, 1996 this sequence version replaced gi:1528951
                                                                                                                                                                                                                                        Contact: Marra M/Mouse EST Project
WashU-HHMI Mouse EST Project
WashIngton University School of Medicinep
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /clone_lib="Soares mouse embryo NbME13.5 14.5"
/sex="unknown"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 464;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /tissue_type="embryo"
/dev_stage="13.5-14.5dpc total fetus"
/lab_host="DH108"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 27.7%; Score 464; DB 29; Best Local Similarity 100.0%; Pred. No. 1.9e-79; Matches 464; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                         Seq primer: -28M13 rev2 from Amersham
High quality sequence stop: 437.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                    organism="Mus musculus"
                                                                                                                                                                              The WashU-HHMI Mouse EST Project
                                                                                                                                                                                                                                                                                                                                 mouseest@watson.wustl.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /db_xref="taxon:10090"
/clone="IMAGE:479043"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         130 g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /strain="C57BL/6J
AA049280.1 GI:1755311
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           144 C
                             house mouse.
Mus musculus
                                                                                                                                                                  Waterston, R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         102
                                                                                                                                                                                                                                                                                                                Fax: 31
Email:
                                                                                                                                                                                                                                                                                                                                                                                                                                        source
                                           ORGANISM
                                                                                                                                                                        TITLE
JOURNAL
COMMENT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      BASE COUNT
ORIGIN
VERSION
KEYWORDS
SOURCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           .738
                                                                                     REFERENCE
                                                                                                     AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                     FEATURES
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Email: mouseest@watson.wustl.edu
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
                                                                                                                                                          360
                                                                                                                                                                                                                                                                                                                                                                                                 W66776. 482 bp mRNA EST 14-JUN-1996 mel7bll.rl Soares mouse embryo NbME13.5 14.5 Mus musculus cDNA clone IMAGE:387741 5' similar to PIR:B38252 B38252 granulocyte colony-stimulating factor receptor precursor; mRNA sequence.
181 CCCTCTTCACTCCCTATGAGATCTGGGTGGAAGCCACCAATCGCCTAGGCTCAGCAAGAT 240
                                                       917
                                                                                                                                                                                              97.7
                                                                                                                                                                                                            301 ACGIGAGCCGCGTIGGGGGCCTGGAGGACCAGCIGAGTGTGCGCTGGGTCTCACCACCAG
                                                                                                                 acgtgagccgcgttgggggcctggaggaccaccaccag
                                                                                                                                                                                        ctctcaaggatttcctcttccaagccaagtaccagatccgctaccgcgtggaggacagcg
                                     ctgatgtcctcacactggatgtcctggacgtggtgaccacggacccccacccgacgtgc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      On Apr 14, 1993 this sequence version replaced gi:785250
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Washu-HHMI Mouse EST Project
Washington University School of MedicineP
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /clone_lib="Soares mouse embryo NbME13.5 14.5"
/sex="unknown"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MGI:239573
Possible reversed clone: similarity on wrong strand
                                                                                                                                                                                                                                                                /dev_stage="13.5-14.5dpc total fetus"
|lab_host="DH10B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Contact: Marra M/Mouse EST Project
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Waterston, R.
The WashU-HHMI Mouse EST Project
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        organism="Mus musculus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          High quality sequence stop: 359
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /strain="C57BL/6J"
/db_xref="taxon:10090"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           tissue_type="embryo"
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W66776.1 GI:1375694
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Tel: 314 286 1800
Fax: 314 286 1810
Email: mouseest@wa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Unpublished (1996
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RESULT 1
AAO49280
LOCUS
DEFINITION
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NID
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                                                                                                                                                                                    3; Search time 2095.87 Seconds (without alignments) 1574.548 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                       4.5
Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2546578 seqs, 986266752 residues
version 4
- 1998 (
                                                                                                                                                                                           September 28, 1999, 15:38:03
                                                                                                                       nucleic search, using sw model
GenCore
Copyright (c) 1993
                                                                                                                                                                                                                                                                                                                      US-09-037-657-14
1673
1 ggcacgagetteget
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gb_est22
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em_est2:*
em_est3:*
em_est4:*
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gb_est32
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em_est6:
em_est7:
em_est8:
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Perfect sc
Sequence:
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Database

Run on:

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A1074921 0Y04d08.s
AA925924 UT-R-A1-e
AA377893 EST90550
H14009 EST00035 Ch
N78873 Zb17h05.s1
A1535068 UI-R-C3-s
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A1575060 UI-R-G0-u
AA043001 ZK56f01.r
W46604 ZC3Zh10.s1
R87407 ym88d09.s1
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                                                                                                                                                                                        AA049280 mj45d02.
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AI185780 qe44h04
W17583 mb75b01.r
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                                                                       Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AV010798
                                                                                                                            SUMMARIES
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AA925924
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W66776
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AA270365
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AA043001
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R87407
em_est22:*
em_est23:*
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em_est25:*
                                                                                                                                                                 DB
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Query
Match
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318.8
311.4
2296.8
2284.4
2246.4
206.4
206.4
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AA049280 464 bp mRNA EST 30-DEC-1996 mj45d02.rl Soares mouse embryo NDME13.5 14.5 Mus musculus CDNA clone IMAGE:479043 5' similar to SW:ILGB_MOUSE Q00560 INTERLEUKIN-6 RECEPTOR BETA CHAIN PRECURSOR; mRNA sequence.

ALIGNMENTS

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Anotes—Weetor: pT713D-pac (Pharmacia) with a modified polylinker; Site_1: Not I; Site_2: Eco R: The UI-R-C2 library is a subtracted library derived from the UI-R-C1 library, which is a subtracted library derived from the UI-R-C0 library, which is a subtracted library derived from the UI-R-C0 library. The UI-R-C0 library consisted of a mixture of individually tagged normalized libraries constructed from rat placenta, adult lung, brain, liver, kidney, heart, spleen, ovary, muscle, 8, 12 and 10-day between the Not I site and the oligo-dr track which allows identification of the library of origin of a clone within
                                                                                                                                                                                                                                                                                                                                                                                                                                Email: msoares@blue.weeg.ulowa.edu
The sequence tag present in the cDNA between the NotI site and the oligo-dr track served to identify it as a clone from the normalized adult Lung library. cDNA Library Preparation: M. Fatima Bonaldo, Ph.D. Clone distribution: clones.will be available through Research Genetics
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          library in the form of single-stranded circles. The remaining single-stranded circles (subtracted library) was
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                converted to double-stranded circles and electroporated into DH10B bacteria (Life Technologies) to generate the ULT-C.2 library. This procedure has been previously described (Bonaldo, Lennon and Soares, Genome Research 6:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             the mixture. The subtracted library (UI-R-C2) was constructed as follows: PCR amplified cDNA inserts from UI-R-C1 clones from which 3' ESTs had been derived was
                                                         Bonaldo, M.F., Lennon, G. and Soares, M.B. Normalization and subtraction: two approaches to facilitate gene
                                                                                                                                                                                                                                                                                                                                            451; pčkstein Medical Research Building Iowa City, IA 52242, USA
Tel: 319 335 8250
Fax: 319 335 9565
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          cacaagacccgaaaccaggacgagggatcctgccttcgggcagacgggggtgcggcgaga 1387
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Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus
1 (bases 1 to 464)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       purified by hydroxyapatite column chromatography,
                                                                                                                                                                                                                   On Sep 12, 1996 this sequence version replaced gi:1404537
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             19;
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Pred. No. 9.1e-52;
); Mismatches 42; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          lab_host="DH10B (Life Technologies)"
                                                                                                                                                                                                                                                                                Contact: Soares, MB Program for Rat Gene Discovery and Mapping
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             db_xref="taxon:10116"
clone="UI-R-C2-nb-d-08-0-UI"
clone_lib="UI-R-C2"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      organism="Rattus norvegicus"
                                                                                                                                            Genome Res. 6 (9), 791-806 (1996)
97044477
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      strain="Sprague-Dawley
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Location/Qualifiers
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Best Local Similarity 86.9%;
Matches 403; Conservative
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A70384 Sequence 14
A70394 Sequence 24
AF059293 Homo Sapi
AC003112 Human DNA
Y07862 Plasmid PEA
X76228 H.Sapiens m
A49139 Sequence 1
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AF061795 Homo Sapi
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Nicola,N.A., Fabri,L., Farley,A., Nash,A., Willson,T., Rakar,S.,
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Kikuchi,Y.
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888; Conservative 0; Mismatches 0;
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Fabri,L., Farley,A., Nash,A., Willson,T., Rakar,S.,
Lexander,W., Hilton,D.J., Kojima,T., Maeda,M. and
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                                                                                                                                                                                                                                                 11163 CAGTGGCGTGCTTGGATGCAGAAGTCACAAGACCCGAAACCAGGTAGGAAAGTTGGGG 11222
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                                                                                                                                                                                                                                                                                                                                              cacttggatataccccagtgtgggtaaggttgggggtattgcagggctcccaacaatctc
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gtgtgcgagccgcgggggcgagcccagctcgggcccggtgcgggcgcgagctcaagcag
                     11043 Grereceaecceceeecceceaeccaacreeecceereceecceaecreaacae
                                             tteeteggetggeteaagaageacgeatactgetegaacettagttteegeetgtaegae
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Sequence 12 from Patent WO9811225.
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Nicola,N.A., Fabri,L., Farley,A., Nash,A., Willson,T., Rakar, Shang,J., Alexander,W., Hilton,D.J., Kojima,T., Maeda,M. and Kikuchi,Y.
                                                                    . 1 ggcaccgtttacttcgtccaagtgcgttgtaacccattcgggatctatgggtcgaaaaag
                                                                                                                                        gegggaatctggagegagtggagceacceacegetgeetceaceectegaagtgagege
                                                                                                                                                                                                           ccgggcccgggcgggggggggggggggccggcggggggcgaqcccagctcgggccggtg
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32.5%; Score 305; DB 5; 100.0%; Pred. No. 2.5e-48; ive 0; Mismatches 0;
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/organism="unidentified"
/db_xref="taxon:32644"
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/db_xref="PlD:e1433703"

/db_xref="PlD:e1433703"

/db_xref="G1:4774673"

/db_xref="G1:4774673"

/translation="TLMGRR.PPELSRVLNASTLALALANLNGSRQRSGDNLVCHARD

GSILAGSCLYVGLPPERPVNISCWSRNMKDLTCRWTPGAHGETFLHTNYSLKYKLRNY

GODNTCEEVHTYGPHSCHIPKDLALFTPYPEIWPERSKBYULLDLIDVYTD

PPPDVHVSRVGGLEDOLSVRWVSPPALKDELFQAKQIRKRRDSVDRKVVDDVSNQT

SCRLAGLKRGTVYFVQVRCNPFGIYGSKRAGIWSEWSHPTAASTPRSERRGPGGGARE

PRGGEPSSGPVRRELKQFLGWLKKHAYCSNLSFRLYDQWRAWMQKSHKTRNQHRTRGS
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A NOVEL HAEMOPOIETIN RECEPTOR AND GENETIC SEQUENCES ENCODING SAME PALENT: WO 9811225-A 19-MAR-1998;
NICOLA NICOS ANTONY (AU)
., Farley, A., Nash, A., Willson, T., Rakar, S.,
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'codon_start=1
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                                                                                                                                                                                                                                  1391 bp DNA
24 from Patent WO9811225.
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Nicola, N.A., Fabri, L
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 1716)

Elson, G.C.A., Graber, P., Losberger, P., Herren, S., Gretener, D., Menoud, L.N., Wells, T.N.C., Kosco-Vilbois, M.H. and Gauchat, J.F. C.F.1, a Novel Soluble Protein Shares Homology With Members of the Cytokine Type-I Receptor Family

J. Immunol. (1998) in press

E 2 (bases 1 to 1716)

S Elson, G.C.A., Graber, P., Losberger, P., Herren, S., Gretener, D., Menoud, L.N., Wells, T.N.C., Kosco-Vilbois, M.H. and Gauchat, J.F. Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /joince="similar to cytokine type-1 receptor family members; similar to the sequence presented in GenBank Accession Number ACO03112"
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PREDSVDWRYVDDVSRQTSCRLAGIRRGTVIRVOVRCRPFGIYGSKRAGIWSEWSHPT
AASTPRSERPGPGGGACEPRGEPSSGPVRRELKQFLGWLKKHAYCSNLSFRLYDQWR
AWQKSHKTRNQDGGILPSGRRGTARGPAR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Submitted (14 APR-1998) Dept. of Immunology, Serono Pharmaceutical Research Institute, 14, Chemin des Aulx, Plan-les-Ouates, GE 1228,
                            02-AUG-1998
cggcgcgagctcaagcagttcctcggctggctcaagaagcacgcatactgctcgaacctt
                                                                                                     241 agtttccgcctgtacgaccagtggcgtgcttggatgcagaagtcacacaagacccgaaac
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Homo sapiens cytokine-like factor-l precursor (CLF-1) mRNA,
AFOS9293
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/profein_d="AAC2835.1"
/db_xref="PDi:3372627"
/db_xref="GI:3372627"
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/gene="CLF-1"
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/gene="CLF-1"
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Best Local Simi Matches 270; Query Match

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Juliary. Lissal for Analysis and School and Lone deposes pregnant uterus NbHPU Homo sapiens cDNA clone 490063 5' (193. .394); 94% identity..-DDS similarity to AA000412 assessor. Is soares fetal heart NbHH19W Homo sapiens cDNA clone 365523 5' (145. .346); 96% identity.--(11121. .11331) DDS similarity to AA009693 assessor. Is soares fetal heart NbHH19W Homo sapiens cDNA clone 365523 3' (429. .307); 95% identity.--(11127. .11246) DDS similarity to AA047548 at 1127. .11246) DDS similarity to AA047548 at 15502. Is soares fetal heart NbHH19W Homo sapiens cDNA clone 377018 5' (222. .341); 97% identity.--(11061. .11331) predicted exon, program; grail2exons_human_1.3, frame: 0, quality; good, score: 73.000--(11061. .11209) DDS similarity to AA452628 xx33f04.rl Scares total fetus NB2HR8 by Homo sapiens cDNA clone 788287 5' (167. .313); 98% identity."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           heart NbHH19W Homo sapiens CDNA clone 377018 5' (1. .138): 96% identity. --Other overlapping matches:-(10435. .1048) DDS similarity to AA136115 zk90b04.r1 Scares pregnant uterus NbHPU Homo sapiens CDNA clone 490063 5' (1. .110); 93% identity. --(10466 .10548) DDS similarity to AA455628 zx33104.r1 Scares total fetus Nb2HF8 9W Homo sapiens CDNA clone 788287 5' (1. .82); 95% identity. --(10486. .10548) DDS similarity to AA0455628 similarity to AA0455628 similarity to AA0455628 clone 788287 5' (1. .82); 95% identity. --(10486. .10548) DDS similarity to AA00912 ze82h02.r1 Scares fetal heart NbHH19W Homo sapiens CDNA clone 365523 5' (1. .61); 97%
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  frame: 1, quality: excellent, score: 100.000--DDS similarity to Add7548 zf15e02.r1 Scores fetal heart NbHH19W Homo sapiens cDNA clone 377018 5' (139. .221); 100% identity.--DDS similarity to AA136115 xg0b04.r1 Scores pregnant uterus NbHPU Homo sapiens cDNA clone 490063 5' (111. .192); 9% identity.--DDS similarity to AA452628 zx33f04.r1 Scores total fetus NbZHFB 9W Homo sapiens cDNA clone 788287 5' (83. .165); 100% identity.--DDS similarity to AA409412 ze82h02.r1 Scores fetal heart NbHH19W Homo to AA009412 ze82h02.r1 Scores fetal heart NbHH19W Homo sapiens cDNA clone 365523 5' (62. .144); 100% identity."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      frame: 1, quality: good, score: 63.000"
complement(9629. .9672)
/note="predicted exon, program: grail2exons_human_l.3,
frame: 1, quality: excellent, score: 75.000"
/rpt_family="Alu"
10409. .10548
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          note-"predicted exon, program: grail2exons_human_1.3,
               gra112exons_human_1.3, 71.000"
                                                                                          gra112exons_human_1.3,
62.000"
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                                                                                                                                                                    /standard_name="endogenous retroviral sequence"
                                                                                                                                                                                            /note="HERV9 retroviral sequence" complement(3269. 3544)
                                       frame: 1, quality: good, score:
complement(1383. .1444)
/note="predicted exon, program:
                                                                                                                     rame: 1, quality: good, score:
257. .8516
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/rpt_family="Alu"
12502, .12581
                                                                                                                                                                                                            /rpt_family="Alu"
5425, .5722
                                                                                                                                                                                                                                                                                                                 /rpt_family="Alu"
complement(7505, 7700, /rpt_family
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complement(9445. .9505)
/note="predicted exon,
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9358. .9535
                                                                                                                                                                                                                                                                                               /rpt_family="Alu"
complement(6486.
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/cell_line="5HL2-B"
/cell_line="5HL2-B"
/clone_lib="LL19NCO3 R chromosome 19 cosmid library"
/note="LL19NCO3 cosmid library constructed at LLNL from
flow-sorted chromosomes from hybrid 5HL2-B, which carries
                                                                                                                                               ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Lamerdin, J.E.
Direct Submission
Submitted (21-NOV-1997) Human Genome Center, Lawrence Livermore
National Laboratory, 7000 East Ave., Livermore, CA 94551, USA
Location/Qualifiers
1. 40668
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1208 cGGCGCGAGCTCCAGGCTGCCTGGCTCAAGAAGCACGCGTACTGCTCCAACCTC 1267
                                                                                                                                                                                                                                          1028 GGCACCGTGTACTTCGTGCAAGTGCGCTGCAACCCCTTTGGCATCTATGGCTCCAAGAAA 1087
                                                                                                                                                                                                                                                                                                                                                                                                       cggcgcgcgagctcaagcagttcctcggctggctcaagaagcacgcatactgctcgaacctt 240
                                                                                                                                                                                                                                                                                                       gogggaatctggagogagtggagocacccaccgctgcctccaccctcgaagtgagogc 120
                                                                                                                                                    Gaps
                                                                                                                                                                                                  ggcaccgtttacttcgtccaagtgcgttgtaacccattcgggatctatgggtcgaaaag 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      40668 bp DNA PRI 21-NOV-199;
from chromosome 19 specific cosmid R30292, genomic
complete sequence.
                                                                                                  DB 11; Length 1716;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         chromosome 19 as its only human chromosome
                                                                                                                                               34; Indels
                                                                                               Score 249.6; DB 1:
Pred. No. 6.2e-38;
0; Mismatches 34.
273
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/db_xref="taxon:9606"
/clone="R30292"
/chromosome="19"
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  623
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RESULT 9
AC003112/c
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VERSION KEYWORDS SOURCE ORGANISM

ACCESSION

REFERENCE AUTHORS

REFERENCE AUTHORS TITLE JOURNAL

FEATURES

JOURNAL

TITLE

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Comptanient (1227). 14042)

frame: 2 quality: good, score: 61.000-other overlapping matches: -(13766. 13836) DDS similarity to Ano99412 se82002.11 Soares fetal heart NbHH19W Homo saplens cDNA clone 365523 5' (428. 496); 97% identity.--(13756. 13984) DDS similarity to Ano99403 ze82002.12 Soares fetal heart NbHH19W Homo saplens cDNA clone 365523 3' (227. 1); 98% identity.--(13756. 13984) DDS similarity to And50010 zx33f04.51 Soares total fetus NbZHF8 9w Homo saplens cDNA clone 788287 3' (228. 1); 99% identity.--(13756. 13984) DDS similarity to And50010 zx33f04.51 Soares total fetus NbZHF8 9w Homo saplens cDNA clone 783348 3' (1. 433); Score: 88% identity.--(1356. 1397) DDS similarity to And6406 zv11e07.51 Soares Fetal lung NbHH19W Homo saplens cDNA clone 783348 3' (1. 433); Score: 88% identity.--(1527. 14885) DDS similarity to And12532 zaplens cDNA clone 30266 5' (1. 355) 94% identity.--(1527. 14885) DDS similarity to And12759 zaplens cDNA clone 30266 5' (1. 355) 94% identity.--(1527. 14885) DDS similarity to And12759 zaplens cDNA clone 30266 5' (1. 355) 94% identity.--(1527. 14887) DDS similarity to And12759 zaplens cDNA clone 30266 5' (1. 355) 9% identity.--(1527. 14897) DDS similarity to And12759 zaplens cDNA clone 300004 3' (1342. 1); 99% identity.--(1527. 14897) DDS similarity to And604 zaplens cDNA clone 324067 3' (322. 465); 96% identity.--(1527. 1527) zaplens cDNA clone 324067 3' (322. 465); 96% identity.--(1527. 15713) DDS similarity to And604 zaplens cDNA clone 324067 3' (322. 465); 96% identity.--(15735. 15713) DDS similarity to W46604 zaplens cDNA clone 324067 3' (322. 465); 96% identity.--(15735. 15713) DDS similarity to W46604 zaplens cDNA clone 324067 3' (322. 465); 96% identity.--(15735. 15713) DDS similarity to W46604 zaplens cDNA clone 324067 3' (322. 465); 96% identity.--(15735. 15713) DDS similarity to W46604 zaplens cDNA clone 324067 3' (322. 465); 96% identity.--(15735. 15713) DDS similarity to W46604 zaplens cDNA clone 324067 3' (229). 100% identity.--(15735. 15713) DDS similarity conserved
                                                                                                                                          similarity
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Anote—"predicted exon, program: grail2exons_human_1.3, frame: 0, quality: excellent, score: 81.008--other overlapping matches:-(15936. .15895) pbs similarity to AA121332 zk89c11.s1 Soares pregnant uterus NbBHD Homo identity.--(15970. .15895) bbs similarity to AA1215970. .15895) bbs similarity to AA1216970. .15895) bbs similarity to AA127694 zk89c11.r1 Soares pregnant uterus NbHPD Homo sapiens cDNA clone 490004 5' (1. .76); 100% identity."
pregnant uterus NDHPU Homo sapiens CDNA clone 490063 5' (395. 477); 92% identity.—DDS similarity to AA009412 cae82h02.rl Scares fetal heart NDHH19W Homo sapiens CDNA clone 365523 5' (347. 427); 94% identity.—DDS similarity to AA009693 seg2h02.sl Scares fetal heart NDHH19W Homo sapiens CDNA clone 365523 3' (306. 228); 99% identity.—DDS similarity to AA450010 zx33f04.sl Scares total fetus ND2HF8 9W Homo sapiens CDNA clone 788287 3' (309. 229); 99% identity.—
                                                                                                                                                                                                                                                                                                            (309, .229); 99% identity."
complement(12966, .13240)
/rpt_family="Alu"
                                                                                                                                                                                                                                                                                                                                                                                                                           complement(13274. .13531) /rpt_family="Alu"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     complement(13756. .14029)
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Complement(18540. .18697)

// note="predicted exon, program: grail2exons_human_1.3, frame: 1; quality: excellent, score: 100.000--DDS slmilarity to W66776 me17bll.r1 Soares mouse embryo NbME13.5 14.5 Mus musculus cDNA clone 387741 5' similar to FIR:B38252 B38252 granulocyte colony stimulating factor receptor precursor (316. .158); 92% identity.--DDS slmilarity to AA049280 mj45602.r1 Soares mouse embryo NbME13.5 14.5 Mus musculus cDNA clone 479043 5' similar to SW:IL6B_MOUSE Q00560 INTERLEUKIN-6 RECEPTOR BETA CHAIN PRECURSOR (274. .431); 93% identity.--"
(157. .1); 82% identity. --(18438. .18406) DDS similarity to IAA049280 mj45d02.rl Soares mouse embryo NDME13.5 14.5 Mus musculus cDNA clone 479043 5' similar to SW:LLGB_MOUSE Q00560 INTERLEUKIN-6 RECEPTOR BETA PRECURSOSR (432. .464);
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Plasmid pEAV030 containing cDNA of Equine arteritis virus, complete
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An infectious arterivirus cDNA clone: identification of a replicase
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di gene; glycoprotein; Gs gene; membrane protein; nucleocapsid protein; ORFIab; ORF3; ORF4; replicase; replicase
protein; ORF1ab; ORF3; ORF4; replicase; replicase
polyprotein; ribosomal frameshift signal.
Equine arteritis virus:
Equine arteritis virus:
Viruses; SRNA positive-strand viruses, no DNA stage; Nidovirales; Arteriviridae; Arterivirus.
Arteriviridae; Arterivirus.
I (Dases 1 to 15528)
van Dinten, L.C., den Boon, J.A., Wassenaar, A.L., Spaan, W.J. and Shijder, E.J.
                                                                                                                                                                                                                                                                                                                                                                                                                15973 GTACTGCTCCAACCTCCAGCTCTACGACCAGTGGCGAGCCTGGATGCAGAAGTC 15914
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                                                                                                                                                                                                                                                                                                                                                                                 Indels 35;
                                                                                                                                                                                                                                                                                                                                               Length 40668;
                                                                                                                                                                                                                                                                                                                                          Score 218; DB 11;
Pred. No. 4.3e-32;
0; Mismatches 85;
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                                                         Q00560 INTERI
88% identity.
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14; Conservative
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Matches 314;
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REFERENCE AUTHORS TITLE JOURNAL

COMMENT FEATURES

CDS

JOURNAL MEDLINE

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VWTRINEVVVLTASHVVGRANMATLKIGDAMLTLTFKKNGDFAEAVTTQSELPGNWPQ
LHFAQPTTGPASWCTATGDEEGLLSGEVCLAWTTSGDSGSAVVQGDAVVGVHTGSNTS
GVAYVTTPSGKLLGADTVTLSSLSKHFTGPLTSIPKDIPDNIIADVDAVPRSLAMLID
                                                                                                                                     Snijder, E.J.

Direct Submission
Submitted (10-SEP-1996) E.J. Snijder, Dept. of Virology, Institute
of Medical Microbiology, Leiden University, Azl. Building 1, Room
P4-26, Postbus 9600, 2300 RC Leiden, NETHERLANDS
Related sequences: X53459, X52275, X52276, X52277 & A02710.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            'translation-"MATFSATGFGGSFVRDWSLDLPDACEHGAGLCCEVDGSTLCAEC
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POATLVTMGYWACVAALAVYSLMGLRVKVNVPMCVTPAHFLLLARSAGOSREOMLRVS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DGFCWLKLLPPDRREAGLRLYYNHYREQRTGWLSKTGLRLWLGDLGLGINASSGGLKF
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GSALQCLNVMWKRPIGSTVLGEQTGAVVTAVKSISFSPPCCVSTTLPTRPGVTVVDHA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       rvvdarlaieeasvfistdhasakrfpgarfaltpvyanawvvspaanslivītdoec
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       eplasagvasdsapkwrvaktvyssaerfrtelvorarsvgdvlvoalplktpavory
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 <u> 2yrnilnaslovdrdaarsrrlmakladfaveqevtagdrvvvidgldrmahfkddl</u>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      join(225. .5405,5405. .9751)
/note="ORFlab; slippery sequence causes -1 frameshift"
point mutation that abolishes discontinuous mRNA transcription
Proc. Natl. Acad. Sci. U.S.A. 94 (3), 991-996 (1997)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1. 15528
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dD_xref="taxon:57026"
/lab_host="Escerichia coli strain K12-PC2495"
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(db_xref-"taxon:57026"

(lab_host-"Escerichia coli strain K12-PC2495"
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'db_xref="PID:e280813"
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                                                                                                                                                                                                                                                                                                                                                                                                                                         /organism="Equine arteritis virus"
/db_xref="taxon:11047"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              db_xref="PID:g1835170"
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                                                                                                                                                                                                                                                                                                                                                                              .ocation/Qualifiers
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/note="ORF1a"
                                                                                                          (bases 1 to 15528)
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FDHLESSSYAPFINAYRQAILSQYPQELQLEAINCKLLAVVAPALYHNYHLANLTGPA
TWVVPTVGQLHYYASSSIFASSVEVLAAIILLFACIPLVTRVYISFTRLMSPSRRTSS
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PQATLVTMGYWACVAALAVYSLMGLRVKVNVPWCVTPAHFLLLARSAGQSREQMLRVS
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LCCLFTPLSMRLCLFHLVCATVTGNVISLWFYITAAGTSYLSEWWFGGYPTMLFVPRF
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/translation-"MATFSATGFGGSFVRDWSLDLPDACEHGAGLCCEVDGSTLCAEC
FRGCEGMEQCPGLFMGLLKLASPVPVGHKFLIGWYRAAKVTGRYNFLELLQHPAFAQL
                                                                                                                                                                                         HIMRGSPQRAWHITTRSCKLKSYYVCDISEADWSCLPAGNYGGYNPPGDGACGYRCLA
                                                                                                                                                                                                                                          FMNGATVVSAGCSSDLWCDDELAYRVFQLSPTFTVTIPGGRVCPNAKYAMICDKQHWR
                                                                                                                                                                                                                                                                                                                                 PRPVPAPRVRPSANSSGDVKDPAPVPPVPKPRTKLATPNPTQAPIPAPRTRLQGASTQ
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TWTLKMMRSRFSWHCDVWYPLAVIACLLPIWPSLALLLSFAIGLIPSVGNNVVLTALL
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VWTRNNEVVVLTASHVVGRANMATLKIGDAMLTLTFKKNGDFAEAVTTQSELPGNWPQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LHFAQPTTGPASWCTATGDEEGLLSGEVCLAWTTSGDSGSAVVQGDAVVGVHTGSNTS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GLCHRTIDSIQGCTFPVVTLRLPTPQSLTRPRAVVAVTRASQELYIYDPFDQLSGLLF
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                                                                                                                                   DGFCWLKLLPPDRREAGLRLYYNHYREORTGWLSKTGLRLWLGDLGLGINASSGGLKF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          VSSANYVASMDHQCEGAACLALLEEEHYYRAVRWRPITGALSLVLNLLGQVGYVARST
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              YVLGKGSYEGLDQDKVLDLTNMLKVDPTELSSKDKAKARHVAHLLLDLANPVEAVNQ)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SVPTNALEATACYRAGCEAVIDGTNVIATIGPFPEQQPIPDIPKSVLDNCADISCD
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   KSLVLYTQHMLLCGLEGYFPEIAEKYLDGSLELRDMFKYVRVYIYSDDVVLTTPNQH)
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/note="ribosomal frameshift slippery sequence"
9824, .10507
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codon_start=1
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588 c
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                                           /protein_id="CaA69189.1"
/db_xref="PID:e255621"
/db_xref="PID:91835173"
/db_xref="GI:B35173"
/tb_xref="GI:B35173"
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VFANASCVQVVCSHTNSTTGLGQLSFSFVDEDLRLHIRPTLICWFALLLVHFLPMPRC
                                                                                                                                                                                                                                                                                                 /translation="MKIYGCISGLLEFVGLPCCWCTFYPCHAAEARNFTYISHGLGHV
HGHEGCRNFINVTHSAFLYLNPTAPATITHCLLLVLAAKMEHPNATIWLQLQPFGY
HVAGDVIVNLEEDKRHPYFKLLRAPALPLGFVAIVIVLLRLVRWAQRCYL"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LLRYDEHTALYNCSASKTCWYCTFLDEOIIFFGTDCDDTYAVPVAEVLEQAHGPYSAL
FDDMPPFIYYGREFGIVVLDVFMFYPVLVLFFLSVLPYATLILEMCVSILFIIYGIYS
GAYLAMGIFAATLAIHSIVVLROLLMLCLAMRYRCTLHASFISAEGKVYPVDPGLPVA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /translation="MLSMIVLLFLLWGAPSHAYFSYYTAQRFTDFTLCMLTDRGVIAN
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Submitted (02-NOV-1993) M. Lipinski, Lab. de Biologie des Tumeurs
Humaines, CNRS URA 1156, Inst. Gustave Roussy, 94805 Villeuif
Cedex, FRANCE
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Bukaryota; Metazoa; Chordata; Vertebrata; Mammalla; Butheria;
Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 1319)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Ouery Match 7.6%; Score 71.2; DB 17; Length 15528; Best Local Similarity 71.1%; Pred. No. 0.00016; Matches 108; Conservative 0; Mismatches 43; Indels 1;
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H.sapiens mRNA for vacuolar H+ ATPase E subunit.
X76228
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11901. .12389
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'protein_id="CAA69183.1"
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                                                                                                                                                                                                                                   /protein_id="CAA69182.1"
/db_xref="PID:e265622"
/db_xref="PID:g1835174"
/db_xref="GI:1835174"
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'db_xref="GI:1835175"
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/product="vacuolar H+ ArPase E subunit"
/product="vacuolar H+ ArPase E subunit"
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/db_xref="G1:q5643"
/db_xref="SWISS-PROT:P36543"
/db_xref="SWISS-PROT:P
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Eukaryota; Metazoa; Chordata; Vertebrata; Mammalia; Eutheria;
Eukaryota; Metazoa; Chordata; Vertebrata; Mammalia; Eutheria;
Sciurognathi; Muridae; Murinae; Rattus.
1 (bases 1 to 1934)
Enmark,E. and Gustafsson,J.A.
Enmark,E. and Gustafsson,J.A.
Oril ON ORPHAN RECEPPOR BELONGING TO THE NUCLEAR RECEPTOR FAMILY
PATENT: WO 9605300-A 1 22-FEB-1996;
KAROBIO AB (SE)
Other publication AU 3384495 960307.
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Baud'y., Mears,A.J., Lamour,V., Scamps,C., Duncan,A.M.,
McDermid,H.E. and Lipinski,M.
The E subunit of vacuolar H(+)-Arpase localizes close to the
centromere on human chromosome 22
Hum. Mol. Genet. 3 (2), 335-339 (1994)
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    1934
/organism="Rattus norvegicus"

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/cell_line="IARC-EW11"
/clone="61EW"
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1. 1319
Cycganism="Homo sapiens"
Ab_Arsef="taxon:9606"
/chromosome="22q11"
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AF061795.1 GI:3126873
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Matches 80; Conserv
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                                                                                                                                                                                                                                                                                                             A NOVEL HAEMOPOLETIN RECEPTOR AND GENETIC SEQUENCES ENCODING SAME PATENT: WO 9811225-A 19-MAR-1998; NICOLA NICOS ANTONY (AU)
                                                                      1824 GTIGGGAGACCACAGGCCCCCTCTTCTGCCCCTTTTATTAATAAAAATAAAA 1883
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2394 bp mRNA PRI 12-SEP-1998 dynamin-like protein Dymple isoform mRNA, complete
                                                   Gaps
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NicoLa,N.A., Fabri,L., Farley,A., Nash,A., Willson,T., Rakar, Shang,J., Alexander,W., Hilton,D.J., Kojima,T., Maeda,M. and Kikuchi,Y.
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          Length 1934;
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1larity 100.0%; Pred. No. 0.0019;
Conservative 0; Mismatches 0;
           DB 5;
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          Score 66.2; DB 5
Pred. No. 0.0016;
0; Mismatches 2:
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Sequence 18 from Patent W09811225.
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/db_xref="taxon:32644"
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          y Match 7.1%;
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/db_xref="PID:93126874"
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DFDEIRQEIENETERISGNNKGVSPEPIHLKIFSPNVVNLTLVDLPGMTKVPVGDQPK
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LMDAGTDAMDVLMGRVIPVKLGIIGVVNRSQLDINNKKSVTDSIRDEYAFLQKKYPSL
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QLITKFATEYCNTIEGTAKYIETSELGGARICYIFHETFGRTLESVDPLGGLNTIDI
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TORELLREFRHDAIVEVYTCLLEKRKLEYTNEWYHNLYAIELAYINTKHEPPEADAGCLM
NONIEEORRNRLARELEPSAASRDKVASGGGGVGDGOPETTGWRGMLKTSKAEELLA
EEKSKPIPIMPASPOKGHAVNLLDVPVPVARKLSAREORDCEVIERLIKSYFLIVRKN
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                                                                                                                                                                                                                                                                                                                                                                           Submitted (18-APR-1998) Graduate Institute of Biochemistry, No.100, Shih-Chuan 1st Road, Raohsiung, Taiwan, ROC 80708, Taiwan, ROC Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /note="large G-protein; dyn IV; expressed in heart, brain, placenta, lung, liver, skeletal muscle, kidney and pancreas; 37 amino acid in frame deletion"
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                                                                                                                    Hong Y.R., Chen,C.H., Cheng,D.S., Howng,S.L. and Chow,C.C. Human dynamin-like protein interacts with the glycogen synthase
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Homo sapiens
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Butheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 2394)
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Hong, Y.R., Chen, C.H., Cheng, D.S. and Chou, C.K.
Direct Submission
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76.9%; Pred. No. 0.0021;
tive 0; Mismatches 24;
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22. .2121
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ferential expression of four human dynamin-like protein variants
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                                                                                                                                                                                                                                     Direct Submission
Submitted (14-MAY-1999) Graduate Institute of Biochem Kaohsiung
Medical College, No. 100, Shih-Chuan 1st Road, Kaohsiung 80708,
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 2472)
                                                                        Chen, C.H., Hwang, S.L., Howng, S.L., Liao, C.H., Chou, C.K. and
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protein_id="AAD39541.1"
db_xref="PID:95081794"
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/db_xref="taxon:9606"
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Hong, Y.R. and Chen, C.H.
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Gaps .; 0 Length 2472; Indels Query Match 7.0%; Score 65.6; DB 42; Best Local Similarity 76.9%; Pred. No. 0.0021; Matches 80; Conservative 0; Mismatches 24;

822

835 attgcagggcctcccaacaatctctttaaataaataaaggagttgttcaggtaaaaaaa 894

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Search completed: September 28, 1999, 16:39:42 Job time: 6969 sec

Sequence encoding Mus musculus Tub I

Q83532 V11858

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44 45

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GenCore version 4.5
Copyright (c) 1993 - 1998 Compugen Ltd.
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OM nucleic - nucleic search, using sw model

September 28, 1999, 16:45:17; Search time 303.81 Seconds (without alignments) 772.457 Million cell updates/sec Run on:

Title: Perfect score: Sequence:

IDENTITY_NUC Scoring table: 311585 segs, 125096042 residues Searched:

N_Geneseq_36:*

Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Description		haemopoiet1	Unspliced murine N	Nucleotide sequenc	ectide seguen	Novel haemopoietin	Novel haemopoietin	Nucleotide sequenc	cDNA encoding rat	Nucleotide sequenc.	cDNA encoding an a	Nucleotide sequenc	cDNA encoding huma	Expressed sequence	Equine arteritis v	e c	ά	9 Fi	Nucleotide sequenc	ò		ŭ	Ĕ	ć ń	\mathbf{z}	ğ	Ä	ij	Human foetal brain		n PKR gene	ň	าลก	par	Asparaginylendopep	Asparaginylendopep	uman	lacer	ii	Human tumour antig	r cathepsin Υ	o acid in	to acid inve	Placenta-specific
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Example 8: Page 99-100; 182pp; English.
NR6 is a novel haemopoletin receptor (HR). Interaction between the novel HR and a ligand facilitates proliferation, differentiation and survival of a wide variety of cells. The HR and it's derivatives can be used for modulating the activity of the receptors e.g. to regulate development, maintenance or regeneration in an array of different cells and tissues in
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Unspliced murine NR6 nucleotide sequence.
Haemopoletin receptor; cell proliferation; cell survival; therapeutic; neuronal proliferation; drug screenin Mouse.
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A, Nicola NA, F
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W09811225-A2.

W09811225-A2.

11-SEP-1997; G02479.

11-SEP-1996; AU-002246.

(AMRA-) AMRAD OPERATIONS PTY LTD.
(ADRA-) DZIEGLEWSKA H E.

Alexander W, Fabri L, Farley A, Hil
KOjima T, Maeda M, Nash A, Nicola N
Zhang J; W8-260970/23.

New isolated haemopoietin receptor
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                                                                           ggcaccgtttacttcgtccaagtgcgttgtaacccattcgggatctatgggtcgaaaaag
vitro and in vivo. They can be present in therapeutics used for modulating neuronal proliferation, differentiation and survival. products can also be used for detection and diagnosis, e.g. for or predisposition to cancers, or for drug screening. sequence 1930 Bp; 375 A; 623 C; 561 G; 371 T;
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                                         94.7%; Scc..
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11463 GAGCCCCAGGITITACTGCATCATCAAGTTGCTGAAGGGTCCAGGCTTAATGTGGCCCTCT 11522
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                                                                                                                                                                                                                                                                                                                                                                                                                                                         The virtue of the control of the control of the control of the control of the control of a novel Haemopoletin receptor (HR). Interaction the NR6 protein is a novel Haemopoletin receptor (HR). Interaction, differentiation and survival of a wide variety of cells. The HR and it's derivatives can be used for modulating the activity of the receptors e.g. to requiate development, maintenance or regeneration in an array of different cells and tissues in vitro and in vivo. They can be present in therapeutics used for modulating neuronal proliferation, differentiation and survival. The products can also be used for detection and diagnosis, e.g. for cancers or predisposition to cancers, or for drug screening.
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                                                                                                                           cancer;
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Nucleotide sequence for murine NR6 containing additional 5N sequence.
Haemopoietin receptor; cell proliferation; cell differentiation; cancer cell survival; therapeutic; neuronal proliferation; drug screening; ss;
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                                                                                                                                                                                                                                                                                                                                                                                                                   New isolated haemopoletin receptor - used for developing products for modulating proliferation, differentiation and survival of cells, e.g. neuronal cells
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(AMRA-) AMRAD OPERATIONS PTY LTD.
(DZIE/) DZIEGLEWH H E
Alexander W, Fabri L, Farley A, Hilton DJ, Kikuchi Y,
Kojima T, Maeda M, Nash A, Nicola NA, Rakar S, Willson T,
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Pred. No. 7.3e-132;
0; Mismatches 27;
V27148

V27148 standard; DNA; 11832 BP V27148; DT 29-5EP-1998 (first entry)

DE Nucleotide sequence for murine RW Haemopotetin receptor; cell provided is used for mouse.

Nus Sp. 10-18 of 198.

PP 19-1896; A0-002246.

PR 11-5EP-1996; A0-002246.

PR 11-5EP-1997.

PR AMRA-) AMRAD OPERATIONS PTY L'ARANA-) AMRAD OPERATIONS COLOUR DE
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Best Local Similarity 96.3%;
Matches 778; Conservative
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New isolated haemopoletin receptor - used for developing products

Tor modulating proliferation, differentiation and survival of cells,

For modulating proliferation, differentiation and survival of cells,

Tor modulating proliferation, differentiation and survival of cells,

Claim 8; Page 108-114; 182pp; English.

Chetween the novel HR and a ligand facilitates proliferation,

differentiation and survival of a wide wariety of cells. The HR and it's

Chetween the novel HR and a ligand facilitates proliferation,

Chetween the novel HR and a ligand facilitates proliferation in an array of

Chetweent cells and tissues in vitro and in vivo. They can be present in

Chermeter cells and tissues in vitro and in vivo. They can be present in

Chermeter cells and tissues in vitro and in vivo. They can be present in

Chermeter cells and tissues in vitro and in vivo. They can be present in

Chermeter cells and tissues and sho be used for detection and diagnosis,

and survival. The products can also be used for drug screening.

Sequence 6663 BP; 1462 A; 1852 C; 1715 G; 1634 T;
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11583 GACCTGGAGGCTCACCTGAATTGGAGCCCCTCTGTACC-ATCTGGGCAACAAAGAAACCT
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                                                                                                                                         gacctggaggctcacctgaattggagccctctgtacctatctgggcaacaaagaaacct
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(AMRA-) AMRAD OPERATIONS PIY LTD.
(DZIE/) DZIEGLEWSKA H E.
Alexander W, Fabri L, Farley A, Hilton DJ, Kikuchi Y,
KOJIMA T, Maeda M, Nash A, Nicola NA, Rakar S, Willson T,
Zhang J;
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/*tag= a
/product= "Murine NR6"
/note= "No start or stop codon given"
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Nucleotide sequence of Murine NR6.
Haemopoietin receptor; cell proliferation; ce cancer; cell survival; therapeutic; neuronal
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113. 1355.
/*tag- a /
/product- "Haemopoletin receptor NR6.1"
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V27140;
29-SEP-1998 (first entry)
Novel hemopoietin receptor NR6.1 gene.
Haemopoietin receptor; cell proliferation; cell difficell survival; therapeutic; neuronal proliferation;
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11-SEP-1997; G02479
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New isolated haemopoietin receptor - used for developing products

Tor modulating proliferation, differentiation and survival of cells,

Tor modulating proliferation, differentiation and survival of cells,

Tor modulating proliferation, differentiation and survival of cells,

Claim 4; Page 77-81; 182pp; English.

Claim 50 person of the novel HR NRG.

Claim 4; Page 77-81; 182pp; English.

Claim 5; Page 77-81; 182pp; English.

Claim 6; Page 77-81; 182pp; English.

Claim 7; Page 77-81; 182pp; English.

Claim 7; Page 77-81; 182pp; English.

Claim 7; Page 77-81pp; English.

Claim 7; Page 77-81pp; Eng
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proliferation; cell differentiation; cancer;
neuronal proliferation; drug screening; ss;
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11-SEP-1997; G02479.
11-SEP-1996; AU-002246.
6AMRA-) AMRAD OPERATIONS FTY LTD.
(D2.1E/) D21EGLEWSKA H E.
Alexander W, Fabri L, Farley A, Hilton DJ, Kikuchi Y,
Kojlma T, Maeda M, Nash A, Nicola NA, Rakar S, Willson
L, Farley A, Hilton DJ, Kikuchi Y,
Nash A, Nicola NA, Rakar S, Willson
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1..1278
½-tag= /
/product= "Haemopoietin receptor NR6.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               32.5%; Score 305; DB 1; 1
100.0%; Pred. No. 8.6e-50;
tive 0; Mismatches 0;
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Alexander W, Fabri
Kojima T, Maeda M,
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Best Local Similarity
Matches 305; Conserv
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17-MAR-1999
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                                                    e.g. neuronal cells
Claim 5; Page 84-87; 182pp; English.
The haemopoletin receptor (HR) NR6.2 is a form of the novel HR NR6.
Interaction between the novel HR and a liqand facilitates proliferation, differentiation and survival of a wide variety of cells. The HR and it's derivatives can be used for modulating the activity of the receptors e.g. to regulate development, maintenance or regeneration in an array of different cells and tissues in vitro and in vivo. They can be present in therapeutics used for modulating neuronal proliferation, differentiation and survival. The products can also be used for detection and diagnosis, e.g. for cancers or predisposition to cancers, or for drug screening.
Sequence 1673 BP; 344 A; 550 C; 474 G; 305 T;
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WPI; 98-260970/23.
P-PSDB; W55012.
New isolated haemopoletin receptor - used for developing products for modulating proliferation, differentiation and survival of cells,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Murine, U4 protein; haematopoietin receptor superfamily; cell proliferation; immune response; antibody; cell differentiation; autoimmune disease; cancer; allergy; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    New nucleic acid encoding U4 haematopoietin receptor superfamily chain - potentially useful, e.g. for modulating cell proliferation or immune response, for treating cancer and auto:immune disease Claim 1; Pages 25-26; 38pp; English.
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                                                                                                                                                                                                                                                          Length 1673;
                                                                                                                                                                                                                                                       32.4%; Score 304; DB 1; Length 16
100.0%; Pred. No. 1.3e-49;
tive 0; Mismatches 0; Indels
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16-JAN-1997; US-784863.
(GEMY ) GENETICS INST INC.
COLILAS M, DOMALGSON DD, Neben T, Whitters M;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               V41688 standard; cDNA; 1656 BP.
V41688;
26-cCT-1998 (first entry)
Nucleoride sequence of the murine U4 gene.
Murine; U4 protein; haematopoletin recepto
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Location/Qualifiers
122. .1399
/*tag= a
/product= "U4 protein"
                                                                                                                                                                                                                                                    Query Match
Best Local Similarity 100.
Matches 304; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WPI; 98-414109/35.
P-PSDB; W59804.
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This is the nucleotide sequence encoding the murine U4 protein from the haematopoletin receptor superfamily, used in the method of the invention for the immune response. Transformed mammalian cells are used to produce recombinant U4 protein. The U4 protein is used to screen for specific binding agents, raise antibodies. It is also used as reagents for assays and as issue markers for isolation of cognate ligands and receptors, and in pharmaceutical compositions which may modulate cell proliferation, cell differentiation, and the immune system (e.g. for treating immune deficiency, inherited or the result of infection, autoimmune diseases, sequence 1656 BP; 318 A; 552 C; 478 G; 308 T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1040 GGCACCGITTACITCGTCCAAGTGCGTTGTAACCCATTCGGGATCTATGGGTCGAAAAAG 1099
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1100 GCGGGAATCTGGAGCGAGTGGAGCCACCCCACCGCTGCCTCCACCCCTCGAAGTGAGCGC 1159
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1160 cc666cc66Gc6Gc6GGGGTGCGAGCCGCGGGGCGGCGAGCCCAGCTCGGGCCCGGTG 1219
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 ggcaccgtttacttcgtccaagtgcgttgtaacccattcgggatctatgggtcgaaaag
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              cDNA encoding rat Zcytor5.
Zcytor5; cytokinin-like receptor; down-regulation; growth factor; maintenance factor; thyroid; heart; skeletal muscle; cardiotrophicardiac pathology; heart enlargement; Zcytor5 ligand; ss.
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                                                                                                                                                                                                                                                                                                                                                                                                       32.4%; Score 304; DB 1; Length 1656;
100.0%; Pred. No. 1.3e-49;
ive 0; Mismatches 0; Indels (
                                                                                                                                                                                                                                                                                                                                                                                                                                                      Indels
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Disclosure; Page 72-75; 55pp; English.
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159. .1436
/*tag= a
/product= Zcytor5
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Adams RL, Foster DC, Gilbert T,
Lok S, Presnell SR, Whitmore TE;
WPI: 99-034662/03.
P-PSDB; W70862.
                                                                                                                                                                                                                                                                                                                 318 A;
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Best Local Similarity 100.0
Matches 304; Conservative
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13-FEB-1998; US-023890.
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01-MAY-1997; US-045287
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New isolated haemopoietin receptor - used for developing products for modulating proliferation, differentiation and survival of cells, e.g. neuronal cells claim 7; Page 102-104; 182pp; English.
The NR6 gene encodes a novel Haemopoietin receptor (HR). Interaction
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ccgggcccgggcggcgggtgtgcgagccgcggggcggcgagcccagctcgggcccggtg 180
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  gogggaatctggagcgagtggagccaccccaccgctgcctccaccctcgaagtgagcgc 120
The present sequence encodes a protein designated Zcytor5, which is a cytokinin-like receptor. Soluble Zcytor5 may be administered to down-regulate the effects of a growth and/or maintenance factor in thyroid, heart, and skeletal muscle for example to lessen the effect of cardiotrophin-1 on cardiac pathologies, so preventing heart enlargement. Zcytor5 could be used to detect cardiotrophin-1 in the blood, and to discover other possible Zcytor5 ligands. A probe comprising Zcytor5 DNA or RNA can be used to determine the presence and integrity of the Zcytor5 gene on chromosome 19. Antibodies and therapeutically to modify Zcytor5 ligand effects. Sequence 1724 BP; SSO C; SSO G; SSO T;
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Nucleotide sequence of clone HFK-66 encoding human NR6.
Haemopoletin receptor; cell proliferation; cell differentiation; cell survival; therapeutic; neuronal proliferation; drug screenir
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                                                                                                                                                                                                                                                                                                                                                                                                                                Length 1724;
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(DZIE/) DZIEGLEWSKA H E.
Alexander W. Pebri L. Farley A, Hilton DJ, Kikuchi Y,
Kojima T. Maeda M, Nash A, Nicola NA, Rakar S, Willson
                                                                                                                                                                                                                                                                                                                                                                                                                                       DB 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                Score 297.6; DB 1
Pred. No. 2.2e-48;
0; Mismatches 4
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1. .1053
/*tag= a
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98.78;
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V27144;
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11-SEP-1996; AU-002246.
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Best Local (
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between the novel HR and a ligand facilitates proliferation, differentiation and survival of a wide variety of cells. The HR and it's derivatives can be used for modulating the activity of the receptors e.g. to requiate development, maintenance or regeneration in an array of different cells and tissues in vitro and in vivo. They can be present in therapeutics used for modulating neuronal proliferation, differentiation and survival. The products can also be used for detection and diagnosis, e.g. for cancers or predisposition to cancers, or for drug screening. Sequence 1391 BP; 281 A; 459 C; 417 G; 234 T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                cDNA encoding an allelic varaint of human Zcytor5.
Zcytor5, cytokinin-like receptor; down-regulation; growth factor;
maintenance factor; thyroid; heart; skeletal muscle; cardiotrophin-l;
cardiac pathology; heart enlargement; Zcytor5 ligand; allelic varaint;
                                                                                                                                                                                                                                                                                                                                                                                                        180
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Disclosure; Page 68-70; 55pp; English.
The present sequence encodes an allelic varaint of protein designated
Zcytor5, which is a cytokinin-like receptor. Soluble Zcytor5 may be
                                                                                                                                                                                                                                                                                                                                   61 gogggaatetggagegagtggageeacceaccgetgeetceaccetegaagtgagege 120
                                                                                                                                                                                                                                                                                                                                                                                                                                           861
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                                                                                                                                                                                                                                                                                                    682 GGCACCGTGTACTTCGTGCAAGTGCGCTGCAACCCCTTTGGCATCTATGGCTCCAAGAAA
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                                                                                                                                                                                           Length 1391;
                                                                                                                                                                                                                              Indels
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01-MAY-1998; U08865.
13-FEB-1998; US-074721.
01-MAY-1997; US-045287.
01-MAY-1997; US-0850030.
13-FEB-1998; US-023890.
(ZXMO) ZXMOGENETICS INC.
Adams RL, Foster DC, Glibert T, Jelmberg AC, Lehner JM, Lok S, Presenl SR, Whitmore TE;
WPI: 99-034662/03.
                                                                                                                                                                               red. No. 2.4e-39;
0; Mismatches 42:
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/product= Zcytor5
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                                                                                                                                                                                          26.6%;
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                                                                                                                                                                                           Query Match 26.6
Best Local Similarity 86.8
Matches 275; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      301 caggtaggaaagttggg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       982 CAGCACAGGACGAGGGG
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V70895
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administered to down-regulate the effects of a growth and/or maintenance factor in thyroid, heart, and skeletal muscle for example to lessen the effect of cardiotrophin-1 on cardiac pathologies, so preventing heart enlargement. Zcytor5 could be used to detect cardiotrophin-1 in the blood, and to discover other possible Zcytor5 ligands. A probe and integrity of the Zcytor5 gene on chronsome 19. Antibodies and the anti-idiotypic antibody could be used to purify Zcytor5 and therapeutically to modify Zcytor5 ligand effects. Sequence 1813 BP; 415 A; 604 C; 519 G; 275 T;
                                                                                                                                                                                                                                                                                                                                                     994 GCCACCGTGTACTICGTGCAAGTGCGCTGCAACCCCTTTGGCATCTATGGCTCCAAGAAA 1053
                                                                                                                                                                                                                                                                                                                                                                                                                            New nucleic acid encoding U4 haematopoietin receptor superfamily chain - potentially useful, e.g. for modulating cell proliferation or immune response, for treating cancer and auto:immune disease Claim 1; Page 28; 38pp; English.

This is the nucleotide sequence encoding the human U4 protein from the haematopoietin receptor superfamily, used in the method of the invention for the modulation of cell proliferation, or the immune response. Transformed mammalian cells are used to produce recombinant U4 protein. The U4 protein is used to screen for specific binding agents, raise antibodies. It is also used as reagents for assays and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1234 AGCTICCGCCTCTACGACCAGTGGCGAGCCTGGATGCAGAAGTCGCACAAGACCCGCAAC 1293
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                                                                                                                                                                                                                                                                                     ggcaccgtttacttcgtccaagtgcgttgtaacccattcgggatctatgggtcgaaaaag 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human; U4 protein; haematopoietin receptor superfamily; cell proliferation; immune response; antibody; cell differentiation; autoimmune disease; cancer; allergy; ds.
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                                                                                                                                                                                                                   Length 1813;
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                                                                                                                                                                                                                26.6%; Score 249.8; DB 1;
86.8%; Pred. No. 2.5e-39;
ive 0; Mismatches 42;
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16-JAN-1997; US-784863.
(GEMY ) GENETICS INST INC.
WPI; 98-414109/35.
P-PSDB; W59805.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1. .1228
/*tag= a
/product= "U4 protein"
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Nucleotide sequence of the human U4
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Best Local Similarity 86.8
Matches 275; Conservative
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1049 CGGCGCGAGCTCAAGCAGTTCCTGGGCTGAAGAAGCACGCGTACTGCTCCAACCTC 1108
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as tissue markers for isolation of cognate ligands and receptors, and in pharmaceutical compositions which may modulate cell proliferation, cell differentiation, and the immune system (e.g. for treating immune defliciency; inherited or the result of infection, autoimmune diseases, cancer, and allergy). 304 A; 535 C; 473 G; 267 T;
                                                                                                                                                                                                                                                                           gogggaatctggagcgagtggagccacccaccgctgctccaccctcgaagtgagcgc 120
                                                                                                                                                                                                                                                                                                                                                cggcgcgagctcaagcagttcctcggctggctcaagaagcacgcatactgctcgaacctt 240
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                                                                                                                                                                                                                                       869 GCCACCGTGTACTTCGTGCAAGTGCGCTGCAACCCCTTTGGCATCTATGGCTCCAAGAAA 928
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17-MAR-1999 (first entry)
CDNA encoding human Zcytor5.
Zcytor5; cytokinin-like receptor; down-regulation; growth factor; maintenance factor; thyroid; heart; skeletal muscle; cardiotrophin-l; eardiac pathology; heart enlargement; Zcytor5 ligand; ss.
                                                                                                                                                                            Gaps
                                                                                                                                                                                                         ggcaccgtttacttcgtccaagtgcgttgtaacccattcgggatctatgggtcgaaaag 60
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down-regulating Zcytor5 natural ligands or detecting cardiotrophin-1
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The present sequence encodes a protein designated Zcytor5, which is a cytokinin-like receptor. Soluble Zcytor5 may be administered to down-regulate the effects of a growth and/or maintenance factor in thyroid, heart, and skeletal muscle for example to lessen the effect of cardiotrophin-1 on cardiac pathologies, so preventing heart enlargement. Zcytor5 could be used to detect cardiotrophin-1 in the
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                                                                                                                                            Length 1579;
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01-MAY-1997; US-045287.
01-MAY-1997; US-850030.
13-FEB-1998; US-023890.
(ZYMO ) ZYMCGENETICS INC.
Adams RL, Foster DC, Gilbert T, Jelmberg AC, Lehner Cok S, Presnell SR, Whitmore TE;
P-PSDB; W70860.
                                                                                                                                     Score 249.6; DB 1;
Pred. No. 2.7e-39;
0; Mismatches 34;
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                                                                                                                                       26.6%;
88.8%;
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/*tag= a
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Best Local Similarity 88.8
Matches 270; Conservative
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Gaps

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32; Indels

Score 92.8; DB 1; Pred. No. 1.1e-09; 0; Mismatches 32;

9.9%;

Length 259

46 T;

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therapeutically to modify 2cytor5 ligand effects. Sequence 259 BP; 53 A; 64 C; 81 G;
                                                                                                  Query Match
Best Local Similarity 76.8
Matches 106; Conservative
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Matches 108
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V09039
ID V09039
AC V09039
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V09036
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blood, and to discover other possible Zcytor5 ligands. A probe comprising Zcytor5 DNA or RNA can be used to determine the presence and integrity of the Zcytor5 gene on chromosome 19. Antibodies and the anti-idiotypic antibody could be used to purify Zcytor5 and therapeutically to modify Zcytor5 ligand effects. Sequence 1690 BP; 319 A; 592 C; 505 G; 274 T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         961 GCCACCGTGTACTTCGTGCAAGTGCGCTGCAACCCCTTTGGCATCTATGGCTCCAAGAAA 1020
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Expressed sequence tag used to identify human Zcytor5.
Zcytor5: cytokinin-like receptor; down-regulation; growth factor; maintenance factor; thyroid; heart; skeletal muscle; cardiotrophin-l; cardiac pathology; heart enlargement; Zcytor5 ligand; EST; SS. Unidentified.
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                                                                                                                                                                                                       Length 1690;
                                                                                                                                                                                                                                                          34; Indels
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                                                                                                                                                                                                     26.6%; Score 249.6; DB 388.8%; Pred. No. 2.7e-39; tive 0; Mismatches 34
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US-045287.
US-850030.
US-023890.
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01-MAY-1998; U08865.
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Best Local Similarity
Matches 270; Conserv
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arteritis virus - ....

T arteritis virus - ....

T useful therapeutically

Claim 1; pages 15-19; 36pp; English.

Claim 1; pages 15-19; 36pp; English.

CC The sequence 1s that of at least part of the RNA genome of the equine

CC The sequence 1s that of a least part of a recombinant

CC DAN vector comprising a DNA sequence complementary to part of

CC adjacent to its 3'-end a non-EAV specific promoter for a non-EAV

CC adjacent to its 3'-end a non-EAV specific promoter for a non-EAV

CC specific RNA polymerase. The RNA and the vector can be used to

CC specific and for therapeutic use. The vector can be

CC make viral particles and for therapeutic use. The vector can be

CC stably incorporated into host cells and produces infectious RNA.

12827 BP; 2831 A; 3258 C; 3295 G; 3443 T;
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12-JUL-1997: NLO408.
12-JUL-1996: NL-003579.
(UVLE-) RIJKSUNY LETDEN.
Bredenbeek PJ. Wassenaar ALM;
Van Dinten LC, Wassenaar ALM;
Van 110596/LO.
Recombinant DNA vector that produces infectious RNA of equine arteritis virus - and derived RNA, host cells and virus particles,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             catgatggtcacacttggatataccccagtgtgg-gtaaggttggggtattgcagggcct
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therapy; ss.
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Pred. No. 2.2e-05;
0; Mismatches 43;
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22-JAN-1998.
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21-JUL-1998 (first entry)
Equine arterilis virus expression vector pEAV030.
equine arteritis; genome; EAV; detection; therapy; cyclic; circular;
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                                                                                                                                                                                                                                                                                                                              "synthetic sequence with unique XhoI site"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The sequence is that of of a recombinant DNA vector, pEAV030, comprising a DNA sequence complementary to part of the genome of equine arteritis virus (EAN) which has adjacent to its 3 -end a non-EAV specific promoter for a non-EAV specific RNA polymerase. It can be used to make viral particles and for therapeutic use. The vector can be stably incorporated into host cells and produces infectious RNA. 3972 G; 4123 T; sequence 15528 BP;
                                                                                                                                                                                                                                                      "Bacteriophage T7 promoter sequence"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              UYLE-) RIJKSUNIV LEIDEN.
Gredenbeek PJ, Den Boon JA, Snijder EJ, Spaan WJM, '
an Dinten LC, Wassenaar ALM;
PI; 98-110596/10.
                                                                                                                                                                                                                                                                                                                                                                                                          "pUC18 vector sequence"
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; Pages 21-24; 36pp; English.
                                                                                                                                                                                Location/Qualifiers
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1; Gaps Score 71.2; DB 1; Length 15528; Pred. No. 2.2e-05; 0; Mismatches 43; Indels 1; 43; Indels 7.6%; 71.1%; Ouery Match Best Local Similarity 71.1 Matches 108; Conservative

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12635 CAGGGCCGTAAGACGTGGATATTCTCCTGTGTGGCGTCATGTTGAAGTAGTTATTAGCCA 12694 788 catgatggtcacacttggatataccccagtgtgg-gtaaggttgggggtattgcagggcct 846 a a

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Search completed: September 28, 1999, 16:45:44 Job time: 7329 sec

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September 28, 1999, 16:39:36; Search time 152.56 Seconds (without alignments) 563.664 Million cell updates/sec
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/cgn2_6/ptodata/2/ina/PCTUS9_COMB.seq:*
/cgn2_6/ptodata/2/ina/PCTUS9_COMB.seq:*
GenCore version 4.5
Copyright (c) 1993 - 1998 Compugen Ltd
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TYPE: nucleic acid
STRANDEDNESS: single
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MEDIUM TYPE: Floppy
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Pred. No. 8.5e-06;
                                                                                                                               APPLICANT: Takeshita, Sunao
APPLICANT: Okazaki, Makoto
APPLICANT: Kawai, Shinji
APPLICANT: Tsujimura, Atsushi
APPLICANT: Amann, Egon
TITLE OF INVENTION: Bone-Related Cadherin-Like Protein and
TITLE OF SEQUENCES: 12
CORRESPONDENCE: 12
                                                                                                                                                                                                                                                                                                 ADDRESSEE: Finnegan, Henderson, Farabow, Garrett & ADDRESSEE: Dunner
STREET: 1300 I Street, N.W.
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     02481.1323-00000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STRAIN: osteoblastic cell line MC3T3E1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/738,349
FILING DATE: 25-0CT-1996
CLASSIFICATION 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/364,439
FILING DATE: 26-AUG-1993
ATTORNEY/AGENT INFORMATION:
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                                                                                      Sequence 1, Application US/08738349
Patent No. 5869638
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NAME: Barker, M. P.
REGISTRATION NUMBER: 32,013
REFRENCE/DOCKET NUMBER: 0248:
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-408-4000
TELEFAX: 202-408-4400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 3581 base pairs
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ilarity 82.0%;
Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NAME/KEY: CDS
LOCATION: 284..2671
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity <sup>f</sup>
Treater 73; Conservat
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                                                                                                                                                                                                                                                                                                                                                                                                          20005-3315
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MOLECULE TYPE: c
ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                     COUNTRY: D.C.
                                                       RESULT 2
US-08-738-349-1
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GENERAL INFORMATION:
APPLICANT: Gaynor, Richard B
APPLICANT: Wu, Foon W.
APPLICANT: Wu, Foon W.
TITLE OF INVENTION: Cellular Nucleic Acid Binding Protein
TITLE OF INVENTION: and Uses Thereof in regulating Gene Expression and in the
TITLE OF INVENTION: Treatment of AIDS
NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
ADDRESSEE: Arnold, White & Durkee
STREET: P.O. Box 4433
CITY: Houston
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
CORFATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Version #1.25
CURREMY APPLICATION DATA:
APPLICATION NUMBER: US/08/242,677
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 63.2; DB 2;
Pred. No. 1.1e-05;
^. wismatches 13;
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APPLICANT: Sonenberg, Nahum
APPLICANT: Katze, Michael G.
APPLICANT: Roy, Sophie
APPLICANT: Koromilas, Antonis E.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 1, Application US/08143219
Patent No. 5670330
RESULT 3
US-08-242-677-1
Sequence 1, Application US/08242677
; Patent No. 5677143
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ATTORNEY/AGENT INFORMATION:
NAME: Mayfield, Denise L.
REGISTRATION NUMBER: 33,732
REFRENCE/DOCKET NUMBER: UTSD
TELECOMMUNICATION INFORMATION:
TELEPHONE: 713-787-1400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity 84.5%;
Matches 71; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELEFAX: 713-789-2679
INFORMATION FOR SEO ID NO: 1:
SEQUENCE CHARACTERISTICS:
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us-09-037-657-16.rni

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SSEE: Howell & Haferkamp, L.C.
7733 Forsyth Blvd., Suite 1400
St. Louis
                                                                                                                                                                         MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 2, Application US/08467607
                                                                                                                                                                                                                                                                                                                                 ATTORNEY/AGENT INFORMATION:
NAME: Henderson, Melodie W.
REGISTRATION NUMBER: 37,848
                                                                                                                                                                                                                                                                                                                                                                                                  REFERENCE/DOCKET NUMBER: 6C
TELECOMMUNICATION INFORMATION:
TELEPHONE: 314-727-5188
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              800 F. Gateway Blvd
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ; MOLECULE TYPE: DNA (genomic)
US-08-520-678A-30
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LENGTH: 270 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   161 AAAAAAAAAAAAA 146
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELEFAX: 314-727-6092
                                                                                                                                               COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      JAY S.
            CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ZIP: 94080
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               nucleic acid
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Best Local Similarity
Matches 67; Conserva
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             linear
                                                                                                                                                                                                                                                                                                                      CLASSIFICATION:
                                                                                                           COUNTRY: US
                                                                                                                                                                                                                                                                                                                                                                                                                                           TELEPHONE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Rice, Charles M.
APPLICANT: Kolykhalov, Alexander A.
TITLE OF INVENTION: NOVEL 3' TERMINAL SEQUENCE OF HEPATITIS
TITLE OF INVENTION: C VIRUS GENOME AND DIAGNOSTIC AND THERAPEUTIC USES THEREOF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ö
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Pred. No. 1.2e-05;
0; Mismatches 9; Indels 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Indels
PPLICANT: Barber, Glen N.
(TLE OF INVENTION: TUMOR-CELL ASSAY METHOD AND KIT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ORIGINAL SOURCE:
INDIVIDUAL ISOLATE: HUMAN PKR GENE, FIGURE 5
                                                                                                                                                                                                                                                                                                                                                                                      PRIOR APPLICATION DATA:
PRIOR APPLICATION DATA: including application
PRIOR APPLICATION DATA: including application
PRIOR APPLICATION DATA: described below:
FILING DATE: 08/141,244
FILING DATE: 0ctober 22, 1993
APPLICATION WUMBER: 07/953,681
FILING DATE: September 29, 1992
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                 SYSTEM: PC-DOS (Version 5.0)
WordPerfect (Version 5.1)
                                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER: US/08/143,219
FILING DATE: October 25, 1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         REGISTRATION NUMBER: 22,798
REFERENCE/DOCKET NUMBER: 204/139
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Application US/08520678A
                                                                                  ADDRESSEE: Lyon & Lyon
STREET: 611 West Sixth Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELEPHONE: (213) 489-1600
TELEFAX: (213) 955-0440
TELES: 67-3510
INFORMATION FOR SEQ ID NO: 1:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match 6.7%;
Best Local Similarity 88.3%;
Matches 68; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE CHARACTERISTICS:
LENGTH: 2628 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                922 aaaaaaaaaaaaaaa 938
                                                                                                                                                                                                                                                                                                     CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Douglas E. Olson
                                                             DRRESPONDENCE ADDRESS
                                                                                                                                                                                                      COMPUTER READABLE FORM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NUMBER OF SEQUENCES:
                                                                                                                        Los Angeles
CA
                                                                                                                                                                                                                                          COMPUTER: IBM COMPOPERATING SYSTEM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                     CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      JS-08-520-678A-30/c
                                                                              ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NAME/KEY:
                                                                                                                                                                COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Patent No.
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6.6%; Score 61.6; DB 4; Length 270;
88.2%; Pred. No. 9.7e-06;
tive 0; Mismatches 9; Indels
SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA: APPLICATION NUMBER: US/08/520,678A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: TATSUNO, GWEN
APPLICANT: ANDERSON, JOHN
APPLICANT: CHRYSLER, SUSANNA
TITLE OF INVENTION: NOVEL CATHEPSIN AND I
TITLE OF INVENTION: COMPOSITIONS FOR INH
NUMBER OF SEQUENCES: 20
CORRESPONDENCE ADDRESS:
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1373 TCMCCATICITAITICACYTTAGRAICMAGGGIGGGRGRGRGRGGGGAGGGAATIGICART 1432
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 1558;
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APPLICANT: SEMKO, CHRISTOPHER M.F.
TITLE OF INVENTION: NOVEL CATHEPSIN AND METHODS AND
TITLE OF INVENTION: COMPOSITIONS FOR INHIBITION THEREOF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compartible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/469,362
FILING DATE: 06-JUN-1995
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEE: ATHENA NEUROSCIENCES: 800 F. Gateway Blvd.
South San Francisco
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 2, Application US/08850392
Patent No. 5858982
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TUNG, JAY S.
SINHA, SUKANTO
                                                                       1558 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NAME: DUVALL, JEAN M. REGISTRATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER READABLE FORM:
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CORRESPONDENCE ADDRESS:
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                                                                                              nucleic acid
                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity
Matches 86; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ZIP: 94080
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US-08-469-362-2
                                                                                                                                                                                                          NAME/KEY:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               784 tecacatgatggtcacaettggatataceceagtgtgggtaaggttgggggtattgeaggg 843
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
6.5%; Score 61.4; DB 3; Length 1558;
Best Local Similarity 55.5%; Pred. No. 1.8e-05;
Matches 86; Conservative 13; Mismatches 56; Indels 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: TUNG, JAY S.
APPLICANT: SINHA, SUKANTO
APPLICANT: SINHA, LISA
APPLICANT: SEMKO, LISA
APPLICANT: SEMKO, CHRISTOPHER M.F.
TITLE OF INVENTION: NOVEL CAPHEPSIN AND METHODS AND
TITLE OF INVENTION: COMPOSITIONS FOR INHIBITION THEREOF
NUMBER OF SEQUENCES: 20
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1493 AAAAAAAAAAAAAAAGAAAAAAAAAAAAAAAAAA 1527
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          904 аааааааааааааааааааааааааааааа 938
FILING DATE: 06-UN-1995
CLASSIFICATION: 435
TTONEY_AGENT INFORMATION:
NAME: DUVALL, JEAN M.
REGISTRATION NUMBER: 32,731
REFERENCE/DOCKET NUMBER: 002010-007
TELEPHONE: (415) 877-0900
TELEPHONE: (415) 877-0900
TELEPHONE: (415) 877-0900
TELEPHONE: (415) 877-0900
STELEPHONE: (415) 877-0900
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER: US/08/469,362 FILING DATE: 06-JUN-1995 CLASSIFICATION: 514
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ADDRESSEE: ATHENA NEUROSCIENCES
STREET: 800 F. Gateway Blvd.
SITY: South San Francisco
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 2, Application US/08469362
Patent No. 5849711
GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                        nucleic acid
EDNESS: single
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LOCATION:
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                                                                                                                                                                                                                                                                                                                              1373 TCMCCATTCTTATTTCACYTTAGRATCMAGGGTGGGRGGGRGGGAGGGGAATTGTCART 1432
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                                                                                                                                                                                                                                                                                                      0; Gaps
                                                                                                                                                      Length 1558;
                                                                                                                                                                                         Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NUMBER OF SEQUENCES: 19
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genetics Institute Inc.- Legal Affairs
STREET: 87 CambridgePark Drive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SOFTWARE: Patentin Release #1.0, Version #1.25
UNRENT APPLICATION DATA:
                                                                                                                                                  6.5%; Score 61.4; DB 4; 55.5%; Pred. No. 1.8e-05;
                                                                                                                                                                   .8e-05
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                                                                                                                                                                                         13; Mismatches
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TITLE OF INVENTION: RECEPTOR PROTEINS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER: PCT/US94/10080
FILING DATE: HEREWITH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ATION NUMBER: US 08/123,934
DATE: 17-SEP-1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 5, Application PC/TUS9410080 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: LAZAR, Steven R
REGISTRATION NUMBER: 32,618
REFERENCE/DOCKET NUMBER: 520:
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ...verunGY: linear
MOLECULE TYPE: DNA (genomic)
IMMEDIATE SOURCE:
CLONE: CFK1-10a
FEATURE:
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TELEFAX: (617) 876-5851
INFORMATION FOR SEQ ID NO: 5:
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LENGTH: 3238 base pairs
                                                                                                                                                                   Best Local Similarity 55.59
Matches 86; Conservative
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EDNESS: single
STRANDEDNESS: single
TOPOLOGY: linear
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MEDIUM TYPE: Floppy
                                                         CDS
103..1011
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LOCATION:
PCT-US94-10080-5
                                                     ; NAME/KEY;
; LOCATION;
US-08-850-392-2
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                 Length 3238,
            Score 61; DB 5; Length 323; Pred. No. 2.8e-05; 0; Mismatches 15; Indels
                                                                                                                                                                                                                                                                                                                 APPLICANT: Nishikura, Kazuko
TITLE OF INVENTION: RNA Editing Enzyme and Methods of
TITLE OF INVENTION: Thereof
TUMBER OF SEQUENCES: 39
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                  Spring House Corporate Cntr, P.O. Box 457
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SYSTEM: PC-DOS/MS-DOS
Patentin Release #1.0, Version #1.25
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0; Mismatches
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APPLICATION DATA:
APPLICATION NUMBER: US 08/197,794
FILING DATE: 17-FEB-1994
ATTORNEY/AGENT INFORMATION:
NAME: Bak, Mary E.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CURRENT APPLICATION DATA: US/08/280,443 FILING DATE:
                                                                                                                                                                               3187 AAAAAAAAAAAAAAAAAAAATA 3211
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                                                                                                                                                                                                                                             US-08-280-443-1
: Sequence 1, Application US/08280443
; Patent No. 5643778
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
                 6.5%;
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Best Local Similarity 80.7%;
Matches 71; Conservative
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Query Match
Best Local Similarity 82.4.
The TO Conservative
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NFORMATION FOR SEQ ID NO:
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155..3832
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STATE: Pennsylvania
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APPLICANT: NIShik
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Length 6671;
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CORRESPONDENCE ADDRESS:
ADDRESSEE: ADDRESSEE: Spring House Corporate Cntr, P.O. Box 457
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Indels
                                                          SEE: Howson and Howson : Spring House Corporate Cntr, P.O. Box 457 Spring House
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: Spring House Corporate Cntr, P.O. Box 457
Spring House
                                                                                                                                                                                                                                                       SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/555,678
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3.9e-05;
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                                                                                                                                                                                                                                                                                                                                     CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE: 17-FEB-1994
PRIOR APPLICATION NUMBER: US 08/280,443
FILING DATE: 25-UTL-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/280,743
FILING DATE: 25-UTL-1994
APPLICATION NUMBER: US 08/457,459
FILING DATE: 01-UN-1995
ATTORNEY/AGENT INFORMATION:
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REFERENCE/DOCKET NUMBER: WST49DUSA
of Use Thereof
                                                                                                                                                                                                                        COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 1, Application PC/TUS9502275 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELECOMMUNICATION INFORMATION TELEPHONE: 215-540-9206 TELEFAX: 215-540-5818
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Best Local Similarity 80.7°
Matches 71; Conservative
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                  NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
ADDRESSEE: Howson an
STREET: Spring House
                                                                                                                                                                                  COMPUTER READABLE FORM:
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STRANDEDNESS: double
                                                                                                    CITY: Spring House
STATE: Pennsylvania
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                                                                                                                                                                                                     MEDIUM TYPE:
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                                                                                                                                          COUNTRY:
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STATE:
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Pred. No. 3.9e-05;
0; Mismatches 17; Indels 0
                                                                                                                                      APPLICANT: Nishikura, Kazuko
IITLE OF INVENTION: RNA Editing Enzyme and Methods of Use
IITLE OF INVENTION: Thereof
                                                                                                                                                                                                                          ADDRESSEE: Howson and Howson
STREET: Spring House Corporate Cntr, P.O. Box 457
CITY: Spring House
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Nishikura, Kazuko
TITLE OF INVENTION: RNA Editing Enzyme and Methods
                                                                                                                                                                                                                                                                                                                                                                                                                                            Patentin Release #1.0, Version #1.25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CLASSIFICATION: 435
PRIOR APPLICATION DATA:
PRIOR APPLICATION NUMBER: 08/197,794
FILING DATE: 17-FEB-1994
PRIOR APPLICATION NUMBER: US 08/280,443
FILING DATE: 25-UUL-1994
ATTORNEY/AGENT INFORMATION:
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APPLICATION NUMBER: US/08/457,459
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                                                                           pplication US/08457459
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REFERENCE/DOCKET NUMBER: WS:
                                                                                                                                                                                                                                                                                                                                                                                                    IBM PC compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity 80.77
Matches 71; Conservative
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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                                                                                                                                                                                                 NUMBER OF SEQUENCES: 3
CORRESPONDENCE ADDRESS:
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MEDIUM TYPE: Floppy
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155..3832
                                                                                                                                                                                                                                                                                                 Pennsylvania
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TOPOLOGY: unknown MOLECULE TYPE: CDNA
                                                                                                                                                                                                                                                                                                                                                                                                                       OPERATING SYSTEM:
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; LOCATION:
US-08-457-459-1
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US-08-555-678-1
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APPLICATION NUMBER: US/08/967,101
FILING DATE: 10-NOV-1997
CLASSIFICATION: 435
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COMPUTER: IBM PC compatible
COMPRATION SYSTEM: PC-DOS/MS-DOS
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Patent No. 5840540
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/592,541
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E: DNA (genomic)
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                                               ATTORNEY/AGENT INFORMATION:
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Best Local Similarity 79.1
Matches 72; Conservative
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MEDIUM TYPE: Floppy
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                                                                                                                                                                                                                                                                                                                                                                                             nucleic acid
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; LOCATION:
US-08-473-981A-5
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: deFougerolles, Antonin R
APPLICANT: Springer, Timothy A
TITLE OF INVENTION: METHODS OF IDENTIFYING AGENTS WHICH MODULATE
TITLE OF INVENTION: I.AM-3 BINDING TO LFA-1 (AS AMENDED)
NUMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESS:
ADDRESSEE: STERNE
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                                                                                                                                      SOFTWARE: Patentin Release #1.0, Version #1.30 UNRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/02275
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                                                                                                                                                                                                                                                                            CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/280,443
FILING DATE: 25-JUL-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/197,794
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 5, Application US/08473981A Patent No. 5629162
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 IBM PC compat.
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Best Local Similarity 80.7.
Best Local 71; Conservative
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STRANDEDNESS: double
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MEDIUM TYPE: Floppy
COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                     OPERATING SYSTEM:
SOFTWARE: Patentl
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; LOCATION:
PCT-US95-02275-1
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Length 1817;
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                               Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Patentin Release #1.0, Version #1.30
 6; DB 1;
2.9e-05;
Score 60.6; DB
Pred. No. 2.9e-
0; Mismatches
                                                                                                                                                   1778 AAAAAAAAAAAAAAAAAAAAAAAAAAAA 1808
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LENGTH: 2285 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                      ; TOPOLOGY: linear
; MOLECULE TYPE: CDNA
US-08-967-101-136
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0; Gaps Score 60.6; DB 4; Length 2285; Pred. No. 3.1e-05; 0; Mismatches 12; Indels 0; Query Match
Best Local Similarity 84.6%;
Matches 66; Conservative

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Search completed: September 28, 1999, 16:40:05 Job time: 6991 sec

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COMMENT
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Butheria; Rodentia; Sciurognathi, Muridae, Murinae; Mus.
1 (bases 1 to 503)
Marra,M., Hillier,L., Allen,M., Bowles,M., Dietrich,N., Dubuque,T.,
Galsal,S., Kucaba,T., Lacy,M., Le,M., Martin,J., Morris,M.,
Schellenberg,K., Steptoe,M., Tan,F., Underwood,K., Moore,B.,
Theising,B., Wylie,T., Lennon,G., Soares,B., Wilson,R. and
                                                                                                                                                                                                                                                     Contact: Marra M/Mouse EST Project
Washigton University School of MedicineP
4444 Forest Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
Final: mouseest@watson.wustl.edu
This clone is available royalty-free through LLNL; contact the IMAGE Consortium (info@image.linl.gov) for further information.
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On Dec 30, 1996 this sequence version replaced g1:1528949.
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Pred. No. 2e-35;
0; Mismatches 4; Indels 4;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /tissue_type="embryo"
/dev_stage="13.5-14.5dpc total fetus"
/lab_host="DH10B"
                                                                                                                                                                                                                                                                                                                                                                                                                                  Seq primer: -28M13 rev2 from Amersham
High quality sequence stop: 486.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /db_xref="taxon:10090"
/clone="IMAGE:479046"
/clone_lib="Soares mouse
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /organism="Mus musculus"
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The WashU-HHMI Mouse EST Project
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Best Local Similarity 97.3
Matches 283; Conservative
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                                    Mus musculus
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ORIGIN
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JOURNAL
KEYWORDS
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                                                                                                        AUTHORS
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Mis musculus
Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 445)
Marta, M., Hillier, L., Allen, M., Bowles, M., Dietrich, N., Dubuque, T.,
Marta, M., Hillier, T., Lacy, M., Le, M., Martin, J., Morris, M.,
Schellenberg, K., Steptoe, M., Tan, F., Underwood, K., Moore, B.,
Theising, B., Wylle, T., Lennon, G., Soares, B., Wilson, R. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 This clone is available royalty-free through LLNL ; contact the IMAGE Consortium (info@image.llnl.gov) for further information.
                                                                                                                            AA039053 445 bp mRNA EST 29-AUG-1996 mi99407.rl Soares mouse embryo NbME13.5 14.5 Mus musculus cDNA clone_IMAGE:474733 5', mRNA sequence.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Contact: Marra M/Mouse EST Project WashO-HMI Mouse EST Project Washington University School of MedicineP 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 445;
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/dev_stage="13.5-14.5dpc total fetus"
/lab_host="DH108"
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Pred. No. 1.6e-34;
0; Mismatches 7;
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The WashU-HHMI Mouse EST Project
Unpublished (1996)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Email: mouseest@watson.wustl.edu
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Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /db_xref="taxon:10090"
/clone="IMAGE:474733"
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ilarity 96.6%;
Conservative
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Fax: 314 286 1810
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AAV49278 503 bp mRNA EST 30-DEC-1996 m145C04.rl Soares mouse embryo NbME13.5 14.5 Mus musculus CDNA clone IMAGE:479046 5', mRNA sequence.
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67.8
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AA049278/c
LOCUS
DEFINITION
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VERSION
                                                         September 28, 1999, 15:38:09 ; Search time 2095.87 Seconds (without alignments) 882.801 Million cell updates/sec
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938
1 gycaccgtttacttcgtcca......aaaaaaaaaaaaaaa 938
GenCore version 4.5
Copyright (c) 1993 - 1998 Compugen Ltd
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                                         - nucleic search, using sw model
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9b_est6:**
9b_est6:**
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gb_est1:*
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Perfect score:
Sequence:
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AA039053 mi99d07.r
AV032198 AV032198
AA043001 zk56f01.r
W17583 mb75b01.rl
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                                                                                                  Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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Gaps

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Length 262

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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

[ (bases 1 to 458)
Hillier, L. Lennon, G., Becker, M., Bonaldo, M.F., Chiapelli, B., Chissoe, S., Dietrich, N., DuBuque, T., Favello, A., Gish, W., Hawkins, M., Hultman, M., Kucaba, T., Laoy, M., Le, M., Le, N., Mardis, E., Moore, B., Morris, M., Parsons, J., Prange, C., Rifkin, L., Rohlfing, T., Schlenberg, K., Soares, M.B., Tan, F., Thierry-Meg, J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        !revaskis,E., Underwood,K., Wohldmann,P., Waterston,R., Wilson,R
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Generation and analysis of 280,000 human expressed sequence tags Genome Res. 6 (9), 807-828 (1996)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AA043001 458 bp mRNA EST 10-MAY-1997 zk56f01.rl Soares_pregnant_uterus_NDHPU Homo sapiens cDNA clone IMAGE:486841 5', mRNA sequence.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          629 caggtcctgccggctaaactctaaggataggccatcctcct-gctgggtcagacctggag 687
                                                                                                                                                                                                                                                                                                         748 ctggggcacaatgagctccacacaccacagctttggtccacatgatggtcacacttggat 807
                                                                                                                                                                                                                                                                                                                                                                                                                                       geteacetgaattggageeeetetgtacetatetgggeaacaaagaaacetaceatgagg
                                                                                                                                                                                                                                                                                                                                                          120 CTGGGGCACAATGAGCTCCCACAACCACAGCTTTGGTCCACATGATGGTCACACTTGGAT
                                                                                                                                                                                                                                                                                                                                                                                                           808 ataccccagtgtgggtaaggttggggtattgcagggcctcccaacaatctctttaaataa
                                                                                                                                                                                                                                                 62 GCTCACCTGAATTGGAGCCCCTTTGTACC-ATTTTGGCAACAAAGAAACCTACCA-GAGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              On May 9, 1995 this sequence version replaced gi:802616
                                                                     Indels
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4444 Forest Park Parkway, Box 8501, St. Louis, MO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         clone_lib="Soares_pregnant_uterus_NbHPU"
                 DB 50;
                                                                  18;
                 Score 194.2; DB 5
Pred. No. 1.7e-27;
0; Mismatches 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Seq primer: -28M13 rev2 from Amersham
High quality sequence stop: 305.
Location/Qualifiers
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/db_xref="GDB:3760555"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /db_xref-"taxon:9606
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /dev_stage="adult"
/lab_host="DH10B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AA043001.1 GI:1522545
            Query Match 20.7%;
Best Local Similarity 91.9%;
Matches 238; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               868 ataaaggagttgttcaggt 886
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             240 ATAAAGGAGTTGTTCAGGT 258
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Contact: Wilson RK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Homo sapiens
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AA04300
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AA043001/c
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Thermostabilization and thermoactivation of thermolabile enzymes by
trehalose and its application for the synthesis of full length cDNA
(Proc. Natl. Acad. Scl. U.S.A. 95(2):520-524 (1998))
Transcriptional sequencing: A method for DNA sequencing using RNA
polymerase (Proc. Natl. Acad. Scl. U.S.A. 95(7):3455-3460 (1998))
Please visit our web site (http://genome.rtc.riken.go.jp) for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AVU32198 262 bp mRNA EST 03-JUN-1999
VN32198 Mus musculus adult C57BL/6J cerebellum Mus musculus CDNA
Clone 1500034F20, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. (Dasse 1 to 262)
Carninci, P., Shibata, K., Ozawa, Y., Konno, H., Ito, M., Aizawa, K., Akahira, S., Akiyama, J., Fukuda, S., Fukunishi, Y., Funayama, T., Akahira, S., Akiyama, J., Fukuda, S., Fukunishi, Y., Funayama, T., Kawai, J., Kakuchi, M., Kojima, Y., Matsuyama, T., Nitsuma, H., Oda, Owa, C., Sato, K., Shibata, Y., Shigemoto, Y., Shiraki, T., Sogabe, Y. Sugahara, Y., Suzuki, H., Tateno, M., Tomaru, Y., Tominaga, N., Watanabe, S., Yagame, M., Yamamura, T., Yokota, T., Yoshino, M., Muramatsu, M., Okazaki, Y. and Hayashizaki, Y.
                                                                                                                                                                                                                                              265 AGGICCIGCCGCTAAACICTAAGGATAGGCCATCCICCIGCTGGGTCAGACCTGGAGGC 206
                                                                                              205 TCACCTGAATTGGAGCCCCTCTGTACC-ATCTGGGCAACAAAGAAACCTACCA-GAGGCT 148
                                                                                                                                               750 ggggcacaatgagctcccacacaccacagctttggtccacatgatggtcacacttggatat 809
                                                                                                                                                                                                        88
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/clone="1500034F20"
/clone_lib="Mus musculus adult C57BL/6J cerebellum"
                                                                                                                                                                           Unpublished (1999)
On Jun 22, 1998 this sequence version replaced g1:3246782
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Koyadai, Tsukuba, Ibaraki 305-0074, Japan
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    .262
    /organism="Mus musculus"

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Fax: 81-298-36-9098
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Contact: Chie Owa
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VERSION KEYWORDS SOURCE ORGANISM

REFERENCE AUTHORS

DEFINITION

RESULT AV032198

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BASE COUNT ORIGIN

FEATURES

TITLE JOURNAL COMMENT

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       source
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AA925924/c
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COMMENT
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TITLE
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Marra,M., Hillier,L., Allen,M., Bowles,M., Dietrich,N., Dubuque,T.,
Geisel,S., Kucaba,T., Lacy,M., Le,M., Martin,J., Morris,M.,
Schellenberg,K., Steptoe,M., Tan,F., Underwood,K., Moore,B.,
Theising,B., Wylie,T., Lennon,G., Soares,B., Wilson,R. and
                                                                    Not
double-stranded CDNA was ligated to Eco RI adaptors (Pharmacla), digested with Not I and cloned into the No and Eco RI sites of the modified p1773 vector. Library went through one round of normalization. Library constructed by M. Fatima Bonaldo.*

136 c 146 g 89 t 8 others
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      This clone is available royalty-free through LLNL; contact the IMAGE Consortium (info@image.llnl.gov) for further information. MGI:216609
                                                                                                                                                                                                                                                                         184 egegageteaageagtteeteggetegagteaagaageacgeataetgetegaacett-ag 242
                                                                                                                                                                                                                                                                                                                                                ggaatctggagcgagtggagccacccaccgctgctccaccctcgaagtgagcgcccg 123
                                                                                                                                                                                                                                                                                                                                                                                                                   ggcccgggcggcggtgtgcgagccgcggggggggggggcgagcccagctcgggcccggtgcgg 183
                                                                                                                                                                                                                                              Gaps
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   115 CGCGAGCTCAAGCAGTTCCTGGGCTGGCTCAAGAAGCACGCGTACTGCTCCAACCNTCNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          W17583 390 bp mRNA EST 10-SEP-
mb75b01.rl Scares mouse p3NMF19.5 Mus musculus cDNA clone
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The WashU-HHMI Mouse EST Project
Unpublished (1996)
On May 9, 1995 this sequence version replaced g1:804170.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Washington University School of MedicineP
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
                                                                                                                                                                                                     Length 458;
                                                                                                                                                                                                     20.0%; Score 187.6; DB 27; Length
85.7%; Pred. No. 3.1e-26;
.ive 0; Mismatches 38; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Contact: Marra M/Mouse EST Project
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Email: mouseest@watson.wustl.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       High quality sequence stop: 384.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            IMAGE:335209 5', mRNA sequence.
W17583
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W17583.1 GI:1291995
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                                                                                                                                                                                                                          Similarity
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                                                                                                                                    79
                                                                                                                                                                                                        Query Match
                                                                                                                                                                                                                            Local
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JOURNAL
COMMENT
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                                                                                                                                                                                                                                                                                                                                                                                                               124
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AUTHORS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Rattus norvegicus
Eukaryota: Metazoa: Chordata: Craniata: Vertebrata: Mammalia;
Eutheria: Rodentia: Sciurognathi: Muridae: Murinae; Rattus.
1 (bases 1 to 455)
Bonaldo.M.F., Lennon, G. and Soares, M.B.
Normalization and subtraction: two approaches to facilitate gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       749
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   220 TCACCTGAATTGGAGCCCCTCTGTACC-ATCTGGGCAACAAAAAAAACTACCA-GAGGCT 277
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
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UI-R-Al-es-g-11-0-UI.S1 UI-R-Al Rattus norvegicus CDNA clone
UI-R-Al-es-g-11-0-UI 3', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   tcacctgaattggagcccctctgtacctatctgggcaacaaagaaacctaccatgaggct
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            On Apr .21, 1998 this sequence version replaced gi:3073060
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                                                                                                                                                                                                                                                                                                                                                                                                                 Length 390;
                                                                                                                                                                                                                                                                                                                                                                                                                                                        Indels
                                                                                                                                                                                                                                                                                                                                                                                                                  26;
                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
19.8%; Score 185.4; DB 26;
Best Local Similarity 95.7%; Pred. No. 7.8e-26;
Matches 223; Conservative 0; Mismatches 6;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Genome Res. 6 (9), 791-806 (1996)
/organism="Mus musculus'
/db_xref="taxon:10090"
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Rat

(REST) Catalog &

MD 20850, USA

FEATURES

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1 470 bp mRNA EST 30-OCT-1998
99 Normalized rat kidney, Bento Soares Rattus sp. cDNA clone
3' end, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /clone_lib="Normalized rat kidney, Bento Soares"
/note="Organ: Kidney; Vector: pT7T3Pac; Site_l: EcoRI;
Site_2: NotI"
143 c 124 g 115 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    146 agccgcgggggggggggcccagctcgggcccggtgcggcgcgagctcaagcagttcctcg 205
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AV010798 Mus musculus 18-day embryo C57BL/6J Mus musculus cDNA
clone 1110029C24, mRNA sequence.
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Eutherla; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
                                                                                                                                                                                                                                                                                                                                                                                                                       1 (bases 1 to 470)
Lee, N. H., Glodek, A., Chandra, I., Mason, T. M., Quackenbush, J.,
Kerlavage, A.R. and Adams, M.D.
Rat Genome Project: Generation of a Rat EST (REST) Catalog &
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                On May 8, 1995 this sequence version replaced gi:801255
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 151; DB 43; Length 470;
Pred. No. 2.3e-19;
0; Mismatches 5; Indels
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Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
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9712, Medical Center Drive, Rockville,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /organism="Rattus sp."
/db_xref="taxon:10118"
/clone="RKIDD49"
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AI233311.1 GI:3817191
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Tel: (301)-838-3529
Fax: (301)-838-0208
Email: nhlee@tigr.org
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96.9%;
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1 (bases 1 to 229)
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ATCC
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Rattus sp.
Rattus sp.
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                                                                                                                                                            RKIDD49
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                                                                                                                                                                                                                                                                                                                                                                 /dev_stage="adult"
//dev_stage="adult"

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oligo-dr track served to identify it as a clone from the normalized adult Brain library. cDNA Library Preparation: M. Fatima Bonaldo, Ph.D. Clone distribution: clones will be available through Research Genetics The following repetitive elements were found in this cDNA sequence: 1-35, >POLY_A#Simple_repeat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  library in the form of single-stranded circles. The remaining single-stranded circles (subtracted library) was purified by hydroxyapatite column chromatography,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         converted to double-stranded circles and electroporated into DHIOB bacteria (Life Technologies) to generate the UI-R-Al library. This procedure has been previously described (Bonaldo, Lennon and Soares, Genome Research 6:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             369 AGCGTCAGGCTTCACTGCATCATCCAGCTGCTGAAAGGGAGTCATCTCAAGACTCCCAGG 310
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  cctcctgctgggt-cagacctggaggctcacctgaattggagcccctctgtac---ctat 719
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Pred. No. 1.5e-22;
0; Mismatches 75;
                                                                                                                                                                                                                                                             /strain="Sprague-Dawley"
/db_xrsf="taxon:10116"
/clone="UI-R-Al-es-g-11-0-UI"
/clone_lib="UI-R-Al"
                                                                                                                                                                                                                                  organism="Rattus norvegicus"
                                                                                                                                                                         Location/Qualifiers
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74.18;
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Matches 274; Conservative
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Transcriptional sequencing: A method for DNA sequencing using RNA polymerase (Proc. Natl. Acad. Sci. U.S.A. 95(7):3455-3460 (1998))

Please visit our web site (http://genome.rtc.riken.go.jp) for further details.
Carninci, P., Shibata, K., Ozawa, Y., Konno, H., Ito, M., Aizawa, K., Akahira, S., Akiyama, J., Fukuda, S., Fukunishi, Y., Funayama, T., Hara, A., Hayatsu, N., Hori, F., Ishikawa, T., Itoh, M., Izawa, M., Rawai, J., Kikuchi, N., Kojima, Y., Matsuyama, T., Niltsuma, H., Oda, H. Owa, C., Sato, K., Shibata, Y., Shigemoto, Y., Shiraki, T., Sogabe, Y., Sugahara, Y., Suzuki, H., Tateno, M., Tomaru, Y., Tominaga, N., Watanabe, S., Yagame, M., Yamamura, T., Yokota, T., Yoshino, M., Muramatsu, M., Okazaki, Y. and Hayashizaki, Y.
                                                                                                                                                                                                                                                                                                                                                                              Email: genome-resertc.riken.go.jp
Thermostabilization and thermoactivation of thermolabile enzymes
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Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
                                                                                                                                                                                          Unpublished (1999)
On Feb 18, 1999 this sequence version replaced g1:4296972.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1. 229
/organism="Mus musculus"
/strain="C57BL/61"
/db_xref="taxon:10090"
/clone="1110029C24"
/clone="110029C24"
/sex="mixed"
/sex="mixed"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 150; DB 49; Length 229;
Pred. No. 3.2e-19;
0; Mismatches 20; Indels
                                                                                                                                                                                                                                                                                                                   Koyadai, Tsukuba, Ibaraki 305-0074, Japan
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50 c 60 g 59 t
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89.4%;
                                                                                                                                                                                                                                                                                                                                       Tel: 81-298-36-9145
Fax: 81-298-36-9098
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Rattus norvegicus
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AI071408/c
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    AUTHORS
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/dev_stage="adult"
/lab_host="adult"
/lab_host="belion Life Technologies)"
/lab_host="belion Life Technologies)"
/lab_host="belion Life Technologies)"
/loce="vector: pT733-pac (Pharmacia) with a modified polylinker; Site_1: Not I; Site_2: Eco Ri; The UI-R-C2 library is a subtracted library derived from the UI-R-C3 library, which is a subtracted library consisted of a mixture of individually tagged normalized libraries constructed from rat placenta, adult lung brain, liver, kidney, heart, spleen, ovary, muscle, 8, 12 and 18-day embryo. The tag is a string of 3-5 nucleotides present between the Not I site and the oligo-dT track which allows identification of the library of origin of a clone within the mixture. The subtracted library (UI-R-C2) was constructed as follows: PCR amplified CDNA inserts from UI-R-C1 clones from which 3' ESTS had been derived was
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The sequence tag present in the cDNA between the NotI site and the oligo-dI track served to identify it as a clone from the normalized adult Lung library. cDNA Library Preparation: M. Fatima Bonaldo, Ph.D. Clone distribution: clones will be available through Research
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          used as a driver in a hybridization with the UI.R-CI
library in the form of single-stranded circles. The
remaining single-stranded circles (subtracted library) was
purified by hydroxyapatite column chromatography,
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Bonaldo,M.F., Lennon,G. and Soares,M.B.
Normalization and subtraction: two approaches to facilitate gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          converted to double-stranded circles and electroporated into DH10B bacteria (Life Technologies) to generate the
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                                                                                                                                                                                                                                                                                                                                         451 Eckstein Medical Research Building Iowa City, IA 52242, USA Tel: 319 335 9200
Fax: 319 335 9565
Email: msoares@blue.weeg.uiowa.edu
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       284 AGGICCIGCGGCIAAACICIGAGGAIAGGCCAICCICCIGCIGGAIGCAGGACCIGGAGG 225
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           689 ctcacctgaattggagccctctgtac---ctatctgggcaacaaagaaacctaccatga 745
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                97044477
On Sep 12, 1996 this sequence version replaced gi:1404537
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Indels 17;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 137.4; DB 41; Length 464;
Pred. No. 8e-17;
0; Mismatches 46; Indels 17;
                                                                                                                                                                                                                                        Contact: Soares, MB
Program for Rat Gene Discovery and Mapping
University of Iowa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /clone="UI-R-C2-nb-d-08-0-UI"
/clone_lib="UI-R-C2"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /organism="Rattus norvegicus"
/strain="Sprague-Dawley"
/db_xref="taxon:10116"
                                                                                                    Genome Res. 6 (9), 791-806 (1995)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Seq primer: M13 Forward.
Location/Qualifiers
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Best Local Similarity 77.9%;
Matches 222; Conservative
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836 ttgcagggcctcccaacaatctctttaaataaatgagttgttc
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SOURCE
ORGANISM
                                                                                                                              RESULT 11
AA377893
                                                                                                                                                                                      DEFINITION
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Thermostabilization and thermoactivation of thermolabile enzymes by
trehalose and its application for the synthesis of full length cDNA
(Proc. Natl. Acad. Sci. U.S.A. 95(2):520-524 (1998))
Transcriptional sequencing: A method for DNA sequencing using RNA
polymerase (Proc. Natl. Acad. Sci. U.S.A. 95(7):3455-3460 (1998))
Please visit our web site (http://genome.rtc.riken.go.jp) for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ä
                                                                                                                                                                                                                                                                                                                                                                                                                                                      Carninci, P., Shibata, K., Ozawa, Y., Konno, H., Ito, M., Alzawa, K., Akahira, S., Akiyama, J., Fukuda, S., Fukunishi, Y., Funayama, T., Hara, A., Hayatsu, N., Hori, F., Ishikawa, T., Itoh, M., Izawa, M., Kawai, J., Kikuchi, N., Kojima, Y., Matsuyama, T., Nitsuma, H., Oda, H. Owa, C., Sato, K., Shibata, Y., Shigemoto, Y., Shiraki, T., Sogabe, Y., Sugahara, Y., Watenaba, M., Muramata, Y., Yoshino, M., Muramatsu, M., Yamamura, T., Yokota, T., Yoshino, M., Muramatsu, M., Okazaki, Y. and Hayashizaki, Y.
                                                                                                                                                                                                                  AV011309 167 bp mRNA EST 03-JUN-1999 AV011309 Mus musculus 18-day embryo C57BL/6J Mus musculus cDNA clone 1110031J03, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                716 ctatctgggcaacaaagaaacctaccatgaggctggggcacaatgagctcccacaaccac 775
                                  105 ATGTACCCCAATATGGGTAGGGTTGGAGTAATGACAAGGGTTATGCAGGACCCTCCAAGA 46
                                                                                                                                                                                                                                                                                                                                                                                                Eukaryota; Metazoa; Chordata; Cranlata; Vertebrata; Mammalla;
Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /clone_lib="Mus musculus 18-day embryo C57BL/6J"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Unpublished (1999)
On Jun 5, 1998 this sequence version replaced g1:3189141
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1;
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Pred. No. 1.4e-16;
0; Mismatches 12; Indels 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          3-1-1 Koyadai, Tsukuba, Ibaraki 305-0074, Japan
Tel: 81-298-36-9145
Fax: 81-298-36-9098
                                                                             /dev_stage="18-day embryo"
40 c 42 g 38 1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /db_xref="taxon:10090",
/clone="1110031J03"
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1. .167
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /strain="C57BL/6J"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Genome Science Laboratory
806 atataccccagtgtgggtaaggttg
                                                                                                                                                                                                                                                                                                94788296
AV011309.1 GI:4788296
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92.28;
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Best Local Similarity 92.2
Matches 154; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Contact: Chie Owa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 further details.
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AV011309
LOCUS
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KEYWORDS
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AUTHORS
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Loases to 247)

Sadams, M.D., Kerlavage, A.R., Fleischmann, R.D., Fuldner, R.A.,
Bult, C.J., Lee, N.H., Kirkness, E.F., Weinstock, K.G., Gocayne, J.D.,
White, O., Sutton, G., Blake, J.A., Brandon, R.C., Man-Wai, C.,
Clayton, R.A., Cline, T.R., Cotton, M.D., Earle-Hughes, J., Fine, L.D.,
Fitzgerald, L.M., Fitzhugh, W.M., Fritchman, J.L., Geoghagen, N.S.,
Glodek, A., Gnehm, C.L., Hanna, M.C., Hedblom, E., Hinkle, P.S.JT.,
Kelley, J.M., Kelley, J.C., Liul, L.I., Marmaros, S.M., Merrick, J.M.,
Moreno-Palanques, R.F., McDonald, L.A., Nquyen, D.T., Pelligrino, S.M.,
Phillips, C.A., Ryder, S.E., Scott, J.L., Saudek, D.M., Shifey, R.,
Bednarik, D.P., Cao, L., Cepeda, M.A., Coleman, T.A., Collins, E.J.,
Dimke, D., Feng, D.-F., Ferrie, A., Fischer, C., Hastings, G.A.,
Kozak, D.L., Kunsch, C., Hungjun, J., Li, H., Melssner, P.S., Olsen, H.,
Rymond, L., Well, Y.F., Wing, J., Xu, C., Yu, G.L., Ruben, S.M.,
Dillion, P.J., Fannon, M.R., Rosen, C.A., Haseltine, W.A., Fields, C.,
Intial assessment of human gene diversity and expression patterns
                                                                                                                                                                                   AA377893 247 bp mRNA EST 21-APR-1997
EST90550 Synovial sarcoma Homo sapiens cDNA 5' end, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Email: arkerlav@tigr.org
For clone availability, additional sequence and expression
Information related to this EST, please check the TIGR Human Gene
Index (http://www.iigr.org/tdb/hgi/hgi.html)
Seq primer: M13 Reverse.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /tissue_type="synovial membrane"
/dev_stage="adult, 20 yrs"
/note="Vector: pBluescript SK-; Site_1: EcoRI; Site_2:
XhoI"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                     Chordata; Craniata; Vertebrata; Mammalia;
Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             On Sep 12, 1996 this sequence version replaced gi:1404677
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ij
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  based upon 83 million nucleotides of cDNA sequence
Nature 377 (6547 Suppl), 3-174 (1995)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The Institute for Genomic Research
9712 Medical Center Drive, Rockville, MD 20850 USA
Tel: 3018699056
121 TTGCAGGGCTCCCAAGAGTCTCTTTAAATAAATAAAGGAGTTGTTC 167
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 108.2; DB 32; Length
Pred. No. 2.2e-11;
0; Mismatches 23; Indels
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/db_xref-"taxon:9606"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /clone_lib="Synovial sarcoma"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      33 t
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                                                                                                                                                                                                                                                                                                                        AA377893.1 GI:2030231
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Best Local Similarity 84.4%;
Matches 130; Conservative (
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Eutheria; Primates;
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COMMENT
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AI074921
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/lab_host="DH10B (Life Technologies)"
/lab_host="DH10B (Life Technologies)"
/lab_host="DH10B (Life Technologies)"
/lab_host="WetCor: pT73D-Pac (Pharmacia) with a modified
/note="WetCor: pT73D-Pac (Pharmacia) with a modified
polylinker; Site_1: Not I; Site_2: Eco RI; The UI-R-C3
library is a subtracted library of a series, ultimately
derived from a mixture of individually tagged normalized
libraries from rat placents of adult lung, brain, liver,
kidney, heart, spleen, ovary, muscle, and 8, 12 and 18-day
embryos, after a series of subtractions to reduce the
representation of CONAS from which ESTS had already been
generated. The following serially subtracted libraries
were generated in this process: UI-R-C3, UI-R-C2P,
UI-R-C1, UI-R-C0, UI-R-A1, The tag is a string of
3-5 nucleotides present between the Not I site and the
oligo-dit track whichallows identification of the library
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    University of Iowa 451 Eckstein Medical Research Building Iowa City, IA 52242, USA Tel: 319 335 8250
Fax: 319 335 9565
Email: mscarese&blue.weeg.ulowa.edu
The sequence contained an oligo-dr track that was present in the oligonucleotide that was used to prime the synthesis of first strand cDNA and therefore this may represent a bonafide poly A tail. The sequence tag present in the cDNA between the Noti Site and the oligo-dr track served to identify it as a clone from the normalized 18 day embryo library cDNA Library Preparation: M.B. Soares Lab Clone distribution: clones will be available through Seg primer: M.3 Forward.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eukaryota; Metazoa; Chordata; Craniata; Muridae; Murinae; Rattus. 1 (bases 1 to 234)
Bonaldo, M.F., Lennon, G. and Soares, M.B.
Normalization and subtraction: two approaches to facilitate gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              origin of a clone within themixture. The subtracted
                                                                                                            224 catactgctcgaaccttagtttccgcctgtacgaccagtggcgtgcttggatgcagaagt 283
AI535068 234 bp mRNA EST 18-MAR-1999 UI-R-C3-sx-d-03-0-UI.SI UI-R-C3 Rattus norvegicus CDNA clone UI-R-C3-sx-d-03-0-UI 3', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Genome Res. 6 (9), 791-806 (1996)
97044477
On May 18, 1998 this sequence version replaced g1:3136453.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Contact: Soares, MB
Program for Rat Gene Discovery and Mapping
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /db_xref="taxon:10116"
/clone="UI-R-C3-sx-d-03-0-UI"
/clone_l1b="UI-R-C3"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /organism="Rattus norvegicus
/strain="Sprague-Dawley"
                                                                                                                                                                                284 cacacaagacccgaaaccaggtaggaaagttggg 317
                                                                                                                                                                                                                              120 CGCACAAGACCNGNAACCAGCACAAGGACGAGGGG 153
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               .ocation/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Norway rat.
Rattus norvegicus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            discovery
                                                                                                                                                                                                                                                                                                               RESULT 12
AI535068/c
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KEYWORDS
SOURCE
ORGANISM
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MEDLINE
COMMENT
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TITLE
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cDNA inserts from UI-R-C2p clones from which 3' ESTs had been derived was used as a driver in a hybridization with the UI-R-C2p library in the form of single-stranded circles. The remaining single-stranded circles (subtracted library) was purified by hydroxyapatite column chromatography, converted to double-stranded circles and electroporated into BHIOB bacteria (lifeTechnologies) to generate the UI-R-C3 library. This procedure has been previously described (Bonaido, Lennon and Soares, Genome Research 6:791-906, 1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             'n
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NCI-GGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 יייייי EST 24-SEP-1998 Coures_senescent_fibroblasts_NbHSF Homo sapiens cDNA clone IMAGE:1664847 3', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Tel: (301) 496-1550
Email: Robert_Strausberg@nih.gov
Email: Robert_Strausberg@nih.gov
This clone is available royalty-free through LENL ; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
Insert Length: 761 Std Error: 0.00
Seq primer: -40ml3 fwd. ET from Amersham
High quality sequence stop: 367.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               683 tggaggotcacctgaattggagoccctctgtac---ctatctgggcaacaaagaaaccta 739
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           740 ccatgaggctggggcacaatgagctcccacaaccacagctttggtccacatgatggtcac 799
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   847
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   234 TGGAGGCTCACCTGAACTGGAGACCATCTGTACTGTCACTTTGGGGCAATGAAGAAACAA 175
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       16; Gaps
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Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    800 acttggatataccccagtgtgggtaaggttg-----gggtattgcagggcctc
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/organism="Homo sapiens"
/organism="Homo sapiens"
/db_xref="taxon:960"
/map="17q21; between D1751321 and D1751325; Xp11.4
between AFMA2127G1 and DX6745"
/clone="IMAGE:1664847"
/clone="type="senescent_fibroblasts_NbHSF"
/tissue=_type="senescent_fibroblasts_NbHSF"
/tab_host="bH10B (ampicillin resistant)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Unpublished (1997)
On Jan 17, 1998 this sequence version replaced gi:1900484.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 101; DB 47; Length 234;
Pred. No. 4.9e-10;
0; Mismatches 45; Indels 1
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AIO74921.1 GI:3401565
                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity 74.0%;
Matches 174; Conservative 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (bases 1 to 404)
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BASE COUNT
ORIGIN
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AA270365
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                                                                                        /note="Vector: pT7T3D (Pharmacia) with a modified polylinker V_TYPE: phagemid; Site_1: Not I; Site_2: Eco RI; 1st strand cDNA was primed with a Not I - oligo(dT)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Washington University School of MedicineP
Washington University School of MedicineP
4444 Porest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1810
Fax: 314 286 1810
Fax: 315 286 1810
Fax: 316 280
Fax: 316 280
Fax: 317 286 1810
Fax: 317 286 1810
Fax: 318 280
Fax: 318 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            176 cggtggggggggggggtcaagcagttcctcggctggctcaagaagcacgcatactgctcga 235
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                me17bll.rl Soares mouse embryo NbMEl3.5 14.5 Mus musculus cDNA clone IMAGE:387741 5' similar to PIR:B38252 B38252 granulocyte colony-stimulating factor receptor precursor ;, mRNA sequence. W66776
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  236 accttagtttccgcctgtacgaccagtggcgtgcttggatgcagaagtcacacaagaccc 295
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
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Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 100.2; DB 42; Length 404; Pred. No. 7.5e-10; 0; Mismatches 18; Indels 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         18; Indels
                                                                                                                                                                                                                                                                                                                                                                              3 others
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /organism="Mus musculus"
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The WashU-HHMI Mouse EST Project
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Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         10.7%;
86.0%;
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W66776.1 GI:1375694
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W66776/c
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AUTHORS
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Rodentia; Sciurògnathi; Muridae; Murinae; Mus.

1 (bases 1 to 27)
Marra,M., Hillier,L., Allen,M., Bowles,M., Dietrich,N., Dubuque,T., Gelsel,S., Kucaba,T., Lacy,M., Le,M., Martin,J., Morris,M., Schellenberg,K., Steptoe,M., Tan,F., Underwood,K., Moore,B., Theising,B., Wylie,T., Lennon,G., Soares,B., Wilson,R. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    This clone is available royalty-free through LLNL; contact the IMAGE Consortium (info@image.llnl.gov) for further information.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               103 GGCACCGTTTACTTCGTCCAAGTGCGTTGTAACCCATTCGGGATCTATGGGTCGAAAAAG 44
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 ggcaccgtttacttcgtccaagtgcgttgtaacccattcgggatctatgggtcgaaaaag
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AA270365 227 bp mRNA EST 26-MAR.
va63h12.rl Soares mouse 3NME12 5 Mus musculus cDNA clone
IMAGE:736103 5', mRNA sequence.
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WashU-HHMI Mouse EST Project
WashIngton University School of MedicineP
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
Email: mouseest@watson.wustl.edu
                           embryo NbME13.5 14.5"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   26; Length 482;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Indels
                                                               /tissue_type="embryo"
/dev_stage="13.5-14.5dpc total fetus"
/lab_host="DH10B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 92.4; DB 26,
Pred. No. 2.2e-08;
0; Mismatches 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         vector to vector length is 405
Seq primer: -28ml3 rev2 ET from Amersham
                                                                                                                                                                                                                                                                                                                                                                                               101 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   43 GCGGGAATCTGGAGCGAGTGGAGCCACCCCATCG 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            94
                    clone_lib-"Soares mouse
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        61 gegggaatetggagegagtggageeacecace
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The WashU-HHMI Mouse EST Project Unpublished (1996)
clone-"IMAGE:387741"
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                                             /sex="unknown
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                               96.86
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity 98.9
Matches 93; Conservative
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3'), on total mouse RNA [provided by Minoru Ko, Wayne State Univ.]; double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of the modified pT713 vector. Library went through one round of normalization, and was constructed by Bento Soares and M. Fatima Bonaldo. "
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9.1%; Score 85; DB 30; Length 227;
Best Local Similarity 100.0%; Pred. No. 4.9e-07;
Matches 85; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                    clone_lib="Soares mouse 3NME12 5"
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Location/Qualifiers
                                                                                                      /db_xref="taxon:10090"
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Search completed: September 28, 1999, 15:38:13 Job time: 3281 sec

A70382 Sequence 12
A70384 Sequence 14
A70392 Sequence 22
AF099293 Homo sapl
A70394 Sequence 23
A70398 Sequence 23
A70398 Sequence 23
A70398 Sequence 38
A7048 Sequence 38
A7048 Sequence 16
J04510 Rabbit prol
U37273 Gallus gall
U95823 Gallus gall
U95823 Cervus elaptus m
D26597 Chicken mRN
M31661 Human prola
AF08249 Bos taurus
L02549 Bos

07-MAY-1999

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A NOVEL HAEMOPOIETIN RECEPTOR AND GENETIC SEQUENCES ENCODING PATENT: WO 9811225-A 19-MAR-1998; NICOLA NICOS ANTONY (AU)
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Nicola,N.A., Fabri,L., Farley,A., Nash,A., Willson,T., Re
Zhang,J., Alexander,W., Hilton,D.J., Kojima,T., Maeda,M.
Kikuchi,Y.
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Pred. No. 7e-181;
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541 c 453 g 299
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WO 9811225-A 19-MAR-1998;
NICOS ANTONY (AU)
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Euthoria; Primates; Catarrhini; Hominidae; Homo.

Elson, G.C. A., Graber, P., Losberger, P., Herren, S., Gretener, D., Menoud, L.N., Wells, T. N.C., Kosco-Vilbols, M.H. and Gauchat, J. F. Cytokine Type-I Receptor Family

J. Immunol. (1988) In press

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Elson, G.C. A., Graber, P., Losberger, P., Herren, S., Gretener, D., Menoud, L.N., Wells, T.N.C., Kosco-Vilbols, M.H. and Gauchat, J. F.
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Research Institute, 14, Chemin des Aulx, Plan-les-Ouates, GE
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           tgcctctatgttggcttgcccctgagaagccctttaacatcagctgctggtccggaac
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Nicola,N.A., Fabri,L., Farley,A., Nash,A., Willson,T., Rakar,S.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  unclassified.
1 (bases 1 to 6663)
Nicola,N.A., Fabri,L., Farley,A., Nash,A., Willson,T., Rakar,S.,
2hang,J., Alexander,W., Hilton,D.J., Koʻjima,T., Maeda,M. and
Kikuchi,Y.
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                                             tccaggcagtcagtcaggagacaatctggtgtgtcacgcccgagacggcagcattctggct
                                                          1 TCCAGGCAGCGGTCGGGGGACAACCTCGTGTGCCACGCCGTGACGGCAGCATCCTGGCT
                                                                                                                                                         AAGAACATGAAGGACTTGACCTGCCGCTGGACGCCCAGGGGCCCACGGGGACTTCCTC
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                                                                                                                                                                                                   ccctatgagatctgggtggaagccaccaatcgcctaggctcagcaagatctgatgtcctc
                                                                                                                                                                                                                                                                                                       301 CCCTATGAGATCTGGGTGGAGGCCACCAACCGCCTGGGCTCTGCCCGCTCCGATGTACTC
                                                                                                                                                                                                                                                                                                                                                    254.4; DB 5; Length 6663; No. 5.4e-49;
Length 560;
                       65; Indels
54.7%; Score 456; DB 5;
ilarity 88.4%; Pred. No. 4.7e-95;
Conservative 0; Mismatches 65;
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Sequence 28 from Patent WO9811225
A70398
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/db_xref="taxon:32644"
1852 c 1715 g 1634
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99.6%;
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unidentified
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Best Local Similarity
            Similarity
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A70398.1
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Query Match
Best Local Simi
Matches 495;
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ORIGIN
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JOURNAL
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AUTHORS
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A70398
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A NOVEL HAEMOPOIETIN RECEPTOR AND GENETIC SEQUENCES ENCODING SAME PATENT: WO 9811225-A 19-MAR-1998; NICOLA NICOS ANTONY (AU)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  6356 CCCACCTTCTCATCGGCTCCTCCCTGCAAGCTACCTGCTATACATGGAGACACACCT 6415
                                                                                                                                                                                                            1185 CCCACCCTTCTCATCGGCTCCTCCCTGCAAGCTACCTGCTCTATACATGGAGACACACT 124
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                                                                                                                                         tcccqcctccttaacacctccaccttggccctggccctggctaaccttaatgggtccagg
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Nicola,N.A., Fabri,L., Farley,A., Nash,A., Willson,T., Re
Zhang,J., Alexander,W., Hilton,D.J., Kojima,T., Maeda,M.
Kikuchi,Y.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
30.5%; Score 254.4; DB 5; Length 11832;
Best Local Similarity 99.6%; Pred. No. 5.2e-49;
Matches 255; Conservative 0; Mismatches 1; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                  11832 bp DNA

5N Sequence 38 from Patent W09811225.

1 A70408

4774683

A70408.1 GI:47746.
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/organism="unidentified"
/db_xref="taxon:32644"
a 3367 c 3298 g 2720
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us-09-037-657-18.rge

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//orb="DDS similarity" //orb="DDS similarity" //orb="DDS similarity" //orb="DDS similarity" //orb="DDS similarity" //orb="DDS similarity" //orb="DDS similarity" //orb="DDS similarity" //orb="DDS similarity" //orb="DDS similarity" //orb="DDS similarity" //orb="DDS similarity" //orb="DDS similarity" //orb="DDS similarity" //orb="DDS similarity" //orb="DDS similarity" //orb="DDS similarity" //orb="DDS similarity" //orb="DDS similarity" //orb="DDS similarity" //orb="DDS similarity" //orb="DDS similarity" //orb="DDS similarity" //orb="DDS similarity" //orb="DDS similarity" //orb="DDS similarity" //orb="DDS similarity" //orb="DDS similarity" //orb="DDS similarity" //orb="DDS similarity" //orb="DDS similarity" //orb="DDS similarity" //orb="DDS similarity" //orb="DDS similarity" //orb="DDS similarity" //orb="DDS similarity" //orb="DDS similarity" //orb="DDS similarity" //orb="DDS similarity" //orb="DDS similarity" //orb="DDS similarity" //orb="DDS similarity" //orb="DDS similarity" //orb="DDS 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/note="Lij9NC03 cosmid library constructed at LLNL from
flow-sorted chromosomes from hybrid 5HL2-B, which carries
chromosome 19 as its only human chromosome."
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Submitted (21-NOV-1997) Human Genome Center, Lawrence Livermore
National Laboratory, 7000 East Ave., Livermore, CA 94551, USA
Location/Qualifiers
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/note="predicted exon, program: grail2exons_human_1.3, frote="predicted exon, program: grail2exons_human_1.3,
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/note="predicted exon, program: grail2exons_human_1.3,
frame: 1, quality: good, score: 71.000"
complement(1383 ..1444)
/note="predicted exon, program: grail2exons_human_1.3,
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1, score: 62.000"
                                                                                                      40668 bp DNA PRI 21-NOV-1997
from chromosome 19 specific cosmid R30292, genomic
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/cell_line="5HL2-B"
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complement(3269. 3544)
/rpt_family="Alu"
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9358 .9535
/rpt_famlly-"LTR12"
complement(9445. .9505)
/note="predicted exon, pr
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/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="R30292"
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complement(6486. .6772)
/rpt_family="Alu"
complement(7505. .7783)
/rpt_family="Alu"
                                                                                                                                                                                                                             sequence, complete sequence.
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Lamerdin, J.E.
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/note="DDS similarity to AA136115 zk90b04.rl Scares
pregnant uterus NBHPU Homo sapiens cDNA clone 490063 5'
(395. 477); 92% identity.~-DDS similarity to AA009412
ze82h02.rl Scares fetal heart NBHHJWH Homo sapiens cDNA
clone 365523 5' (427); 94% identity.~-DDS similarity
to AA009693 ze82h02.sl Scares fetal heart NBHHJWH Homo
sapiens cDNA clone 365523 3' (306. 228); 99%
identity.~-DDS similarity to AA450010 zx33f04.sl Scares
total fetus ND2HF8 9W Homo sapiens cDNA clone 788287 3'
(309. 229); 99% identity.~"
complement(12966. 13240)
/rpt_family="Alu"
nn /rpt_family="Alu"
nn /rpt_family="Alu"
nn /rpt_family="Alu"
nn /rpt_family="Alu"
nn /rpt_family="Alu"
nn /rpt_family="Alu"
nn /rpt_family="Alu"
ncomplement(13756. 13240)
servedicted exon, program: grail2exons_human_l.3,
frame: 2, quality: good, score: 61.000-other overlapping
matches:-(13756. 13240) DDS similarity to AA009412
ze82h02.rl Scares fetal heart NDHH9W Homo sapiens cDNA
clone 365523 5' (428. 496); 97% identity.--(13756. 13984)
DDS similarity to AA009903 ze82h02.sl Scares fetal heart
NDHH9W Homo sapiens cDNA clone 365523 3' (227. 1); 98%
identity--(13756. 13984) DDS similarity to AA450010
zx33f04.sl Scares total fetus ND2HF8 9W Homo sapiens cDNA
clone 788287 3' (228. 1); 99% identity.-"
14885 115317
96% identity. --other overlapping matches: -(10435, .10548)
DDS similarity to AA136115 zk90b04.rl Scares pregnant
UDS similarity to AA136115 zk90b04.rl Scares pregnant
UDS similarity to AA452628
zx33f04.rl Scares total fetus ND2HF8 9w Home sapiens cDNA
zx33f04.rl Scares total fetus ND2HF8 9w Home sapiens cDNA
clone 788287 5' (1. 382); 95% identity. --(10466. 10548) DDS
similarity to AA009412 ze82102.rl Scares fetal heart
NDHH19W Home sapiens cDNA clone 365523 5' (1. 61); 97%
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /note-"DDS similarity to AA406406 zvlle07.sl Soares NhHMPu Sl Homo sapiens cDNA clone 753348.3' (1. 433); Score: 858 Identity: 431/433 (99%).---(14884. 15237) DDS similarity to W37175 zb21a02.rl Soares fetal lung NbHL19W Homo
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/rpt_family="Alu"
12502. .12581
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identity..~(15227. .14885) .DDS similarity to AA121532
zk89c11.s1 Soares pregnant uterus NbHPU Homo sapiens cDNA
clone 490004 3' (342. .1); 99% identity.~-(1527. .14885)
DDS similarity to AA127694 zk89c11.r1 Soares pregnant
uterus NbHPU Homo sapiens cDNA clone 490004 5' (126. .467);
99% identity.~-(1527. .14897) DDS similarity to W46603
zc32h10.r1 Soares senescent fibroblasts NbHSF Homo sapiens
cDNA clone 324067 5(328. .1); 98%
identity.--(1527. .15088) DDS similarity to W46604
zc32h10.s1 Soares senescent fibroblasts NbHSF Homo sapiens
cDNA clone 324067 3' (322. .465); 96% identity."
[5733. .15760
//octe-*DDS similarity to AA12153 zk89c11.s1 Soares
pregnant uterus NbHPU Homo sapiens cDNA clone 490004 3'
(389. .343); 99% identity.~-DDS similarity to AA127694
zk89c11.r1 Soares pregnant uterus NbHPU Homo sapiens cDNA
clone 490004 5' (77. .125); 90% identity.~-(15735. .15713)
DDS similarity to W46603 zc32h10.r1 Soares senescent
flbroblasts NbHSF Homo sapiens cDNA clone 34067 5'
(351. .329); 100% identity.~-(15755. .15713) DDS similarity
to W46604 zc32h10.s1 Soares senescent fibroblasts NbHSF
Homo sapiens cDNA clone 324067 3' (299. .321); 100%
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ö 21,348 TCCCGTGTACTCAACGCCTCCACCTTGGCTCTGGCCTGGCCAACCTCAATGGGTCCAGG 21289 121 tcccgcctccttaacacctccaccctggccctggccctggctaaccttaatgggtccagg 180 61 ggggccaccgctgaggggctctactggaccctcaatggtcgccgcctgccctctgagctg 120 Gaps DB 11; Length 40668; Query Match 24.1%; Score 200.6; DB 11; Length Best Local Similarity 86.7%; Pred. No. 9.8e-37; Matches 221; Conservative 0; Mismatches 34; Indels g 셤 ö õ S

REFERENCE

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/translation="GTVYFVOVRCNPFGIYGSKKAGIWSEWSHPTAASTPRSERPGPG
GGCDFRGGEPSGPVRRELKQFLGWLKKHAYCSNLSFRLYDOWRAWMOKSHKTRNOV
GKLGBACVGGGEPERPDFGPOHTTLISKHRTRGSCPRADGVRREVRGSG"
1 245 c 272 g 178 t
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                                                                                                                                                                                                                                                                                                                            1 (bases 1 to 938)
Nicola,N.A., Fabri,L., Farley,A., Nash,A., Willson,T., Rakar,S.,
Zhang,J., Alexander,W., Hilton,D.J., Kojima,T., Maeda,M. and
                    769 ggcaccgtttacttcgtccaagtgcgttgtaacccattcgggatctatgggtcgaaaag 828
1 GGCACCGTTTACTTCGTCCAAGTGCGTTGTAACCCATTCGGGATCTATGGGTCGAAAAAG 60
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Eutheria, Lagomorpha, Leporidae, Oryctolagus.

    (bases 1 to 2635)

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Rabbit (14-day pregnant) mammary gland, cDNA to mRNA, clones
PRLR-2[1,4].
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Rabbit prolactin receptor 2 mRNA, complete cds
J04510
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /codon_start=1
/protein_id="CAB42574.1"
/db_xref="PID:e1431693"
/db_xref="PID:g4774666"
/db_xref="GI:4774666"
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Sequence 16 from Patent WO9811225.
A70386
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /organism="unidentified"
/db_xref="taxon:32644"
<1. .468
                                                                                                                                                                                                                                                                                                                                                                                                            Patent: WO 9811225-A 19-MAR-1998;
NICOLA NICOS ANTONY (AU)
Location/Qualiflers
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                                                                               21228 TGCCTCTATGTTGGC 21214
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Matches 66; Conservative
                                                                241 tgcctctatgttggc 255
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GPGMKPTDLDPDNDSGRGSCDSPSLLSEKCEEPQANPSTFHTPEVIEQPEKPRANVTH
TWDPQTISLVGKMPYLSVNGSKSSTWPLLQPGQHNTNSPYHNIADMCKLATSLDKIDK
                                                                                                                                                                                                                                                                                                                                                                                                           translation="MKENVASMIVFLLLFLNIRLLKGQSPPGKPFIFKCRSPEKETF
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Edery, M., Jolicoeur, C., Levi-Meyrueis, C., Dusanter-Fourt, I., Petridou, B., Boutin, J.-M., Lesueur, L., Kelly, P.A. and Djiane, J. Identification and sequence analysis of a second form of prolactin receptor by molecular cloning of complementary DNA from rabbit
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SGWLTLQYEIRLKPEKAAEWETHFAGQQTQFKILSLYPGQKYLVQVRCKPDHGFWSVW
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EESTKEAPPSPSONQAEKDLSSFSTAPSDCRLQQGGLDYLDPACFMHSLH"
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                                                                                                                                     Draft entry and computer-readable sequence for [1] kindly provided by J.Djiane, 14-MAR-1989.
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5.3%; Score 44.2; DB 3; Length 2635;
Best Local Similarity 50.5%; Pred. No. 0.75;
Matches 165; Conservative 0; Mismatches 153; Indels 9
                                                                                                                                                                                                                                                                     note-"prolactin receptor 2 signal peptide"
                                                                                             Proc. Natl. Acad. Sci. U.S.A. 86, 2112-2116 (1989)
89184578
                                                                                                                                                                                                                                                                                                             /note="prolactin receptor 2 precursor"
                                                                                                                                                                                                               /organism="Oryctolagus cuniculus"
/db_xref="taxon:9986"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /note="prolactin receptor
668 c 603 g 647
                                                                                                                                                                                                                                                                                                                                                   'protein_id="AAA31457.1"
'db_xref="PID:g165670"
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bp upstream of BamHI site.
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VYPTSGOPSGYSAACSGALDTSGSYHCSMRAMSLYSGERPGHHCVPPRALEEGLAEHP
TGAPSRLGALSLPSGOEGALGAGHPHGGTAAGQPAASWYLNHGAELSHLPGHTYGSOO
OTFPNVREMFTSHRLGMESEHQVSSNSACQIPYRSAPSLYRHTAPYSYDCTKY"
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                                                                                                                                                                                                                                                                                                                                                                                                                 Submitted (29-SEP-1995) Bettina S. Freyaldenhoven, Department of Molecular and Experimental Medicine, SBR-7, Scripps Research Institute, 10666 North Torrey Pines Road, La Jolla, CA 92037, USA Location/Qualifiers
                                                                        Gallus gallus
Gallus gallus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Archosauria;
Aves; Neognathae; Galliformes; Phasianidae; Phasianinae; Gallus
(bases 1 to 1531)
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                                                                                                                                                                                                             Aberrant cell growth induced by avian winged helix proteins Cancer Res. 57 (1), 123-129 (1997)
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/note="winged helix transcription factor"
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/protein_id="AAC60065.1"
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Freyaldenhoven, B.S. and Freyaldenhoven, M.P.
Direct Submission
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Pred. No. 1.2;
0; Mismatches 101;
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/db_xref="taxon:9031"
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/db_xref="G1:1766075"
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GI:1766074
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CSRRAMSLYSGERPGHMCVPPRALEEGIAEHPTGAPSPRGPOPAVGAGGSAGGRAPAR
RHCAGOPAGSWYLMAGAELSHLPGHTFGSQQQTFPNVREMFTSHRLGMESEHQVSSNS
APSLYRHTAPYSYDCTKY"
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FLRRRRRFKKKDVSKEKEEARERLLKEQPRPPGLPGADLPKEASSSSSSSSSSKVV
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Columba livia
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Archosauria;
Aves; Neognathae; Columbiformes; Columbidae; Columba.
1 (bases 1 to 2713)
Chen,X. and Horseman,N.D.
                                                                                                                                                                                               Direct Submission
Submitted (28 WAR-1997) Molcular Immunology, School of Medicine,
Chiha University, 1-8-1, Inohana, Chuo-ku, Chiba 20, Japan
                 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Archosauria;
Aves; Neognathae; Galliformes; Phasianidae; Phasianinae; Gallus.
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Columba livia prolactin receptor mRNA, complete cds.
U07694
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                                                                                                                                                                                                                                                                                                                                                                        /product="winged helix transcriptional factor MFH-1"
/protein_id="AAB53749.1"
/db_xref="PID:92072324"
/db_xref="GI:2072334"
                                                                   Arase, Y., Koseki, H. and Miura, N. Winged helix transcriptional factor MFH-1 is required for generation of medial structures of the vertebrae and the
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note-"mesenchymal forkhead homolog-1"
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Pred. No. 1.2;
0; Mismatches 101;
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                                                                                                                                                                                                                                                                                        /organism="Gallus gallus"
/db_xref="taxon:9031"
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Best Local Similarity 50.7%;
Matches 104; Conservative
                                                       (bases 1 to 1849)
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                                                                                                                                             Unpublished
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THYKMFSLNPGKKYIVQIHCKPDHHGSWSEWSLEKYLOIPTDFRIKDMYWIIVGVLS
SLICLYMSWTMVLKGYRMIAFILPPVPGPKIKGIDTHLLETGKSEELLSALGCHGFPP
TSDCEELLIEYLEVEDSEDQQLMPSHDNGHPSKNAKMIAKETDSDSGRGSCDSPSLLS
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EVENLYSKTDQTTVQVKQNRPNDKSPFSKPKLMDYVEVHKVRQDEVAAVLLKHKENSG
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SCWWKPGSDGGLPTNYTLFYSKDSEEK IYECPDYGMSGPNSCYFDKNHTNPWTTYNI?
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                                                                                                                                                                                                                                                                                                                                                 /organism="Columba livia"
/db_xref="taxon:8932"
/clone_"pcLLR."
/clone_lib="assembled from a clone of pigeon crop lambda gtll cDNA library and a PCR product."
//tissue_type="crop"
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                                                                                                                                                                                                  Submitted (14-MAR-1994) Xiaojuan Chen, Physiology & Blophysics, University of Cincinnati Medical College, 231 Bethsda Ave., Cincinnati, OH 45267, USA Location/Qualifiers
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expression, and mutational analysis of the pigeon
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Pred. No. 2.2;
0; Mismatches 158;
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/product="prolactin receptor"
/protein_id="AAA20646.1"
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Endocrinology 135 (1), 269-276 (1994)
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GenCore version 4.5
Copyright (c) 1993 - 1998 Compugen Ltd.
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Run on:

September 28, 1999, 16:45:44; Search time 303.81 Seconds (without alignments) 686.811 Million cell updates/sec

US-09-037-657-18 834

1 cccaccetteteateggete.....atgggtegaaaaggeggga 834 Title: Perfect score: Sequence:

IDENTITY_NUC Scoring table:

Searched:

311585 seqs, 125096042 residues

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution. N_Geneseq_36:* Database :

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Length 834; Indels

Query Match
100.0%; Score 834; DB 1; I
Best Local Similarity 100.0%; Pred. No. 3.9e-209;
Matches 834; Conservative 0; Mismatches 0;

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NR6.1 gene.
proliferation; cell differentiation; can
neuronal proliferation; drug screening;
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Pred. No. 3.3e-208;
0; Mismatches 2;
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Novel heemopoietin receptor Ni
Haemopoietin receptor; cell pi
Cell survival; therapeutic; ne
99.6%;
ilarity 99.8%;
Conservative
  Ouery Match
Best Local Similarity
Matches 832; Conserv
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(DZIE/) DZIEGLEWSKA H E.
Alexander W, Fabri L, Farley A, Hilton DJ, Kikuchi Y,
Kojima T, Maeda M, Nash A, Nicola NA, Rakar S, Willson
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Location/Qualifiers
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Matches 832; Conserv
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                                                                                                                   New isolated haemopoietin receptor - used for developing products for modulating proliferation, differentiation and survival of cells, e.g. meuronal cells claim 4; Page 77-81; 182pp; English.

Claim 4; Page 77-81; 182pp; English.

Claim 4; Page 77-81; 182pp; English.

Inhermopoletin receptor (HR) NR6.1 is a form of the novel HR NR6.

Interaction between the novel HR and a ligand facilitates proliferation, differentiation and survival of a wide variety of cells. The HR and 1t's differentiation and survival of a wide variety of cells. The HR and 1t's to requilate development, maintenance or regeneration in an array of different cells and tissues in vitro and in vivo. They can be present in the and survival. The products can also be used for detection and diagnosis, sequence 1629 BP; 336 A; 541 C; 453 G; 299 T;
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/*tag= a
/product= "Haemopoietin receptor NR6.1"
                                                            (DZIE/) DZIEGLEWSKA H E.
Alexander W, Fabri L, Farley A, Hilton DJ, Kikuchi Y,
Kojima T, Maeda M, Nash A, Nicola NA, Rakar S, Willson
                                                                                                                                                                                                                                                                  Query Match 99.6%; Score 830.8; DB 1; Best Local Similarity 99.8%; Pred. No. 3.2e-208; Matches 832; Conservative 0; Mismatches 2;
                                                     AMRA-) AMRAD OPERATIONS PTY LID
                                  11-SEP-1997; G02479.
11-SEP-1996; AU-002246.
                                                                                               98-260970/23.
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for modulating for the modulating form of the movel HR NR6.

7. Fig. neuronal cells

8. Claim 5; Page 84-87; 182pp; English.

8. Claim 6; Page 84-87; 182pp; English.

9. Claim 6; Page 84-87; 182pp; 182
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29-SEP-1998 (first entry)
Novel haemopoietin receptor NR6.2 gene.
Haemopoietin receptor; cell proliferation; cell differentiation; cancer;
cell survival; therapeutic; neuronal proliferation; drug screening; ss;
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P-PSDB; W55012.
New isolated haemopoietin receptor - used for developing products
for modulating proliferation, differentiation and survival of cells,
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(DZIE/) DZIEGLEWSKA H E.
Alexander W, Fabri L, Farley A, Hilton DJ, Kikuchi Y,
Kojima T, Maeda M, Nash A, Nicola NA, Rakar S, Willson.
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V41688.
C5-OCT-1998 (first entry)
Nucleotide sequence of the murine U4 gene.
Murine; U4 protein; haematopoietin receptor superfamily;
cell proliferation; immune response; antibody; cell differentiation; autoimmune disease; cancer; allergy; ds.
                                                                                                                                                                                                                                                                                                                                                 Pages 25-16; 38pp; English.
the nucleotide sequence encoding the murine 04 protein from
                                                                                                                                                                                                                                                                                                                                 superfamily proliferation
                                     atgaaggateteaegtgeegetggaeaeegggtgeaeaeggggagaeattettaeataee
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122. .1399
/*tag= a
/product= "U4 protein
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the haematopoietin receptor superfamily, used in the method of the invention for the modulation of cell proliferation, or the immune response. Transformed mammalian cells are used to produce recombinant U4 protein. The U4 protein is used to screen for specific binding agents, raise markers for isolation of cognate ligands and receptors, and in pharmaceutical compositions which may modulate cell proliferation, cell differentiation, and the immune system (e.g. for treating immune deficiency, inherited or the result of infection, autoimmune diseases, cancer, and allergy). 318 A; 552 C; 478 G; 308 T;
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5.7e-207;
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Pred. No. 5.7e-
0; Mismatches
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Best Local Similarity 99.4%;
Matches 829; Conservative
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The present sequence encodes a protein designated Zcytor5, which is a cytokinin-like receptor. Soluble Zcytor5 may be administered to down-regulate the effects of a growth and/or maintenance factor in thyroid, heart, and skeletal muscle for example to lessen the effect of cardiotrophin-lon cardiac pathologies, so preventing heart blood, and to discover other possible Zcytor5 ligands. A probe and integrity of the Zcytor5 gene on chromosome 19. Antibodies and the and integrity of the Zcytor5 gene on chromosome 19. Antibodies and therapeutically to modify Zcytor5 ligand effects.

Sequence 1724 BP; 350 A; 550 C; 500 G; 324 T;
                                                                          growth factor;
e; cardiotrophin-1;
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                                                                                                                                                                                                                                                                                                           New mammalian cytokinin-like receptor 2cytor5 - useful for, e.g. down-regulating 2cytor5 natural ligands or detecting cardiotrophin-1
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                                       17-MAR-1999 (first entry)

CDNA encoding rat Zcytor5.

Zcytor5: cytokinin-like receptor; down-regulation; growth
maintenance factor; thyroid; heart; skeletal muscle; card
cardiac pathology; heart enlargement; Zcytor5 ligand; ss.

Rattus sp.
                                                                                                                                                                                                                                                                T, Jelmberg AC, Lehner JM,
TE;
                                                                                                                     Socation/Qualifiers
                                                                                                                               159. .1436
/*tag= a
/product= 2cytor5
                       V70896 standard; cDNA; 1724 BP. V70896;
                                                                                                                                                                                                    13-FEB-1998; US-074721.
01-MAY-1997; US-045287.
01-MAY-1997; US-850030.
13-FEB-1998; US-023890.
(ZYMO) ZYMOGENFICS. INC.
Adms RL, Foster DC, Gilbert T,
LOK S, Presnell SR, Whitmore IE
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Best Local Similarity 94.5
Matches 788; Conservative
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                                                                                                                                                                                                                                                                                   WPI; 99-034662
P-PSDB; W70862
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Disclosure; Page 68-70; 55pp; English.

The present sequence encodes an allelic varaint of protein designated Scytors, which is a cytokinin-like receptor. Soluble Zoytor5 may be administered to down-regulate the effects of a growth and/or maintenance factor in thyroid, heart, and skeletal muscle for example to lessen the frifect of cardiotrophin-1 on cardiac pathologies, so preventing heart enlargement. Zcytor5 could be used to detect cardiotrophin-1 in the blood, and to discover other possible Zcytor5 ligands. A probe comprising Zcytor5 DNA or RNA can be used to determine the presence and integrity of the Zcytor5 gene on chromosome 19. Antibodies and the
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CDNA encoding an allelic varaint of human 2cytor5.

Zcytor5; cytokinin-11ke receptor; down-regulation; growth factor; maintenance factor; thyroid; heart; skeletal. muscle; cardiotrophin-1; cardiac pathology; heart enlargement; Zcytor5 ligand; allelic varaint;
New mammalian cytokinin-like receptor Zcytor5 - useful for, e.g. down-regulating Zcytor5 natural ligands or detecting cardiotrophin-1
                                                                                                                                                                                             gagatetgggtggaagecaaceaategeetaggeteageaagatetgatgteeteaeaetg
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01-MAY-1997; US-850030.
13-FEB-1998; US-023890.
(ZYMO ) ZYMOGENETICS INC.
Adams RL, Foster DC, Gilbert T, Jelmberg AC, Lehner JM,
WPI, 99-034662703.
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88. .1365
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Query Match 79.7%;
Best Local Similarity 87.4%;
Matches 728; Conservative
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                                                                Indels
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V41689;
26-oCT-1998 (first entry)
Nucleotide sequence of the human U4 gene.
Human; U4 protein; haematopoietin receptor superfamily;
e used to purify Zong Ilgand effects.
                                                Score 666.6; DB 1;
Pred. No. 2.6e-165;
0; Mismatches 104;
                modify Zcytor5
        could be
                                                79.9%;
ilarity 87.5%;
Conservative
        antibody
                therapeutically to
Sequence 1813 BP;
                                                 Query Match
Best Local Similarity
Matches 729; Conserv
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New nucleic acid encoding U4 haematopoietin receptor superfamily chain - potentially useful, e.g. for modulating cell proliferation or immune response, for treating cancer and auto:immune disease claim 1; Page 28: 38pp; English.

Claim 1; Page 28: 38pp; English.

Chis is the nucleotide sequence encoding the human U4 protein from the haematopoietin receptor superfamily, used in the method of the invention for the modulation of cell proliferation, or the immune response. Transformed mammalian cells are used to produce recombinant U4 protein. The U4 protein is used to screen for specific binding agents, raise antibodies. It is also used as reagents for assays and in pharmaceutical compositions which may modulate cell proliferation, cell differentiation, and the immune system (e.g. for treating immune deficiency, inherited or the result of infection, autoimmune diseases, sequence 1579 BP; 304 A; 535 C; 473 G; 257 T;
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cell proliferation; immune response; antibody; cell differentiation; autoimmune disease; cancer; allergy; ds.
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Pred. No. 6.7e-165;
0; Mismatches 105; Indels
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                                                                     Location/Qualifiers
                                                                                                                                                                                     23-JUL-1998.
15-JAN-1998.
16-JAN-1997. US-784863.
(GEMY ) GENETICS INST INC.
COllins M, Donaldson DD, Neben T,
WPI: 98-414109/35.
P-PSDB: W59805.
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us-09-037-657-18.rng

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CDNA encoding human Zcytor5.

2cytor5; cytokinin-like receptor; down-regulation; growth factor;
maintenance factor; thyroid; heart; skeletal muscle; cardiotrophin-1;
cardiac pathology; heart enlargement; 2cytor5 ligand; ss.
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The present sequence encodes a protein designated Zcytor5, which is a cytokinin-like receptor. Soluble Zcytor5 may be administered to down-regulate the effects of a growth and/or maintenance factor in thyroid, heart, and skeletal muscle for example to lessen the effect of cardiotrophin-1 on cardiac pathologies, so preventing heart enlargement. Zcytor5 could be used to detect cardiotrophin-1 in the blood, and to discover other possible Zcytor5 ligands. A probe and integrity of the Zcytor5 gene on chromosome 19. Antibodies and therapeutically to modify Zcytor5 ligand effects.

Sequence 1690 BP; 319 A; 592 C; 505 G; 274 T;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (ZYMO) ZYMOGENETICS INC.
Adams RL, Foster DC, Gilbert T, Jelmberg AC, Lehner
Lok S, Presnell SR, Whitmore TE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            New mammalian cytokinin-like receptor 2cytor5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Disclosure; Page 63-66; 55pp; English.
                                                                                                                                                                                                                                                                                                                                                                    Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                          /*tag= a
/product= Zcytor5
                                                                                                                                                                                                                                                                      V70894 standard; cDNA; 1690
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01-MAY-1997; US-045287.
01-MAX-1997; US-850030.
13-FEB-1998; US-023890.
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WPI; 99-034662/03.
P-PSDB; W70860.
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01-MAY-1998;
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N27144 Standard; cDNA; 1391 BP.

N27144 Standard; cDNA; 1391 BP.

N27144 Standard; contact of the sequence of clone HFK-66 encoding human NR6.

Nucleotide sequence of clone HFK-66 encoding human NR6.

KW Haemopoletin receptor; cell proliferation; cell differentiation; cance of cell survival; therapeutic; neuronal proliferation; drug screening;
                                    tocogoctcottaacacotcoaccotggccctggccctggctaaccttaatgggtccagg
                                              tgcctctatgttggcttgcccctgagaagccctttaacatcagctgctggtcccggaac
                                                                                                                         atgaaggatotcacgtgccgctggacaccgggtgcacacgggggagacattcttacatacc
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Location/Qualiflers
1. .1053
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/product=
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11-SEP-1996; AU-002246.
(AMRA-) AMRAD OPERATIONS
(DZIE/) DZIEGLEWSKA H E.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /*tag=
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V27159
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                                                  claim 7; Page 102-104; 182pp; English.

The NRG gene encodes a novel Haemopoietin receptor (HR). Interaction between the novel HR and a lighand facilitates proliferation, differentiation and survival of a wide variety of cells. The HR and it's derivatives can be used for modulating the activity of the receptors e.g. to regulate development, maintenance or regeneration in an array of different cells and tissues in vitro and in vivo. They can be present in therapeutics used for modulating neuronal proliferation, differentiation and survival. The products can also be used for detection and diagnosis, e.g. for cancers or predisposition to cancers, or of rary screening. Sequence 1391 BP; 281 A; 459 C; 417 G; 234 T; screening.
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                                           of cells,
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                                    developing products
and survival of cell
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lton DJ, Kikuchi Y,
NA, Rakar S, Willson
                                                                                                                                                                     92;
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Pred. No. 1.3e-147;
); Mismatches 92;
                       WPI; 98-260970/23.
P-PSDB; W55015.
New isolated haemopoletin receptor - used for for modulating proliferation, differentiation
L, Farley A, Hilton
Nash A, Nicola NA, R
                                                                                                                                                                     ;
0
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Best Local Similarity 87.7%;
Matches 654; Conservative
   Alexander W, Fabri
Kojima T, Maeda M,
                       98-260970/23.
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While 90.260970/23.

When 90.260970/23.

New isolated haemopoletin receptor - used for developing products for modulating proliferation, differentiation and survival of cells.

To modulating proliferation, differentiation and survival of cells.

Disclosure; Page 101; 182pp; English.

NR6 is a novel haemopoletin receptor (HR). Interaction between the novel NR6 is a novel haemopoletin receptor (HR). Interaction and survival of a wide variety of cells. The HR and it's derivatives can be used for modulating the activity of the receptors e.g. to regulate development, maintenance or regeneration in an array of different cells and tissues in control and in vivo. They can be present in therapeutics used for modulating neuronal proliferation, differentiation and survival. The products can also be used for detection and diagnosis, e.g. for cancers or predisposition to cancers, or for drug screening.
                                                                                                                                                      V27159;
29-SEP-1998 (first entry)
PCR product for human NR6.
Haemopoletin receptor; cell proliferation; cell differentiation; cancer cell survival; therapeutic; neuronal proliferation; drug screening; ss;
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                                                                                                                                                                                                                                                                                 Homo sapiens.

WO981225-A2.
119-MR-1998.
11-SEP-1996, AU-002246.
(AMRA-) ANRAD OPERATIONS PTY LTD.
(AMRA-) DIEGLEWSKA H E.
Alexander W, Fabri L, Farley A, Hilton DJ, Kikuchi Y,
Kojima T, Maeda M, Nash A, Nicola NA, Rakar S, Willson
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88.4%; Pred. No. 2.1e-110;
ive 0; Mismatches 65;
833
                   gggatctatgggtcgaaaaaggcggg
                                                                                                                                         BP.
                                                                                                                                       standard; DNA; 560
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495; Conservative
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Best Local S:
Matches 495;
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WPI: 98-260970/23

New isolated haemopoietin receptor - used for developing products

Tor modulating proliferation, differentiation and survival of cells,

e.g. neuronal cells

Claim 9; Fig 3; 182pp; English.

Claim 9; Fig 3; Fig 3; Fig 3; Fig 3; Fig 4; F
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Nucleotide sequence for murine NR6 containing additional 5N sequence.
Haemopoietin receptor; cell proliferation; cell differentiation; cancer; cell survival; therapeutic; neuronal proliferation; drug screening; ss;
                             6356 CCCACCCTICTCATCGGCTCCTCCTGCAAGCTACCTGCTCTATACATGGAGACACACCT 6415
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595 gttggggggcctggaggaccagctgagtgtgcgctgggtctcaccaccagctctcaaggat
                                                                                                655 ttcctcttccaagccaagtaccagatccgctaccgcgtggaggacagcgtggactggaag
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Pred. No. 2.3e-57;
0; Mismatches 1; Indels 0;
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(DZIE/) DZIEGLEWSKA H E.
Alexander W, Fabri L, Farley A, Hilton DJ, Kikuchi Y,
Kojima T, Maeda M, Nash A, Nicola NA, Rakar S, Willson T,
                                                                                                                                                                                                                                                         541 GTGGTGGACGATGTGAGCAA 560
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Matches 255; Conservative
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11-SEP-1996; AU-002246
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WO9811225-A2.
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Claim 8; Page 108-114; 182pp; English.

Claim 8 Page 108-114; 182pp; English.

The NR6 gene encodes a novel Haemopoletin receptor (HR). Interaction between the novel HR and a ligand facilitates proliferation, differentiation and survival of a wide variety of cells. The HR and it's products can be used for modulating the activity of the receptors e.g. to requiate development, maintenance or regeneration in an array of different cells and tissues in vitro and in vivo. They can be present in therapeutics used for modulating neuronal proliferation, differentiation and survival. The products can also be used for detection and diagnosis, e.g. for cancers or predisposition to cancers, or for drug screening.

Sequence 6663 BP; 1462 A; 1852 C; 1715 G; 1634 T;
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New isolated haemopoletin receptor - used for developing products
for modulating proliferation, differentiation and survival of cells,
                                                                                AUCLECTICE SEQUENCE OF MULINE NRG.
Haemopoletin receptor; cell proliferation; cell differentiation; cancer; cell survival; therapeutic; neuronal proliferation; drug;
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11-SEP-1997; GD2479.
11-SEP-1996; AU-002246.
(AMRA-) ANRAD OPERATIONS PTY LTD.
(DZIE/) DZIEGLEWSKA H E.
Alexander W, Fabri L, Farley A, Hilton DJ, Kikuchi Y,
Kojima T, Maeda M, Nash A, Nicola NA, Rakar S, Willson
                                                                                                                                                                                                                                                                                                                                                                   /note= "No start or stop codon given'
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Pred. No. 2e-57;
0; Mismatches 1;
                                                                                                                                                                                                                                                                                                                                   /product- "Murine NR6"
                                                                                                                                                                                                                                            Location/Qualifiers
1182. .1744
/*tag= a
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                                                           3 (first entry)
sequence of Murine
V27145 standard; DNA; 6663 BP
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V70897;
17-MAR-1999 (first entry)
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Best Local Similarity 99.6
Matches 255; Conservative
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                            V27145;
02-0CT-1998
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The present sequence represents an expressed sequence tag (EST) used to identify CDNA encoding a protein designated Zcytor5, which is a cytokinin-like receptor. Soluble Zcytor5 may be administrated to down-regulate the effects of a growth and/or maintenance factor in thyroid, heart, and skeletal muscle for example to lessen the effect of cardiotrophin-1 on cardiac pathologies, so preventing heart of cardiotrophin-1 on cardiac pathologies, so preventing heart of cardiotrophin-1 on the possible Zcytor5 ligands. A probe comprising Zcytor5 DNA or RNA can be used to determine the presence and integrity of the Zcytor5 gene on chromosome 19. Antibodies and the anti-idiotypic antibody could be used to purify Zcytor5 and therapeutically to modify Zcytor5 ligand effects.
Sequence 259 BP; 53 A; 64 C; 81 G; 46 T;
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maintenance factor; thyroid; heart; skeletal muscle; cardiotrophin-l;
cardiac pathology; heart enlargement; 2cytor5 ligand; EST; ss.
W09849307-A1.
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             Zcytor5; cytokinin-like receptor; down-regulation; growth factor;
maintenance factor; thyroid; heart; skeletal muscle; cardiotrophin-l;
cardiac pathology; heart enlargement; Zcytor5 ligand; EST; ss.
Unidentified.
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                                                                                                                                                                                                                                                                                                 New mammalian cytokinin-like receptor Zcytor5 - useful for, e.g. down-regulating Zcytor5 natural ligands or detecting cardiotrophin-1
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Adams RL, Foster DC, Gilbert T, Jelmberg AC, Lehner JM,
LOK S, Presnell SR, Whitmore TE;
WPI; 99-034662/03.
 Expressed sequence tag used to identify human 2 cytor5
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Expressed sequence tag used to identify human
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US-045287.
US-850030.
US-023890.
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01-MAY-1997; US-850030
13-FEB-1998; US-023890
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01-MAY-1998; U08865
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Matches 153; Conser
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Search completed: September 28, 1999, 16:45:58 Job time: 7343 sec

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Example 1; Page 77; S5pp; English.

The present sequence represents an expressed sequence tag (EST)

used to identify cone encoding a protein designated zcytor5, which is

used to identify cone encoding a protein designated zcytor5, which is

c stokinin-like receptor. Soluble Zcytor5 may be administered to

down-regulate the effects of a growth and/or maintenance factor in

thyroid, heart, and skeletal muscle for example to lessen the effect

c cardiotrophin-1 on cardiac pathologies, so preventing heart

c cardiotrophin-1 on cardiac pathologies, so preventing heart

blood, and to discover other possible Zcytor5 ligands. A probe

comprising Zcytor5 DNA or RNA can be used to determine the presence

and integrity of the Zcytor5 gene on chromosome 19. Antibodies and the

anti-idiotypic antibody could be used to purify Zcytor5 and

therapeutically to modify Zcytor5 ligand effects.

c therapeutically to modify Zcytor5 ligand effects.
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                                                                                New mammalian cytokinin-like receptor Zcytor5 - useful for, e.g. down-regulating Zcytor5 natural ligands or detecting cardiotrophin-l in blood
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        RL, Foster DC, Gilbert T, Jelmberg AC, Lehner JM,
Presnell SR, Whitmore TE;
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                                                                     WPI; 99-034662/03.
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/cgn2_6/ptcdata/2/ina/FCTUS9_COMB.seq:*
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GenCore version 4.5
Copyright (c) 1993 - 1998 Compugen Ltd.
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парычана		14, Application US/08232463 INFORMATION: ANT: DORNER, F. ANT: SCHEIFLINGER, F. ANT: FALKERR, F. G. OF INVENTION: ECCOMBINANT FOR ESSEE: FOLGY & Lardner IS ALEXANDERS: 52 PRONDENCE ADDRESS: ESSEE: VA TEX: 1800 Diagonal Road, Sul: ESSEE: VA TEX: 1800 Diagonal Road, Sul: EN READABLE FORM: UM TYPE: IBOPY disk UM TYPE: IBOPY disk UM TYPE: IBOPY disk UM TYPE: IBOPY disk UM TYPE: IBOPY disk UM TYPE: BATHON NUMBER: US/07/935,3 ICATION NUMBER: US/07/935,3 ING DATE: INCOMMUNICATION INFORMATION: EN BENT, STEPHON A STRAATION NUMBER: 29,768 RENCE/DOCKET NUMBER: 29,768 RENCE/DOCKET NUMBER: 39,768 RENCE/DOCKET N	Zgpt-Fls larity 1.3 Conservative ttctcatcggct. :::::::: XYYXYXYXXXX ccgctgaggggc: :::::::::::::::::::::::::::::::
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APPLICANT: Little, Michael C.
TILLE OF INVENTION: MYCOBACTERIOPHAGE SPECIFIC FOR THE TILLE OF INVENTION: MYCOBACTERIOM TUBERCULOSIS COMPLEX NUMBER OF SEQUENCES:
CORRESPONDENCE ADDRESS:
ADDRESSEE: Richard J. Rodring Streem
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LOCATION: 222.425
OTHER INFORMATION: /function= "potential open reading
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
SURRIMARE: APPLICATION DATA:
APPLICATION NUMBER: US/08/402,282
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ATORNEY/AGENT INFORMATION:
NAME: FUGHT, DOING R.
REGISTRATION NUMBER: P.
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 15664 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EATURE:
-NAME/KEY: misc_feature
LOCATION: 1109..2014
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Franklin Lakes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                       783 cgtccaagtgcgt 795
                                                                                                                               393 CGCTCCGAGGGT 405
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ZIP: 07417
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FEATURE:
NAME/KEY:
LOCATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COUNTRY:
                                            В
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ö
                                                                                                                                                      121 tecegectecttaacacetecacetggecetggecetggetaacettaatgggtecagg 180
                                                                                                                           241 tgcctctatgttggcttgcccctgagaagccctttaacatcagctgctggtcccggaac 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               663 ccaagccaagtaccagatccgctaccgcgtggaggacagcgtggaaggtggtgg 722
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        273 CCTGGCCATGGAGATGCTCCGGGACATCGACGAGGACAGCGTCGACTTCCAGGACAACTA 332
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 423;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Huang Ph.D, Wai Mun
TITLE OF INVENTION: Method and Compositions for
TITLE OF INVENTION: Identification of Species in a Sample
NUMBER OF SEQUENCES: 207
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/470,179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 35.4; DB 2;
Pred. No. 0.58;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
4.2%; Score 35.4; Di
Best Local Similarity 54.1%; Pred. No. 0.58
Matches 72; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ADDRESSEE: Trask, Britt and Rossa STREET: P.O. Box 2550
CIIY: Salt Lake City
                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 109, Application US/08470179 Patent No. 5645994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ; ORGANISM: Actinomyces naesundii
US-08-470-179-109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Swelgert Ph.D. Susan E.
REGISTRATION NUMBER: 36,289
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  REFERENCE/DOCKET NUMBER: 26
FELECOMMUNICATION INFORMATION:
TELEPHONE: 801-532-1922
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: NO
ANTI-SENSE: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LENGTH: 423 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   not relevant
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELEFAX: 801-531-9168
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ZIP: 84110
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CORRESPONDENCE ADDRESS ADDRESS: Trask, Bi
                                                                                                                                                                                                                                                                                                                                                                                                                              US-08-470-179-109
                                                                                                                                                                                                                                                                                                                                           1440 A 1440
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                                                                          NAME/KEY: misc_feature
LOCATION: 2747.3109
OTHER INFORMATION: /function- "potential open reading
OTHER INFORMATION: frame"
                                                                                                                                                                                    NAME_KEX: misc_feature
LOCATION: 3109..344
OTHER INFORMATION: /function= "potential open reading
OTHER INFORMATION: frame"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME/KEY: misc_feature
LOCATION: 3731..4855
OTHER INFORMATION: /function= "potential open reading
OTHER INFORMATION: frame"
OTHER INFORMATION: /function= "potential open reading OTHER INFORMATION: frame"
EATURE:
                                                                                                                                                                                                                                                                                                                                    NAME/KEY: misc_feature
LOCATION: 3444..3728
OTHER INFORMATION: /function= "potential open reading
OTHER INFORMATION: frame"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NAME/KEY: misc_feature
LOCATION: 5382..5747
OTHER INFORMATION: /function= "potential open reading
OTHER INFORMATION: frame"
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LOCATIONS 5837.6307
OTHER INFORMATION: /function= "potential open reading
OTHER INFORMATION: frame"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NAME/KEY: misc_feature
LOCATION: 6403..7770
OTHER INFORMATION: /function= "potential open reading
OTHER INFORMATION: frame"
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LOCATION: 7770..8006
OTHER INFORMATION: /function= "potential open reading
OTHER INFORMATION: frame"
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LOCATION: 8033..8236
OTHER INFORMATION: /function=."potential open reading
OTHER INFORMATION: frame"
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LOCATION: 8244..943
OCHER INFORMATION: /function= "potential open reading
OTHER INFORMATION: frame"
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LOCATION: 9450..1024
OTHER INFORMATION: /function= "potential open reading
OTHER INFORMATION: frame"
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LOCATION: 10371..10586
OTHER INFORMATION: /function= "potential open reading
OTHER INFORMATION: frame"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /function= "potential open reading frame"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NAME/KEY: misc_feature
LOCATION: 4855..5376
OTHER INFORMATION: /function= "potential coding
OTHER INFORMATION: sequence"
OTHER: INFORMATION: /product= "L5 gp37 homolog".
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LOCATION: 11115..11786
OTHER INFORMATION: /fur
OTHER INFORMATION: fran
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Db 12218 TCGGCAAGCACCGGCCGCTGTTCGATGACCGGCCGAACACGGTAGCGCTTACCGAGGCCC 12277
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  509 taggeteageaagatetgatgteeteacaetggatgteetggaegtggteaceeggaee 568
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               12338 ACCAGGACGACGACGACGACGCCCGTGCAGTCCCTCGGCGACGAGCACCGCGCCCC 12395
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      569 occoaccogacytycacytyayccycyttygygygcotygayyaccayctyaytytycy 626
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               449 tececaaggacetggeeetetteaetecetatgagatetgggtggaageeaetegee
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APPLICANT: Hamilton, Paul T.
APPLICANT: Hamilton, Paul T.
APPLICANT: Little, Michael C.
APPLICANT: Beyer Jr., Wayne F.
ITLE OF INVENTION: MYCOBACTERIOPHAGE SPECIFIC FOR THE TITLE OF INVENTION: MYCOBACTERIUM TUBERCULOSIS COMPLEX NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
ADDRESSEE: Richard J. Rodrick, Becton Dickinson and STREET: I Becton Drive CITY: Franklin Lakes
COUNTRY: US
ZID.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 15664;
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               LOCATION: 11917..12741
OTHER INFORMATION: /function= "potential open reading OTHER INFORMATION: frame"
                                                                            FEATURE:
NAME/KET: misc.feature
NAME/KET: misc.feature
LOCATION: 12748.14499
OTHER INFORMATION: /function- "potential open reading
OTHER INFORMATION: frame"
NAME/KEY: misc_feature
                                                                                                                                                                                NAME/KEY: misc_feature
LOCATION: 14771..15154
OTHER INFORMATION: /function= "potential open reading
OTHER INFORMATION: frame"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /function- "potential open reading frame"
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frame"
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APPLICATION NUMBER: US/08/508,004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           4.1%; Score 34; DB 1;
49.4%; Pred. No. 3.8;
tive 0; Mismatches 90
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER: IBM PC COMPATIBLE OPERATING SYSTEM: PC-DOS/MS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ZIP: 07417
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                 misc_feature
                                                                                                                                                                                                                                                                                                                       NAME/KEY: misc_feature
LOCATION: 15154.,15426
OTHER INFORMATION: /fur
OTHER INFORMATION: fran
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity 49.4
Matches 88; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RESULT 4
US-08-508-004-3
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us-09-037-657-18.rni

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NAME/KEY: misc_feature
LOCATION: 3444.3728
OTHER INFORMATION: /function= "potential open reading
OTHER INFORMATION: frame"
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OTHER INFORMATION: /function= "potential open reading
CATER INFORMATION: frame"
EATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NAME/KEY: misc_feature
LOCATION: 2034..2747
OTHER INFORMATION: /function= "potential open reading
OTHER INFORMATION: frame"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NAME/KEY: misc_feature
LOCATION: 2747..3109
OTHER INFORMATION: /function= "potential open reading
OTHER INFORMATION: frame"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME/KEY: misc_feature
LOCATION: 3109.3444
OTHER INFORMATION: /function= "potential open reading
OTHER INFORMATION: frame"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NAME/KEY: misc_feature
LOCATION: 3731.4855
OCHER INFORMATION: /function= "potential open reading
OTHER INFORMATION: frame"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NAME/KEY: misc_feature
LOCATION: 451..747
OCHER INVENARIUN: /function= "potential open reading
OTHER INFORMATION: frame"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NAME/KEY: misc_feature
LOCATION: 747..1109
OTHER INFORMATION: /function= "potential open reading
OTHER INFORMATION: frame"
                                                                                                                                                                                                                                                                                                                                                                                                                                                NAME/KEY: misc_feature
LOCATION: 222.425
OCHER INFORMATION: /function= "potential open reading
OTHER INFORMATION: frame"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NAME/KEY: misc_feature
LOCATION: 1109..2014
OCHER INFORMATION: /function= "potential open reading
OTHER INFORMATION: frame"
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sequence"
/product= "L5 gp37 homolog"
FILING DATE: 27-JUL-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/402,282
FILING DATE: 10 MAR-1995
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                         NAME: Fugit, Donna R.
REGISTRATION NUMBER: 32,135
REFERENCE/DOCKET NUMBER: P-1
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                   TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NAME/KEY: misc_feature
LOCATION: 4855..5376
OTHER INFORMATION: /func
OTHER INFORMATION: seque
OTHER INFORMATION: /prod
                                                                                                                                                                                                                                                                                       LENGTH: 15664 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NAME/KEY: misc_feature
LOCATION: 5382..5747
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NAME/KEY: misc_feature
LOCATION: 5837.6307
OTHER INFORMATION: /function= 'potential open reading
OTHER INFORMATION: /function= 'potential open reading
OTHER INFORMATION: /function= 'potential open reading
OTHER INFORMATION: /function= 'potential open reading
OTHER INFORMATION: /function= 'potential open reading
OTHER INFORMATION: frame"
                                                                                                                                                                                                                                                                                                                                                                                                        NAME/KEY: misc_feature
LOCATION: 8033.8236
OCHER INFORMATION: /function= "potential open reading
OTHER INFORMATION: frame"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NAME/KEY: misc_feature
LOCATION: 10371..10586
OTHER INFORMATION: /function- "potential open reading
OTHER INFORMATION: frame"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME/KEY: misc_feature
LOCATION: 11115.11786
OTHER INFORMATION: /function= "potential open reading
OTHER INFORMATION: frame"
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LOCATION: 12748..14499
OCHER INFORMATION: /function- "potential open reading
OTHER INFORMATION: frame"
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LOCATION: 14771..15154
OTHER INFORMATION: /function= "potential open reading
OTHER INFORMATION: frame"
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COCATION: 15429..15664
COTHER INFORMATION: /function- "potential open reading of the INFORMATION: frame"
                                                                                                                                                                                                                                                                       NAME/KEY: misc_feature
LOCATION: 770..806
COCHER INFORMATION: /function= "potential open reading
OTHER INFORMATION: frame"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NAME/KEY: misc_feature
LOCATION: 8244..9443
OCHER INFORMATION: /function= "potential open reading
OTHER INFORMATION: frame"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME/KEY: misc_feature
LOCATION: 11917..1274
OCHER INFORMATION: /function- "potential open reading
OTHER INFORMATION: frame"
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frame"
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NAME/KEY: misc_feature
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OTHER INFORMATION: /fur
OTHER INFORMATION: fran
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NAME/KEY:
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449 tececaaggacetggeectetteactecetatgagatetgggtggaagceaceaategee 508

Score 34; DB 1; Length 15664; Pred. No. 3.8; 0; Mismatches 90; Indels

Query Match
Best Local Similarity 49.4%;
Matches 88; Conservative

us-09-037-657-18.rni

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OTHER INFORMATION: /function= "potential open reading OTHER INFORMATION: frame" | FPATURE: NAME/KEY: misc_feature
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NAME/KEY: misc_feature
LOCATION: 5837..6307
OTHER INFORMATION: /function= 'potential open reading
OTHER INFORMATION: frame'
NAME/KEY: misc_feature
LOCATION: 6403..7770
OTHER INFORMATION: /function= 'potential open reading
OTHER INFORMATION: frame"
                                                                                                                                                                                                                                                                 NAME/KEY: misc_feature
LOCATION: 3109..3444
OTHER INFORMATION: /function= "potential open reading
OTHER INFORMATION: frame"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NAME/KEY: misc_feature
LOCATION: 3731.4853
OCHER INFORMATION: /function= "potential open reading
OTHER INFORMATION: frame"
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OTHER INFORMATION: /function- "potential open reading OTHER INFORMATION: frame"
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LOCATION: 8033..8236
OTHER INFORMATION: /function= "potential open reading
OTHER INFORMATION: frame"
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LOCATION: 8244..9443
OTHER INFORMATION: /function= "potential open reading
OTHER INFORMATION: frame"
                                                                                                                                                                                                                                                                                                                                                                                                                                                     "potential open reading
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frame"
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OTHER INFORMATION: /function- "potential open reading OTHER INFORMATION: frame"
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OTHER INFORMATION: /function= "potential open reading OTHER INFORMATION: frame"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LOCATION: 4855_.5376
OTHER INFORMATION: /function= "potential coding OTHER INFORMATION: sequence"
OTHER INFORMATION: /product= "L5 gp37 homolog"
                                                                                                                                            NAME/KEY: misc_feature
LOCATION: 2747.:3109
LOCATEN INFORMATION: /function= "potential open
OTHER INFORMATION: frame"
                                                                                                                                                                                                                                                                                                                                                                                            NAME/KEY: misc_feature
LOCATION: 3444..3728
OTHER INFORMATION: /function=
OTHER INFORMATION: frame"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NAME/KEY: misc_feature
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LOCATION: 7770.8006
OTHER INFORMATION: /fur
OTHER INFORMATION: first
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LOCATION: 10371..10586
12218 TCCGCAAGCACCGGCCGCTGTTCGATGACCGGCCGAACACGGTAGCGCTTACCGAGGCCC 12277
                                                                                                   12278 IGCIGGACGCCGCGACGACGCCATGAAAGCGCAAGAGGCCGCGCGGAGTICACCGCCCGCC 12337
                                                      taggeteageaagatetgatgteeteacaetggatgteetggacgtggtgaccaeggace 568
                                                                                                                                                                                                12338 ACCAGGACGACGACGACGACAGCCCCGTGCAGTCCCTCGGCGACGACGACGCGCCCG 12395
                                                                                                                                                 569 ccccacccgacgtgcacgtgagccgcgtgggggcctggaggaccagctgagtgtgcg 626
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME/KEY: misc_feature
LOCATION: 222..425
OTHER INFORMATION: /function= "potential open reading
OTHER INFORMATION: frame"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LOCATION: 1109_.2014
OTHER INFORMATION: /function= "potential open reading OTHER INFORMATION: frame"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /function- "potential open reading frame"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Beyer Jr., Wayne F.
TITLE OF INVENTION: MYCOBACTERIOPHAGE SPECIFIC FOR THE
TITLE OF INVENTION: MYCOBACTERIUM TUBERCULOSIS COMPLEX
NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               "potential open reading
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ADDRESSEE: Richard J. Rodrick, Becton Dickinson and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SOFTWARE: Patentin Release #1.0, Version #1.25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICATION NUMBER: US/08/402,06
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                equence 3, Application US/08402066
atent No. 5612182
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CLASSIFICATION: 436
-ATTORNEY/AGENT INFORMATION:
NAME: Fugit, Donna R.
-REGISTRATION NUMBER: 32,135
REFERENCE/DOCKET NUMBER: P-
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH 15664 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 32,135
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MOLECULE TYPE: DNA (genomic)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ittle, Michael
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ZIF: 0171.
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPALI
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LOCATION: 747..1109
OTHER INFORMATION: /fun
OTHER INFORMATION: fram
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LOCATION: 451..747
OTHER INFORMATION: /fur
OTHER INFORMATION: fran
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LOCATION: 1109..2014
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: 1 Becton Drive
Franklin Lakes
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NAME/KEY: misc_feature
LOCATION: 451..747
OTHER INFORMATION: /function= "potential open reading
OTHER INFORMATION: frame"
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NAME/KEY: misc_feature
LOCATION: 2034..2747
COTHER INFORMATION: /function= "potential open reading
OTHER INFORMATION: frame"
                                                                                                                                                                                                                                                                                                                                                                                                                          NAME/KEY: misc_feature
LOCATION: 222..425
OCHER INFORMATION: /function= "potential open reading
OTHER INFORMATION: frame"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NAME/KEY: misc_feature
LOCATION: 747-1109
OCHER INFORMATION: /function= "potential open reading
OTHER INFORMATION: frame"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME/KEY: misc_feature
LOCATION: 1109..2014
O'THER INFORMATION: /function- "potential open reading
OTHER INFORMATION: frame"
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LOCATION: 3109..344
OCHER INFORMATION: /function- "potential open reading
OTHER INFORMATION: frame"
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LOCATION: 3444..3728
COCHER INFORMATION: /function= "potential open reading
OTHER INFORMATION: frame"
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LOCATION: 3731.4855
OCHER INFORMATION: /function- "potential open reading
OTHER INFORMATION: frame"
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LOCATION: 5382.5747
OTHER INFORMATION: /function= "potential open reading
OTHER INFORMATION: frame"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /function- "potential open reading frame"
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/402,068
FILING DATE:
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: FUGIt, Donna R.
REGISTRATION NUMBER: 32,135
REFERENCE/DOCKET NUMBER: P-3283
INPORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LOCATION: 4855.5376
OTHER INFORMATION: /function=
OTHER INFORMATION: sequence"
OTHER INFORMATION: /product= ";
FRATURE:
NAME/KEY: misc_feature
                                                                                                                                                                                                                                                                                                                                                TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
FEATURE:
                                                                                                                                                                                                                                                                  LENGTH: 15664 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME/KEY: misc_feature
LOCATION: 2747..3109
OTHER INFORMATION: /fur
OTHER INFORMATION: fram
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    NAME/KEY: misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Db 12218 TCCGCAAGCACCGGCCGCTGTTCGATGACCGGCCGAACACGGTAGCGCTTACCGAGGCCC 12277
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         509 taggetcageaagatetgatgteetcaeactggatgteetggaegtggtgaeeacggaee 568
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 12338 ACCAGGACGACCAGGACGACAGCCCCGTGCAGTCCCTCGGCGACGACGACCGCCCCG 12395
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 449 tececaaggaeetggeeetetteaeteeetatgagatetgggtggaageeaeeaategee 508
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                569 ccccacccgacgtgcacgtgagccgcgttggggggcctggaggaccagctgagtgtgcg 626
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 34; DB 1; Length 15664; Pred. No. 3.8; 0; Mismatches 90; Indels
                                                                             NAME/KEY: misc_feature
LOCATION: 11917..12741
OTHER INFORMATION: frame"
OTHER INFORMATION: frame"
OTHER INFORMATION: frame"
NAME/KEY: misc_feature
LOCATION: 12748..14499
OTHER INFORMATION: function- "potential open reading other INFORMATION: frame"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         , NAME/KEY: misc_feature
; LOCATION: 15429.,15664
; OTHER INFORMATION: /function= "potential open reading
; OTHER INFORMATION: frame"
US-08-402-066-3
OTHER INFORMATION: /function= "potential open reading OTHER INFORMATION: frame"
PATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                      FEATURE:
NAME/KEY: misc_feature
LOCATION: 15154..15426
OTHER INFORMATION: /function= "potential open reading
OTHER INFORMATION: frame"
                                                                                                                                                                                                                                                                                                                                                NAME/KEY: misc_feature
LOCATION: 14771.1517
OCHER INFORMATION: /function= "potential open reading
OTHER INFORMATION: frame"
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APPLICANT: Hamilton, Paul T.
APPLICANT: Little, Michael C.
APPLICANT: Little, Michael C.
APPLICANT: Little, Michael C.
TITLE OF INVENTION: MYCOBACTERIOPHAGE SPECIFIC FOR THE
TITLE OF INVENTION: MYCOBACTERIUM TUBERCULOSIS COMPLEX
NUMBER OF SEQUENCES:
ADDRESSEE: Richard J. Rodrick, Becton Dickinson and
ADDRESSEE: Company
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Patentin Release #1.0, Version #1.25
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Patent No. 5633159
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity 49.4%;
Matches 88; Conservative
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CITY: Franklin Lakes
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569 ccccacccgacgtgcacgtgagccgcgttgggggcctggaggaccagctgagtgtgcg

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LOCATION: 5837..6307
OTHER INFORMATION: /function= "potential open reading
OTHER INFORMATION: frame"
                                                                           NAME/KEY: misc_feature
LOCATION: 6403..7770
OTHER INFORMATION: /function= "potential open reading
OTHER INFORMATION: frame"
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; LOCATION: 15429..15664
; OTHER INFORMATION: /function- "potential open reading
; OTHER INFORMATION: frame"
                                                                                                                                                                                                                                              NAME/KEY: misc_feature
LOCATION: 7770..8006
OTHER INFORMATION: /function= "potential open reading
OTHER INFORMATION: frame"
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LOCATION: 9450..10244
OTHER INFORMATION: /function= "potential open reading
OTHER INFORMATION: frame"
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LOCATION: 10371.10586
OTHER INFORMATION: /function= "potential open reading
OTHER INFORMATION: frame"
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LOCATION: 11115..11786
OTHER INFORMATION: /function= "potential open reading
OTHER INFORMATION: frame"
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OTHER INFORMATION: /function= "potential open reading OTHER INFORMATION: frame"
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LOCATION: 12748..14499
OTHER INFORMATION: /function= "potential open reading
OTHER INFORMATION: frame"
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LOCATION: 14771.1515
OCHER INFORMATION: /function= "potential open reading
OTHER INFORMATION: frame"
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LOCATION: 15154..15426
OTHER INFORMATION: /function= "potential open reading
OTHER INFORMATION: frame"
                                                                                                                                                                                                                                                                                                                                                                                                                                              reading
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LOCATION: 8033..8236
LOCATION: 6733..8236
LOCATION: frame" potential open
OTHER INFORMATION: frame"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME/KEY: misc_feature
LOCATION: 8244..943
LOCATION: 8244..943
OTHER INFORMATION: frame" potential open
OTHER INFORMATION: frame"
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LOCATION: 11917..12741
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     367 TTCAGCTCGGCCTGGCGGGGACACACTGCGTCCAGCAGCGGGGGGAGCGCGGCCAGCGCC 308
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  542 atgtcctggacgtggtgaccacggaccccccaccgacgtgcacgtgagccgcgttggg
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                                                                           APPLICANT: Baker, Joffre
APPLICANT: Chien, Kenneth
APPLICANT: Chien, Kathleen
APPLICANT: Pennica, Diane
APPLICANT: Pennica, Diane
APPLICANT: Wood, William
TITLE OF INVENTION: Cardiac Hypertrophy Factor and INTMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0; Mismatches 131;
                                                                                                                                                                                                                                                                                                                                                             COMPUTER READABLE FORM:
MEDIUM TYPE: 5.25 inch, 360 Kb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                    OPERATING CONTWARE: patin (General CONTWARE: patin (General APPLICATION DATA: APPLICATION NUMBER: US/08/444,083
                                                                                                                                                                                                                                  SEE: Genentech, Inc.
1960 Point San Bruno Blvd
South San Francisco
California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/233609
FILING DATE: 25-APR-1994
FRIDK APPLICATION DATA:
APPLICATION NUMBER: 08/286304
FILING DATE: 05-AUG-1994
ATTORNEY/AGBNT INFORMATION:
NAME: TOTCHIA, TIMOCHY E.
                          Sequence 6, Application US/08444083 Patent No. 5571675
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELECOMMUNICATION INFORMATION TELEPHONE: 415/225-8674 TELEFAX: 415/952-9881
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             46.18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Best Local Similarity 46.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         REFERENCE/DOCKET NUMBER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELERAX: 415/952-9881
TELEX: 910/371-7168
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  REGISTRATION NUMBER:
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                                                                                                                                                                                                                                           ADDRESSEE:
JS-08-444-083-6/c
                                                                                                                                                                                                                                                                                                                      COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           US-08-444-083-6
                                                                                                                                                                                                                                                                                                      STATE:
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Gaps

90; Indels

0; Mismatches

4.1%; Score 34; DB 1; Length 15664; 49.4%; Pred. No. 3.8;

Query Match
Best Local Similarity 49.4
Matches 88; Conservative

Db 12218 TCCGCAAGCACCGGCGCTGTTCGATGACCGGCCGAACACGGTAGCGCTTACCGAGGCCC 12277 449 tececaaggaeetggecetetteaeteeetatgagatetgggtggaageeaetegee 508

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602 gcctggaggaccagctgagtgtgcgctgggtctcaccaccagctctcaaggatttcctct 661
662 tecaagecaagtaccagatecgetacegegtggaggacagegtggactggaaggtggtgg 721
                                            307 GCCGCGTCCAGCCGCAGCCGCTCGTGCACTGGCAGCCCCGCGTGGCTCGGAGCCGGGGCG 248
                                                                                           722 atgaegteageaaceagaeeteetgeegtetegegggeetgaageeeggeaeegtttaet 781
                                                                                                                                       247 CTCAGGCCGGCCACCGGCAGCCGCGGCGAGAAGCTGGGCAGCCCGAAGGGGTCTCCC 188
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    542 atgtcctggacgtggtgaccacggaccccccacccgacgtgcacgtgagccgcgttgggg 601
                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Baker, Joffre
APPLICANT: Chien, Kenneth
APPLICANT: King, Kathleen
APPLICANT: Fennica, Diane
APPLICANT: Wood, William
TITLE OF INVENTION: Cardiac Hypertrophy Factor and Uses Therefor
NUMBER OF SEQUENCES: 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 1018;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDIUM TYPE: 5.25 inch, 360 Kb floppy disk COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 33.4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CLASSIFICATION: 435
PRIOR APPLICATION DATA:
PRIOR APPLICATION NUMBER: 08/233609
FILING DATE: 25-APR-1994
PRIOR APPLICATION DATA:
APPLICATION UNBER: 08/286304
FILING DATE: 05-AUG-1994
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                      Sequence 6, Application US/08442745 Patent No. 5624806
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ADDRESSEE: Genentech, Inc.
STREET: 460 Point San Bruno
IITY: South San Francisco
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TELECOMMUNICATION INFORMATION TELEPHONE: 415/225-8674
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  orchia, Timothy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity 46.1
Matches 112; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SOFTWARE: patin (Genen CURRENT APPLICATION DATA: APPLICATION NUMBER: US
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS
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MEDIUM TYPE: 5.25 in
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STATE: C
COUNTRY:
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                                                                                                                                     247 CICAGGCGGCCACCGGCAGCCGCGGGGGAAGCIGGGCAGCCCGAAGGGGTCTCCC 188
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                                                 307 GCCGCGTCCAGCCGCAGCCGCTCGTGCACTGGCAGCCCCGGGGTGGCTCGGAGCCGGGGCG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TITLE OF INVENTION: Cardiac Hypertrophy Factor and Uses Therefor NUMBER OF SEQUENCES: 8
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Pred. No. 2.5;
0; Mismatches 131; Indels 0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   UMBER: US/08/286,304
05-AUG-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ADDRESSEE: Genentech, Inc.
STREET: 460 Point San Bruno Blvd
CITY: South San Francisco
STATE: Callfornia
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APPLICATION NUMBER: 08/233609
FILING DATE: 25-APR-1994
                                                                                                                                                                                                                                                                                                                                                         Sequence 6, Application US/08286304
Patent No. 5571893
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SOFTWARE: patin (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/
                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Baker, Joffre
APPLICANT: Chien, Kenneth
APPLICANT: King, Kathleen
APPLICANT: Pennica, Diane
APPLICANT: Wood, William
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FILING DATE: 25-APR-1994 ATTORNEY/AGENT INFORMATION:
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Matches 112; Conservative
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 1018 bases
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662 tccaagccaagtaccagatccgctaccgcgtggaggacagcgtggactggaaggtggtgg 721
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                360 Kb floppy disk
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STREET: 460 Point San Bruno Blvd
CITY: South San Francisco
ATATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PC-DOS/MS-DOS
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FILING DATE: 05-AUG-1994
IOR APPLICATION DATA:
APPLICATION NUMBER: 304
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Pennica, Diane
Wood, William
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IEDIUM TYPE: 5.25 inch,
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INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
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US-08-443-129-6
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Gaps

Score 33.4; DB 1; Length Pred. No. 2.5; O; Mismatches 131; Indels

Query Match
Best Local Similarity 46.1
Matches 112; Conservative

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427 AGGGCCCGGGCCTGGCGCGCGCGTCCTCCAGGCGCGCAGCAGCGCGGGGCGCGCGGG 368
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                                                                                                       602 gcctggaggaccagctgagtgtgcgctgggtctcaccaccagctctcaaggatttcctct 661
                                                                                                                                                                                                                                                                                                                   722 atgacgicagcaaccagacciccigccgictcgcgggccigaagcccggcaccgittaci 781
542 atgtcctggacgtggtgaccacggacccccacccgacgtgcacgtgagccgcgttgggg
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: 460 Point San Bruno Blvd
South San Francisco
California
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17-MAY-1995
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FILING DATE: 25-APR-1994
SRICK APPLICATION DATA:
APPLICATION NUMBER: 08/286304
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Wood, William
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Search completed: September 28, 1999, 16:40:33 Job time: 7019 sec

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                                                                                                                                                                                                Length 1018;
                                                                                                                                                                                                Score 33.4; DB 2; Length 19 Pred. No. 2.5; 0; Mismatches 131; Indels
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GENERAL INFORMATION:
APPLICANT: Genentech, Inc.
TITLE OF INVENTION: Cardiotrophin and Uses Therefor
NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech, Inc.
STRET: 460 Point San Bruno Blvd
CITY: South San Francisco
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MEDIUM TYPE: 5.25 inch, 360.Kb floppy disk
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CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/04467
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  IBM PC compatibl
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APPLICATION NUMBER: 08/2.
FILING DATE: 25-APR-1994
ATTORNEX/AGENT INFORMATION:
                                                                                                                                                                                                     4.0%;
                                                                                                                                                                                                                                                     46.18;
                                                                                                                                                                                          Query Match
Best Local Similarity 46.1
Matches 112; Conservative
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; TOPOLOGY: linear
US-08-443-130-6
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                DB 2; Length 1018;
     Score 33.4; DB 2; Length 1 Pred. No. 2.5; 0; Mismatches 131; Indels
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Therefor
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FLESSIFICATION: 435
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STREET: 460 Point San Bruno Blvd
CITY: South San Francisco
STATE: California
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APPLICATION NUMBER: 08/233609
FILING DATE: 25-APR-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/286304
FILING DATE: 05-AUG-1994
ATTORNEY/AGENT INFORMATION:
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     Query Match
Best Local Similarity 46.1%;
Matches 112; Conservative
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Pennica, Diane
Wood, William
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TITLE OF INVENTION: The
NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech,
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APPLICANT:
APPLICANT:
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Best Local Similarity 59.6%; Pred. No. 8.4;
Matches 56; Conservative 0; Mismatches
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                                                                                                                                                                                                                                                                                           307 GCCGCGTCCAGCCGCAGCCGCTCGTGCACTGGCAGCCCCGCGTGGCTCGGAGCCGGGGCG 248
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                           0; Gaps
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Best Local Similarity 46.1%; Pred. No. 2.5;
Matches 112; Conservative 0; Mismatches 131; Indels
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90 PARK AVENUE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELEFAX: (212) 286-0854 or 286-0082
TELEX: TWX 710-581-4766
INFORMATION FOR SEQ ID NO: 1:
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REFERENCE/DOCKET NUMBER: 96700/402
FLECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICATION NUMBER: US/08/614,770A
FILING DATE: MARCH 7, 1996
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NAME: ELIZABETH A. BOGOSIAN
REGISTRATION NUMBER: 39,911
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NUMBER OF SEQUENCES: 1
CORRESPONDENCE ADDRESS:
ADDRESSEE: AMSTER, R
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MEDIUM TYPE: 3.5 INC
MEDIUM TYPE: DISKETT
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STRANDEDNESS: DOUBLE
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TRY: U.S.A.
10016
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DB 3; Length 49272;

4.0%; Score 33.2;

Query Match

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 38; Indels
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                                                                                                          3860 GATCGGCGGGGGACACCGTCAACGTCGACTTC 3893
                                                                                        750 tctcgcgggcctgaagcccggcaccgtttacttc 783
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APPLICATION NUMBER: US/08/804,227C FILING DATE: February 21, 1997
                                                                                                                                                                                                                                                                                                                                                        1: THOMAS G. PLANT 1501
LILLY CORPORATE CENTER
                                                                                                                                                                                               Sequence 7, Application US/08804227C
Patent No. 5876991
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                OLECULE TYPE: DNA (genomic)
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TYPE: nucleic acid
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MEDIUM TYPE: Floppy
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Best Local Similarity
Matches 93; Conserv
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NAME/KEY:
LOCATION:
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LOCATION:
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LOCATION:
FEATURE:
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FEATURE:
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US-08-804-227C-7
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AAV49280 464 bp mRNA EST 30-DEC-1996 mj45602.rl Soares mouse embryo NDME13.5 14.5 Mus musculus cDNA clone IMAGE:479043 5' similar to SW:ILGB_MOUSE Q00560 INTERLEUKIN-6 RECEPTOR BETA CHAIN PRECURSOR ;, mRNA sequence.
                                                                     Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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em_est25:*
em_est26:*
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 em_est22:*
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     GenCore version 4.5
Copyright (c) 1993 - 1998 Compugen Ltd.
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W46603 zc32h10.rl W81301 zd85a12.rl AA788346 r7c10a1.r AA255111 mz79d08.r AIG49345 uc83f01.y

A1575103 UI-R-GO-A1579792 UI-R-AGO A1713798 UI-R-AA1

R87407 ym88d09.s1 W46604 zc32h10.s1 H14009 EST00035 C

A1575060 UI-R-GO-N78873 zb17h05.81

AI074921 0y04d08 AA049278 mj45c04

AA049280 mj45d02

Description

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Mus musculus
Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eukaryota; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 482)
Marra,M., Hillier,L., Allen,M., Bowles,M., Dietrich,N., Dubuque,T., Gelsel,S., Kucaba,T., Lacy,M., Le,M., Martin,J., Morris,M., Schellenberg,K., Steptoe,M., Tan,F., Underwood,K., Moore,B., Theising,B., Wylie,T., Lennon,G., Soares,B., Wilson,R. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     This clone is available royalty-free through LLNL; contact the IMAGE Consortium (info@image.llnl.gov) for further information.
                                                                                     300
                                                                                                                                                                                                                                                                                                                                                                                                     W66776 14-JUN-1996 mRNA mel7blir. Soares mouse embryo NbME13.5 14.5 Mus musculus cDNA clone IMAGE:387741 5' similar to PIR:B38252 B38252 granulocyte colony-stimulating factor receptor precursor ; mRNA sequence.
                                                                                                                          643
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                                                  ctctcaaggatttcctctccaagccaagtaccagatccgctaccgcgtggaggacagcg
                                                                                                                            acqtgagccgcqttgggggcctggaggaccagctgagtgtgcgctgggtctcaccaccag
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Unpublished (1996)
On Apr 14, 1993 this sequence version replaced gi:785250
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Contact: Marra M/Mouse EST Project
WashU-HMMI Mouse EST Project
WashIngton University School of MedicineP
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
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/dev_stage="13.5-14.5dpc total fetus"
/lab_host="DH10B"
                                                                                                                                                                                                                                                                       /clone_lib-"Soares mouse
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Tel: 314 286 1800
Fax: 314 286 1810
Email: mouseest@watson.wustl.edu
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High quality sequence stop: 359.
Location/Qualifiers
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/db_xref="taxon:10090"
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/clone="IMAGE:387741"
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This clone is available royalty-free through LLNL ; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            284 gctgctggtcccggaacatgaaggatctcacgtgccgctggacaccgggtgcacacggggg 343
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The MasNU-HHMI Mouse EST Project
Unpublished (1996)
On Dec 30, 1996 this sequence version replaced gi:1528951.
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Pred. No. 2.3e-107;
0; Mismatches 2; Indels 0:
                                                                                                                                                                                                                                                                                                                              WashU-HHMI Mouse EST Project
Washington University School of MedicineP
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /db_xref="taxon:10090"
/clone="imagE:479043"
/clone_lib="Soares mouse embryo NbMEI3.5 14.5"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /tissue_type="embryo"
/dev_stage="13.5-14.5dpc total fetus"
/lab_host="DH10B"
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High quality sequence stop: 437.
Location/Qualiflers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /organism="Mus musculus"
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AA049280.1 GI:1755311
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14.5dpc embryos [total RNA provided by Minoru Ko, Wayne State Univ., from 2.]; double-stranded cDNA was ligated be Eco Ri adaptors (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of the modified pT7T3 vector. Library went through one round of normalization, and was constructed by Bento Soares and M.Fatina Bonaldo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AA866388 428 bp mRNA EST 05-FEB-1999 UI-R-AO-aj-f-04-0-UI-SJ UI-R-AO-aj-f-04-0-UI-SJ UI-R-AO-aj-f-04-0-UI-SJ UI-R-AO-aj-f-04-0-UI-SJ UI-R-AO-aj-f-04-0-UI-SJ SIMILIAR TO QD|AC003112|AC003112 Human DNA from chromosome 19 specific cosmid R30292, genomic sequence (Homo sapiens), mRNA sequence.
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Eukaryota: Metazoa; Chordata; Craniata; Ver
Eutheria; Rodentia; Sciurognathi; Muridae;
11 (bases 1 to 428)
Bonaldo,M.F., Lennon,G. and Soares,M.B.
                                                                                                                                Score 428.2; DB 26;
Pred. No. 4.4e-99;
0; Mismatches 3;
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Program for Rat Gene Discovery and Mapping
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Matches 441; Conservative
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University of Iowa 451 Eckstein Medical Research Building Iowa City, IA 52242, USA 7Tel: 319 335 8250
Fax: 319 335 9265
Fax: 319 335 9565
Email: mscares@blue.weeg.ulowa.edu
Oligo-df track not found, Not I site shown in beginning of sequence 1s likely internal to the message. CDNA Library Preparation: M. Fatima Bonaldo, Ph.D. Clone distribution: clones will be available through Research Genetics
Seq primer: MJ3 Forward.
                                                                                                                                                                                                                                                                                                                                                                                                     /dev_stage="adult"
/lab_host="DH10B (Life Technologies)"
/lab_host="DH10B (Life Technologies)"
/lab_host="DH10B (Life Technologies)"
/lab_host="DH10B (Life Technologies)"
/lab_host="Interpolation of the consists of a mixture of individually tagged normalized consists of a mixture of individually tagged normalized bibaries constructed from rat placenta, adult lung, brain, liver, kidney, heart, spleen, ovary, and muscle. The tag is a string of 3-5 nucleotides present between the Not I site and the oligo-dT track which allows identification of the library of origin of a clone within
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             446 atatococaaggacotggocotottoactocotatgagatotgggtggaagcoaccaato
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       gcctaggctcagcaagatctgatgtcctcacactggatgtcctggacgtggtgaccacgg
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         182 ACCTCCACCCGACGTGCACGTGAGCCGCGTTGGGGGGCCTGGAGGACCAGCTGAGTGTGC
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Pred. No. 4.7e-89;
0; Mismatches 24; Indels 0;
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/map="between D1151765 and UGB"
/clone="UI-R-A0-aj-f-04-0-UI"
/clone_llb="UI-R-A0"
                                                                                                                                                                                                                                                1. .428 /organism="Rattus norvegicus"
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tf25h01.x1 NCI_CGAP_Brn23 Homo sapiens cDNA clone IMAGE:2097265 3'similar to SW:IL6B_MOUSE Q00560 INTERLEGKIN-6 RECEPTOR BETA CHAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                Tissue Procurement: David N. Louis, M.D., Myrna R. Rosenfeld M.D.,
                                                                                                                                                                                                                                                    National Cancer Institute / National Institute of Neurological Disorders and Stroke, Brain Tumor Genome Anatomy Project (CGAP/BTGAP), Tumor Gene Index Unpublished (1998)
On Apr 7, 1998 this sequence version replaced gi:3034955.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               61 ggggccaccgctgaggggctctactggaccctcaatggtcgccgcctgccctctgagctg 120
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                                                                                                                                                       Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     cDNA Library Preparation: M. Bento Soares, Ph.D., M. Fatima
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  36.9%; Score 307.6; DB 46; Length 474; ilarity 86.1%; Pred. No. 1.8e-68; Conservative 0; Mismatches 55; Indels 0;
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0
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NCI/NINDS-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
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./organism="Homo sapiens"
/db xref="taxon.9606"
/clone="IMAGE:2097265"
/clone=11b="NCI_CGAP_Brn23"
/tissue_type="glioblastoma (pooled)"
/lab_host="DH108"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Insert Length: 1664 Std Error: 0.00 Seq primer: -400P from Glbco High quality sequence stop: 450. Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                Contact: Robert Strausberg, Ph.D. Tel: (301) 496-1550
Email: Robert_Strausberg@nih.gov
                                                                                                                                                                                                                                                                                                                                                                                                          Robert_Strausberg@nih.gov
                                        PRECURSOR ;, mRNA sequence.
                                                                                               AI421423.1 GI:4267354
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                                                                                                                                                                                                                                                                                                                                    AI185924 477 bp mRNA EST 29-OCT-1998 qe50c05.xl Soares_fetal_lung_NbHL19W Homo sapiens cDNA clone IMAGE:1742408 3' similar to TR:Q16354 Q16354 PROLACTIN RECEPTOR;;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutherla; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 47?)
NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP), Unpublished (1997)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Tel: (301) 496-1550
Email: Robert_Strausbergenih.gov
This clone is available royalty-free through LLNL; contact the IMAGE Consortium (info@image.llnl.gov) for further information.
Insert_Length: 1552 Std Error: 0.00
                                                                                                                           301 atgaaggatctcacgtgccgctggacaccgggtgcacacggggagacattcttacatacc 360
380 AIGAAGGACTIGACCIGCCCIGGACGCCCAGGGCCCCACGGNGAGACCTICCICCACACC 439
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Pred. No. 4.5e-68;
0; Mismatches 56;
                                                                                                                                                                                                                                    440 AACTACTCCCTCAAGTACAAGCTTAGGTGGTATGG 474
                                                                                                                                                                                                      361 aactactccctcaagtacaagctgaggtggtacgg 395
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High quality sequence stop: 467
Location/Qualifiers
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85.8%;
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Best Local Similarity 85.8
Matches 339; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AI394468 462 bp mRNA EST 30-MAR-1999
tf79d12.xl NCI_CGAP_Brn23 Homo sapiens cDNA clone IMAGE:2105495 3'
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                                                           9999ccaccgctgaggggctctactggaccctcaatggtcgccgcctgccctctgagctg 120
                                                                        143 GGAGCCACCCCGAGGGCCTCTACTGGACCCTCAACGGGGGCGCCCGCTGCCCCTGAGCTC. 202
                                                                                                                                                             262
                                                                                                                                                                                                                                                     tgcctctatgttggcttgccccctgagaagccctttaacatcagctgctggtcccggaac 300
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1 (Dasse; D. 462)
NCI/NINDS-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute / National Institute of Neurological Disorders and Stroke, Brain Tumor Genome Anatomy Project (CGAP/BTGAP); Tumor Gene Index
Unpublished (1998)
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cocaccetteteateggeteeteetgeaagetacetgetetatacatggagaeacacet .60
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                                                                                                                                           On Feb 17, 1998 this sequence version replaced g1:2887603
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/clone_lib="NCI_CGAP_Brn23"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Contact: Robert Strausberg, Ph.D.
Tel: (301) 496-1550
Email: Robert_Strausberg@nih.gov
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/db_xref="taxon:9606"
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Seq primer: -400P from Gibco
High quality sequence stop: 454.
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1. (Dases: 1 to 466)

NCI-GGAP http://www.ncb1.nlm.nih.gov/ncicgap.
NAI-GGAP http://www.ncb1.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP), Tumor Gene Index
Unpublished (1997)

On Jan 19, 1998 this sequence version replaced gi:2287379.
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Tel: (301) 496-1550
Email: Robert-Strausbergenih.gov
Email: Robert-Strausbergenih.gov
This clone is available royalty-free through LLNL; contact the IMAGE Consortium (info@image.llnl.gov) for further information.
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/tissue_type="glioblastoma (pooled)"
/lab_host="DH10B"
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Pred. No. 3e-66;
0; Mismatches 53; 3
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Best Local Similarity 86.2%;
Matches 330; Conservative
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FEATURES

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Eutheria; Primates; Catarrhin; Hominidae; Homo.

1 (Dasa 1 to 466)

NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.

NATional Cancer Institute, Cancer Genome Anatomy Project (CGAP), Tumor Gene Index

Unpublished (1997)

On Jan 19, 1998 this sequence version replaced gi:2151491.
                                                                                                                              Contact: Robert Strausberg, Ph.D.
Tel: (301) 496-1550
Email: Robert_Strausbergenih.gov
This clone is available royalty-free through LLNL; contact the IMAGE Consortium (info@image.llnl.gov) for further information.
Insert Length: 1622 Std Error: 0.00
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Chordata; Craniata; Vertebra
Catarrhini; Hominidae; Homo
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/clone="ImAcE:1741879"
/clone=lib="Soares_fetal_lung_NbHL19w"
/dev_stage="19 weeks"
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    466
    /organism="Homo sapiens"

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Seq primer: -400P from Glbco
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/db_xref="taxon:9606"
/map="839CC2; 821G11; 4; 4p15.33-4p16.1; 4p15.33-4p16.1"
/clone="IMAGE:1705398"
/clone_lib="Soares_fetal_heart_NbHH19W"
                                                                                                                                                                                                                                                                                                          normalization to a Cot - 5. Library constructed by M.Fatima Bonaldo. This library was constructed from the same fetus as the fetal lung library, Soares fetal lung
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Soares_fetal_lung_NbHL19W Homo sapiens cDNA clone
379 3', mRNA sequence.
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Insert Length: 1599 Std Error: 0.00 Seq primer: -40ml3 fwd. Er from Amersham High quality sequence stop: 454.
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                                                                                                                           Soares_fetal_lung_NbHL19W Homo sapiens cDNA clone 06 3' similar to TR:Q16354 Q16354 PROLACTIN RECEPTOR;;
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NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Tel: (301) 496-1550
Email: Robert_Strausberg@nih.gov
This clone is available royalty-free through LLNL; contact the
IMAGE Conscitum (info@image.llnl.gov) for further information.
Insert Length: 1615 Std Error: 0.00
Seq primer: -40UP from Gibco
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                                                                                                                                                                                                                                                                                                                                                                                                                                           Vertebrata; Mammalia;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /clone_lib="Soaree_fetal_lung_NbHL19W"
/dev_stage="19 weeks"
/lab_host="DH10B (ampicillin resistant)"
                                                                                                                                                                                                                                                                                                                                                                                                    Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebra
Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Pred. No. 1.1e-58;
0; Mismatches 50;
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/db_xref="taxon:9606"
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Location/Qualifiers
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/clone="IMAGE:1930606"
                                                                                                                                                                                                                                                                                             AI333812.1 GI:4070371
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ilarity 85.7%;
Conservative (
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                                                                                                                                  qp93e12.xl SoE
IMAGE:1930606
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Matches 299; Conserv
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AUTHORS
TITLE
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normalization to a Cot = 5. Library constructed by Bento Soares and M.Fatima Bonaldo. This library was constructed from the same fetus as the fetal heart library. Soares fetal heart NbHH19W." 175 c 128 g 74 t 1 others
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adapters (Pharmacia), digested with Not I and cloned into
the Not I and Eco RI sites of a modified pT/T3 vector
(Pharmacia). Library went through one round of
                                                                                                                                                                                                                                                                                                                           NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        This clone is available royalty-free through LLNL; contact the IMAGE Consortium (info@image.llnl.gov) for further information. Insert Length: 1667 Std Brror: 0.00 Seq primer: -40ml3 fwd. ET from Amersham High quality sequence stop: 431.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ggggccaccgctgaggggctctactggaccctcaatggtcgccgcctgccctctgagctg 120
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AI187074 447 bp mRNA EST 29-OCT-1998
qe38a03.s1 Soares_fetal_lung_NbHL19W Homo sapiens cDNA clone
IMAGE:1741228 3', mRNA sequence.
                                                                                                                                                                                                                      Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
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Pred. No. 2.4e-58;
0; Mismatches 50; Indels 0;
                                                                                                                                                                                                                                                                           Catarrhin1; Hominidae; Homo.
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/db_xref="taxon:9606"
/clone="IMAGE:1741228"
/clone_11b="Soares_fetal_lung_NbHL19W"
                                                                                                                                                                                                                                                                                                                                                                                                                                      On Aug 21, 1998 this sequence version replaced.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Contact: Robert Strausberg, Ph.D
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Tel: (301) 496-1550
Email: Robert_Strausberg@nih.gov
                                                                                                                                 AI187074.1 GI:3737712
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1 (bases 1 to 447)
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Unpublished (1997)
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Conservative
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TITLE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              reaction. The driver was PCR-amplified cDNNs from pools of 5,000 clones made from the same 3 libraries. The pools consisted of I.M.A.G.E. clones 260232-265223, 340488-348479."
                                                                                                                                                                                                                                                                                                                                                   AI269388 417 bp mRNA EST 27-JAN-1999
q126b05.x1 Soares_NhHMPu_S1 Homo sapiens cDNA clone IMAGE:1857585
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/Organism="Homo saplens"
/db_xref="taxon:9606"
/clone="IMAGE:1897585"
/clone_lib="Soares_NhHMPu_S1"
/tissue_type="Pooled human melanocyte, fetal heart, and pregnant uterus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (Dases 1 to 417)
NCI-GGAP http://www.ncbi.nlm.nlh.gov/ncicgap.
NAtional Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
Unpublished (1997)
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Tel: (301) 496-1550
Email: Robert_Strausbergenih.gov
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
Insert Length: 1634 Std Error: 0.00
Seq primer: -40UP from Gibco
High quality sequence stop: 406.
Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                     mRNA sequence
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SOURCE
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NID
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Length 417;

Score 245; DB 44; Pred. No. 1.3e-52;

29.4%;

Query Match Best Local Similarity

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AI670108 385 bp mRNA EST 14-MAY-1999 we65£03.x1 Scares_thymus_NHFTh Homo sapiens cDNA clone IMAGE:2345981 3' similar to TR:075462 075462 CYTOKINE-LIKE FACTOR-1 AI670108
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Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 385)
NCI-GGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
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Tel: (301) 496-1550
Email: Robert_Strausberg@nih.gov
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
Seq primer: -400P from Gibco____
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                                                                                                                                                         ggggccaccgctgaggggctctactggaccctcaatggtcgccgcctgccctctgagctg 120
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                                                                                                                                                                                 161 GGAGCCACCGCCGAGGGCCTCTACTGGACCCTCAACGGGGCGCCCCCTGCCCCTGAGCTC
                                                                                                                                                                                                                                                                                       Tumor Gene Index
Unpublished (1997)
On May 9, 1996 this sequence version replaced g1:1133091.
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  Indels
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/dev_stage="fetal"
/lab_host="DH10B (phage-resistant)"
45;
  Mismatches
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/organism="Homo sapiens"
/db_xref="taxon:9606"
/map="2"
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High quality sequence stop: 372.
Location/Qualifiers
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A1670108.1 GI:4834882
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/clone="IMAGE:486841"
/clone_lib="Soares_pregnant_uterus_NbHPU'
                                                      /dev_stage="adult"
/lab_host="DH10B"
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                                      /sex="female'
                                                                                                                                                                                                                                                                                                           24.08;
                                                                                                                                                                                                                                                                                                             Ouery Match 24.0
Best Local Similarity 84.7
Matches 271; Conservative
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Hiller, L., Lennon, G., Becker, M., Bonaldo, M.F., Chiapelli, B.,
Chissoe, S., Dietrich, N., DuBuque, T., Favello, A., Gish, W.,
Hawkins, M., Hultman, M., Kucaba, T., Lacy, M., Le, M., Le, M., Le, M.
Mardis, E., Moore, B., Morris, M., Parsons, J., Prange, C., Rifkin, L.,
Rohlfing, T., Schellenberg, K., Soares, M.B., Tan, F., Thierry-Mey, J.,
Trevaskis, E., Underwood, K., Wohldmann, P., Waterston, R., Wilson, R.
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2X56f01.sl Soares_pregnant_uterus_NbHPU Homo sapiens cDNA clone
IMAGE:486841 3', mRNA sequence.
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 by Bento Soares and M. Fatima Bonaldo. 108 q 66 t
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4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
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                                                                                    Length
                                                                                                                    Indels
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Eukaryota; Metazoa; Chordata; Craniata; Vertebre
Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                                                                    20;
                                                                                 Score 217.8; DB 50;
Pred. No. 1e-45;
0; Mismatches 42;
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High quality sequence stop: 388.
Location/Qualifiers
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/db_xref="GDB:3760555"
/db_xref="taxon:9606"
/map="12p"
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AA042914.1 GI:1522430
                                                                                 26.1%;
85.3%;
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156 c
                                                                                                 Best Local Similarity 85.3
Matches 243; Conservative
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AUTHORS
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Not
/note="Organ: uterus; Vector: pT7T3-Pac; Site_1: Not I; Site_2: Eco RI; 1st strand cDNA was primed with a Not I oligo(dT) primer [5'
                                                               AACTGGAAGATTCGCGGCCGCCTTTTTTTTTTTTTTT 3'],
double-stranded cDNA was ligated to Eco RI adaptors
(Pharmacia), digested with Not I and cloned into the No
and Eco RI sites of the modified pT773 vector. Library
went through one round of normalization. Library
constructed by M. Fatima Bonaldo I others
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
1 (bases 1 to 312)
Bonaldo,M.F., Lennon,G. and Soares,M.B.
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Program for Rat Gene Discovery and Mapping
University of Iowa
451 Eckstein Medical Research Building Iowa City,
Tel: 319 335 8250
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97044477
On Mar 10, 1998 this sequence version replaced
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Pred. No. 3.4e-41;
0; Mismatches 45;
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UI-R-GO-ut-h-08-0-UI.83 UI-R-GO Rattus
UI-R-GO-ut-h-08-0-UI 3', mRNA sequence.
AI579568
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Query Match
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Bonaldo, M.F., Lennon, G. and Soares, M.B.
Normalization and subtraction: two approaches to facilitate gene
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Email: msoares@blue.weeg.ulowa.edu
Oligo-dT track not found, Not I site shown in beginning is likely internal to the message. cDNA Library Preparat Soares Lab Clone distribution: clones will be available Research Genetics (www.resgen.com)
Seq primer: M13 Forward.
Location/Qualifiers
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Pred. No. 7.9e-41;
0; Mismatches 16; Indels 0;
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
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                                                                                                                                                                                                                                            /organism="Rattus norvegicus"
/Strain="Sprague-Dawley"
/db_xrefe"taxon:10116"
/clone="UI-R-GO-Ut-h-08-0-UI"
/clone_lib="UI-R-GO"
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Matches 208; Conservative
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AUTHORS
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MEDLINE
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KEYWORDS
SOURCE
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                                                                                                                                                                                            FEATURES
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/organism="Rattus norvegicus"
/strain="Sprague-Dawley"
/db_xref="lason:10116"
/db_xref="lason:10116"
/map="6p21:3; 5q3"
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/clone="U1-R-GO"
/dev_stage="adult"
/lab.host="DH10B (Life Technologies)"
/lab.h
451 Eckstein Medical Research Building Iowa City, IA 52242, USA Tel: 319 335 8250
Fax: 319 335 8250
Email: msoares@blue.weeg.ulowa.edu
Oligo-dr track not found, Not I site shown in beginning of sequence is likely internal to the message. CDNA Library Preparation: M.B. soares Lab Clone distribution: clones will be available through
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        229 TCNCGTCTCCTCAACACCTCCACCTGGCCTTGGCCCTGGCTAACCTTAATGGGTCCAGG 288
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 cccaccetteteateggetectecetgcaagetacetgetetatacatggagacacacet
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                61 ggggccaccgctgaggggctctactggaccctcaatggtcgccgcctgccctctgagctg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        . 1 others
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 186; DB 48; Length 3
Pred. No. 1.1e-37;
0; Mismatches 16; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        68 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Search completed: September 28, 1999, 15:38:17
Job time: 3285 sec
                                                                                                                                                                                                                                                                                                                                                                            Research Genetics (www.resgen.com)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   289 CAGCAGTCAGGGGACAATCTGGTGTGTCACG 319
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        88 g
                                                                                                                                                                                                                                                                                                                                                                                                                             Seq primer: M13 Forward
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    22.3%;
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us-09-037-657-24.rge

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misc_feature
                           gene
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RBS
                                                                                                                                     correct initiation codon. Where possible we choose an initiation codon (atg, gtg, ttg or (att)) which is preceded by an upstream ribosome binding site sequence (optimally 5-13bp before the initiation codon). If this cannot be identified we choose the most upstream initiation codon. If this cannot be identified we choose the most IMPORTANT: This sequence MAX NOT be the entire insert of the sequence clone. It may be shorter because we only sequence overlapping sections once, or longer, because we only sequence asmall overlap between neighbouring submissions. Cosmid 9810 lies between 2E9 and 5B8 in the Asel-B genomic restriction fragment.

In 33320
prediction is based on positional base preference in codons using a specially developed Hidden Markow Model (Krogh et al., Nucleic Acids Research, 22(22):4768-4778(1994)) and the FramePlot program of Bibb et al., Gene 30:157-66(1984) as implemented at http://www.nih.go.jp/
lun/cgi-/www.nih.go.jp/
lun/cgi-bin/frameplot.pl CAUTION: We may not have predicted the correct initiation codon. Where possible we choose an initiation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /gene="SC9B10.02"
//gene="SC9B10.02, unknown ATP/GTP binding protein, len:
362 aa; similar in N-terminus to other ATP/GTP binding
proteins eg. COBW_PSEDE P29937 cobw protein from
pseudomonas denitrificans (353 aa), fasta scores; opt: 302
z-score: 390.2 E(): 1.4e-14, 30.1% identity in 366 aa
overlap. Contains PS00017 ATP/GTP-binding site motif A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              KSPSADPHSTTGGRSPDSGVDMVTRKNATGREGSAAAGMLLATAGISLAARRRREAA
WHERLLELEELAIRROSLAHQQRMHWELLTRAIDDPSLAEVIDTYDKSIPARRROF
YANAWYVNLYHVHRAGLLDQEGLGGRLREFFQSPVFREYWEATRNMRAALDQNSDEA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  translation="MRGADVFQGAGPCDPRFPPCASSPPPRRSAPLGTLEAAAPSIAR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    KTDRATDAERVLGLVHSLVGGAAVVPATYGRIDPEELYDCRPGEERVGQLSFDDLHDH
SEGGAHADHLHAAYDTLSFVSGLPLDPRRLMRFLDSRPKGLYRIKGYVDFGPYDTRNR
YAVHAVGRFLRFYPEPWTPAGAAGGSGAPETGRTQLVLIGSGIDAAALGEELDACRRD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    'translation="MGQRSTPQQIPVVVLAGFLGSGKTTLLNHLLHRSGGSRIGAVVN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DFGSIEIDAMAVAGALGDSTVSLGNGCLCCAVDASELDGYLARLARPEAGIDVIVIEA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SGLAEPQELVRMLLASEQPGIVYGGLVEVVDAAEFDDTRARHPEIDRHLALADLVVVN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /note="PS00017 ATP/GTP-binding site motif A (P-loop)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      product="hypothetical protein SC9B10.01c"
protein_id="CAA15791.1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  'note="possible RBS upstream of SC9B10.02"
197. .2085
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           product="hypothetical protein SC9B10.02"
protein_id="CAA15792.1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 complement(159. .905)
/gene="SC9B10.01c"
/hote="SC9B10.01c, unknown, len: 248 aa"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /organism="Streptomyces coelicolor"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               complement(1. .6675)
Anote Noverlap with Cosmid St5B8"
Complement(159. .905)
/gene="SC9B10.01c"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LGLVVDALAKDFEDTDTDEWWVVGTPPHD
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                _xref="SPTREMBL:050508"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     'db_xref-"SPTREMBL:050509"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  db_xref "PID:92661687"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    'db_xref="PID:g2661688"
'db_xref="G1:2661688"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       db_xref="PID:e1202332
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /db_xref="taxon:1902"
/clone="cosmid 9B10"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    'gene="SC9B10.02"
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/gene="SC9B10.02"
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trans1_table=11
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /strain="A3(2)
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gene

CDS

RBS

gene

FEATURES

CDS

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/note="SC9B10.03c, DNA gyrase-like protein, subunit A, len: 818 aa; similarity (strongest in N-terminus, around active site) to DNA gyrase subunit A from many organisms eg. GYRA_MYCTU ON 200 an gyrase subunit a (ec 5.99.1.3) from Mycobacterium tuberculosis (838 aa), fasta scores; opt: 1835 z-score: 1379.9 E(): 0, 42.4% identity in 768 aa subunit a (ec 5.991.3) (864 aa), fasta scores; opt: 1425.4 E(): 0, 42.9% identity in 788 aa overlap.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ALGTEGGVVKRVVPDY PSNKDELEVITLKDGDRIVGGVELRTGDEDLYFITDDAGLLR
YQASQVRPQGRPAGGVAGVKLADGAKVISFTAVDPAADAVVFTVAGSRGTLDDSYQTT
AKLTPFDQYPRKGRATGGVRCQRFLKGEDCLAFAWAGATPALAAQKNGTPAQLPDTDP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (DGQEQEPVALPAAFPNLLVNGASGIAVGMATNMPPHNLREVIAAARHLIRYPNADLD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            almkhvpgpdlptggrivglpgirdayetgrgtfkiratvsvetvtarrkglvvtel/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FAVGPEKVISKIKDLVGAKKIQGIADVKDLTDRAHGLRIVIEIKNGFVPEAVLEOLVI
LTAMEESFGINNVALVDGQPLTLGLKELLEVYLDHRFTVVRRRSEFRRSKRRDRLHLN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AVPLOVADDPCRVLLSSTGLLARTANDEPLVTEAGAKRVKHDLIVSAVPATARGEVG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LTALAY PEGHPYHHTPIGSMADLDAATLEDARAFFRTY YAPNNAVLSVVGDIDPEQTL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MAQSFSMRVPLVDGHGNFGSLGNDDPPAAMRYTECRMAEAAGLMTESIDEDTVDFAP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EGLLTALVDIDEVIRLIRSSENSAQAKQRLMERFSLSDVQTQYILDTPLRRLTKYDR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FETMPAHQLELALWLEADRMGSLLAALDDESMENQRDVVKNERRQRYDNVPYGTAFEK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AWIEKYFGSIASHDGKOPPRDGALPDVMGGELREVVEEEVPARALMAAYRLPEDGTRA
CDAADLALTVLGGGESSRLXNRLVRRDRTAVAAGFGLLRLAGAPSLGWLDVKTSGDVE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             VTSGGRLLRVNVVDLPQLPEAMPTPNLAGGAPLAEFVSLEDDEDVVCLTTLDESSPC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          4874. .6226
/gene="SC9B10.04"
/note="SC9B10.04"
/note="SC9B10.04, probable zinc protease, len: 450 aa;
/eakly similar to many of prokaryotic and eukaryotic
origin eg. TYMA.RHISN P55679 hypothetical zinc protease
y4wa from Rhizobium sp. (512 aa), fasta scores; opt: 617
z-score: 325.0 E(): 6.1e-11, 30 8% identity in 426 aa
overlap; and MPP2_YEAST P10507 mitochondrial processing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            processing
s; opt: 355
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                peptidase beta subunit (462 aa), fasta scores; opt: 35; z-score: 321.6 E(): 9.4e-11, 25.3% identity in 415 aa overlap. The zinc-binding and active site residues are
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WYDVGSRHEVKGRIGLAHLFEHLMFQGSAQVKGNGHFELVQGAGGSLNGTISFI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /note="69% match EM_BA:SCDNAGYR L27063 Streptomyces coelicolor dnaA-gyra region from 5495 to 6921"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                complement(4548. .4553)
/note="possible RBS upstream of SC9B10.03c"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                possible RBS upstream of SC9B10.04"
                                                                                                                                                                                                                                                                                                                                                                                                                                            'trans1_table=11
Tycoduct_nDN gyrase-like protein"
'protein_id="CAAIS'93.1"
db_xref="FID:e1202334"
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/gene="SC9B10.03c"
/note="SC9B10.03c"
/note="SC9B10.03c, DNA a
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/db_xref="PID:e1202335"
/db_xref="PID:92661690"
/db_xref="GI:2661690"
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/gene="SC9B10.04"
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/transl_table=11
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Louis,
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Homo sapiens clone NH0429J10, WORKING DRAFT SEQUENCE, 2 unordered
                                    18469 GCCCGGCTACCACATCTGGTTCATCTTCATGCGGTCGATGATGCTGCTGGACATCAGCAG 18410
                                                                                                               GCACCGCTGGGAGCGGATGGCCCCGATCAACGCGATGGCGTGGGCGATCCAGACCATCGC 18350
                                                                                                                                                                                         CAAGCCCTCCCAGTTCGAGG - - - TCAAGGAGCCGCTGCCGCGCGCGGGTCGTGGCCCGGGA 18293
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Eucheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 183800)
Waterston,R.H.
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Submitted (25-ARR-1999) Genome Sequencing Center, Washington University School of Medicine, 4444 Forest Park Parkway, St. MO 63108, USA
On Jun 5, 1999 this sequence version replaced g1:4680445.
* NOTE: This is a 'working draft' sequence. It currently * consists of 2 contigs. The true order of the pieces * is not known and their order in this sequence record is
  gatccgctaccgagtggaggacagtgtggactggaaggtggtggacgatgtgagcaacca
                                                                           gacetectgecgectggecggectgaaaceeggeaeegtgtaettegtgeaagtgegetg
                                                                                                                                                        18292 Gecceccaagreerrececececacerecacesecreacesecrececentrecrerecrea
                                                                                                                                                                                                                                                                                                               gegggeggagagecgageteggggeeggtgegegegegeteaageagtteetggggetg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
                                                                                                                                                                                                                                    13037: contig of 13037 bp in length
13054: gap of unknown length
183800: contig of 170746 bp in length.
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38622 c 35111 g 51289 t
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/db_xref="taxon:9606"
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Gaps

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Indels

Score 48.4; DB 35; Pred. No. 0.95; 0; Mismatches 136;

3.5%;

3.5 Best Local Similarity 48.9 Matches 130; Conservative

Length 183800;

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Submitted (28-NOV-1997) Streptomyces coelicolor sequencing project, Sanger Centre, Wellcome Trust Genome Campus, Hinxton, Cambridge CBIO ISA E-mail: barrell@sanger.ac.uk Cosmids supplied by Prof. David A. Hopwood, [3] John Innes Centre, Norwich Research Park, Colney, Norwich, Norfolk NR4 7UH, UK
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Usually the highest scoring match found by fasta -o is given for CDS which show significant similarity to other CDS in the database. The position of possible ribosome binding site sequences are given where these have been used to deduce the initiation codon. Gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       agaS; agaZ; DNA gyrase-like protein; FAD-dependent oxidoreductase; ferrochelatase; hemH; phosphocarrier protein hpr; ptsH; putative hydroxlase; putative protease; putative thimidine kinase; suhB; tagatose 6-phosphate Alnase; tagatose-bisphosphate aldolase; thiosulfate sulfurtransferase; transcriptional regulator; zinc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Bacteria; Firmicutes: Actinobacteria; Actinobacteridae;
Actinomycetales; Streptomycineae; Streptomycetaceae; Streptomyces.
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A set of ordered cosmids and a detailed genetic and physical map for the 8 Mb Streptomyces coelicolor A3(2) chromosome Mol. Microbiol. 21 (1), 77-96 (1996)
                                              agtggcgagdctggatgcagaagtcgcacaagacccgcaaccagcacaggacgaggggat 1000
                                                                                                                                                                                                                                                                                                                                                              2954 GECECCEGEAGCECCEGETACAGICGECTEGCTCCGCACCTCGAGITCCGGGCGTCIT 3013
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         10-FEB-1999
                                                                                                                                                                                                                                                           2894 CCCGCGCCCGCCGGGAGGTGGCCGCGGGGAGGTCGGGGGTTGTCTCTCCCCCCGCGAAGG
                                                                                                     cgtgcgaaccgcggggggggagccgagctcggggccggtgcggcgcgagctcaagcagt
                                                                                                                                                   881 tectgggetggeteaagaageaegegtaetgeteeaaceteageiteegeetetaegaee
  ggagecacceacagectecactececgeagtgagegeeeggggeeegggeggeggg
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2 (bases i to 33320)
Parkhili,J., Barrell,B.G. and Rajandream,M.A.
Direct Submission
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AMP-binding, AMP-binding enzyme, a Pfam match to entry Pro10668 Durg4, Domain of unknown function, a Pfam match to entry Pr008975 Thioesterase domain and two Pfam matches to entry Pr00550 pp-binding, Pr05phopantetheine attachment site. Each Pr0501 contains a Prosite match Pr00550 contains a Resphopantetheine attachment site. Phosphopantetheine attachment site.
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TDRPRPATADHTGDRVEFALPADLHTRLTELARATDTTLYMVLQAALATLTTRHGAGE
DIPIGTPVAGRTDDATDHLVGFFVNTLVLRTDTSGNPTFRDLLTRVRDTDLTAYTHQD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /translation="RLRPAETLTGFLRRLQGEQARLIDHQWVGLAEIQRWAGSGELFD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AERFTDLFEEQVARTPGKTALIAPDGRLTYAELDAAANRLARRLVELGVGPERHVAVA
VGRRTELVVGMLAVLKAGGAYVPVDPEYPPDRIRHMIQDADPALVLTTSDVDDRIGEE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EHRALSAFVRHCRSSQAPDISGLSVMQASASFDQSVGSLHAPLISGGCVRLTDLRALA
ETAGSEPGFHRATFWKGTPSHLALLATMPPEVAPSGTLTLGGEELRGEILAPWREAAG
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AARARLALSLPDFMMPSAFVALDALPLSPNGKLDRAALPAPTYTGRTAGRAPRTPAEE
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LARAARHAFDLGAELPVRARLLRLSEREHVLLLLVHHIASDAWSRGPLAQDLTAAYTA
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GRLDPATGHAASAAVPETEGVTAMNPSPEPAPSPESLDSTEVA"
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APEYRTVEGRSPRTPREEALCRLFAEVLGLELVGLDDGFFDLGGHSLLAIRLVERVRA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TAMVFENYPLNSSRGRPPGAAPDADLPTVLGVRSKDQMHYPLGLLALPRETLRFSLG)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TGDLVRHRADGDLEYLGRTDTQVKLRGMRVEPAEIEAVTAGLPGVAQAAVLVREDTPG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DVTVVNVYGPTEATGHCLEHWIAPDRTVEPGPVPIGTPHEGVRVYVLDSALRPVAPGI
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Phosphopantetheine attachment site, score 78.40, E-value
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Anote-"PS00455 Putative AMP-binding domain signature." 2046. 2238 //gene-"SCE63.01"
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/gene="SCE63.01"
/note="PS00012 Phosphopantetheine attachment site."
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AMP-binding enzyme, score 385.20, E-value 6.6e-112"
                                                                                                                                                                                                                                                                                                                                                                                    /product="CDA peptide synthetase III"
/protein_id="CAB38876.1"
/db_xref="PID:e1393918"
AMP-binding, AMP-binding
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /db_xref-"PID:94490979"
                                                                                                                                                                                                                                                                                                                    table-11
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/gene="SCE63.01"
                                                                                                                                                                                                                                                                                   /codon_start=3
                                                                                                                                                                                                                                                                                                                                                /label=cdaPS3
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     . 6e-20
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misc_feature

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to many eq. TR.052809 (EMBL:AJ22399) from the vancomycin blosynthesis cluster of Amycolatopsis orientalis (276 as) fasta scores; opt: 892, z-score: 1028, 9, E(); 0, (50.9% identity in 271 as overlap) and TR.057982 (EMBL:AF003947) Poal; single polypeptide combining 3-oxoadipate enol-lactone hydrolyzing and 4-carboxynuconolactone decarboxylating activityfrom Rhodococcus opacus (400 as) fasta scores; opt: 28% z-score: 335.4, E(): 2.36-11, (32.0% identity in 256 as overlap). Contains Pfeam match to entry PF00561 abhdrolase, alpha/beta hydrolase fold, society 27.80, E-value 2.2e-19.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ä
                                                                                                                                                       note="Pfam match to entry PF00550 pp-binding,
hosphopantetheine attachment site, score 76.90, E-value
.2e-19"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        18889 CCCCGTCACCCCGCACCGCCACGACGACTTCCCCGACGTACCCGGCATGCTCGGCGA 18830
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CGGCGGCCAACGAACTCTGGTACATGTTCGACGAGCCACGCTCTACAACGTGGGCCC 18770
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       18769 GGAGCTGGAGCAGGCGTTCACCGACATCGAGACCGCGCTCGGCGACGGCTGGGAGCGGGC 18710
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GGGCGTGCTCAACGACCCCCGCGGGGCGCCCGGTGCACCATGAACGGCAACCCGCC 18470
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 114 egigicacgecegigaeggeageateciggeiggeigeciecitatgiggeeigee 173
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                174 cccagagaaacccgtcaacatcagctgctggtccaagaacatgaaggacttgacctgccg 233
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ctggacgccagggggcccacgggggagccttcctccacacca---actactccctcaagta 290
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                                                                                       note="PS00455 Putative AMP-binding domain signature.
1232, .5424
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                                                                                                                                                                                                                                                                                 /note="Pfam match to entry PF00975 Thioesterase, Thioesterase domain, score 139.00, E-value 8.5e-38" 6360. 7178 6360. 7178
                 note-"Pfam match to entry PF00501 AMP-binding,
MP-binding enzyme, score 448.70, E-value 5.2e-131"
                                                                                                                                                                                                                       5301. 5348
/gene="SCE63.01"
/note="SOS0012 Phosphopantetheine attachment site.
/5490. 6219
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                                                                                                                                                                                                                                                                                                                                                                                                                                                    /note="SCE29.02, probable hydrolase,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 50.6; DB 1;
Pred. No. 0.47;
0; Mismatches 449;
                                                                                                                       5232. .5424
/gene="SCE63.01"
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/label=SCE29.02
'gene="SCE63.01"
                                                                            gene="SCE63.01"
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                                      AMP-binding
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ALDSFRNYNSGANVTDSIADFTHGADLIDLSALGYTGLGDGYNGTLAIVLNDAGTKTY
LKDRGGDAEGNRFEIALEGNHADQLDASDFIFATAAAATGIEVVGSTPAEEQPVV"
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LDGGVGRDTLTGGAGADTERESAREDSYRTASTSFTDLTTDFDPAQDRIDLSALGFTG
LGDGYDGTLLVTTGSGGSRTYLKSLEADAEGRRFEIALDGDFVGLLDASNLIFERPAI
BGDAGDNALLGTSVAETLLGHAGNDTLDGAGGDDILVGGAGSDSLTGGAGADVFRFDA
                                                                                             VKSY ENGADGYRFEFSLDGNYQGLLGNEDFIFATPSGQQLLEGTAGNDSLQGTAAADEV
IHGGSGRDTLAGGAGADVFRFSELTDSYRTDSASYADLITDFDASEDRIDLSGLGFSG
LGNGYGGTLALQVNSAGTRTYLKSYEANAAGERFELSLDGDLSGLDESHLVFDERVVL
                                                                       LSDSQRNYDTGDNQGDRITDFAVGEDKLDVSALGFTGLGDGYNGTLVLVLNSAGDRTY
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Streptomyces coelicolor
Bacteria; Firmicutes; Actinobacteria Actinomycetales; Streptomycineae, Streptomyces.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1037 GAAGGCGTGCTCCAAGATGACCAGCGACATCACCCTGCAGAACGCCGATATCCACGGC 1096
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     aaggacctggctctttacgccctatgagatctgggtggaggccaccaaccgcctgggc 426
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                                                                                                                                                                                                                                                                                                                                                                                                                                 gocotggocaacotcaatgggtocaggoagoggtoggggacaacotcgtgtgccacgcc 126
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                                                                                                                                                                                                                                                                                                                                   Score 50.6; DB 1; Length 15759;
Pred. No. 0.51;
0; Mismatches 259; Indels 0;
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Streptomyces coelicolor cosmid E29.
AL035707
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                                                                                                                                                                                                                                                                                                                                   3.6%;
al Similarity 44.3%;
206; Conservative (
                                                                                                                                                                                                                                          2992
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Best Local
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DEFINITION
ACCESSION
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ORIGIN
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Saunders, D.C. and Harris, D. Unpublished

AUTHORS

REFERENCE

(bases 1 to 26477

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in acdons is given for each CDS.

Usually the highest scoring match found by fasta -o is given for CDS which show significant similarity to other CDS in the database. The position of possible ribosome binding site sequences are given where these have been used to deduce the initiation codon. Gene prediction is based on positional base preference in codons using a specially developed Hidden Markow Model (Krogh et al., Nucleic Acids Research, 22(22):4768-4778(1994)) and the Frameplot program of Bibb et al., Gene 30:157-66(1984) as implemented at http://www.nih.go.jp/
jun/cgi-bin/frameplot.pl. CAUTION: We may not have predicted the correct initiation codon. Where possible we choose an initiation codon (aty, ttg or (att)) which is preceded by an upstream initiation codon. If this cannot be identified we choose the most upstream initiation codon. If this cannot be identified we choose the most upstream initiation codon. If this cannot be identified we choose the most sequence clone. It may be shorter because we only sequence overlapping sections once, or longer, because we arrange for a small overlapp with cosmids E63 and E39 on the Asel-E genomic
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Jote-"SCESS.01, partial CDS, cdaPS3, CDA peptide synchetase III, len: >332a3. Constitutes the the majority of cdaPS3, CDA peptide synthetase III, part of the calcium-dependent antibiotic (CDA) blosynthetic cluster from Streptomyces coelicolor. CDA is a peptide antibiotic multifunctional peptide synthetase enzyme. This partial CDS encodes a subunit of this enzyme suspected to be
                                                                                                        project,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Details of S. coelicolar sequencing at the Sanger Centre are available on the World Wide Web.

(WLE, http://www.sanger.ac.uk/Projects/S_coelicolor/) CDS are numbered using the following system eg SC/B7.01c. SC (S. coelicolor), 787 (cosmid name), .01 (first CDS), c (complementary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The more significant matches with motifs in the PROSITE database are also included but some of these may be fortuitous. The length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Streptomyces coelicolor sequencing at The Sanger Centre is funded by the BBSRC and Beowulf Genomics
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                                                                                                 coelicolor sequencing proje
Campus, Hinxton, Cambridge
                                                                                  Submitted (12-MAR-1999) Streptomyces coelicolor sequencing projection Centre, Wellcome Trust Genome Campus, Hinxton, Cambridge CB10 15A B-mall: barrellesanger.ac.uk Cosmids supplied by Prof. David A. Hopwood, [3] John Innes Centre, Norwich Research Park, Colney, Norwich, Norfolk.NR4 70H, UK
                                                                                                                                                                                                                                                                                                                      Redenbach, M., Kleser, H.M., Denapaite, D., Eichner, A., Cullum, J., Kinashi, H. and Hopwood, D.A.
2 (bases 1 to 26477)
Bentley, S.D., Parkhill, J., Barrell, B.G. and Rajandream, M.A.
                                                                                                                                                                                                                                                                                                                                                       A set of ordered cosmids and a detailed genetic and pl for the 8 Mb Streptomyces coelicolor A3(2) chromosome Mol. Microbiol. 21 (1), 77-96 (1996)
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/db_xref="taxon:1902"
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/gene="SCE63.01"
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                                                                      Submission
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us-09-037-657-24.rge

ORGANISM

CEYWORDS

REFERENCE AUTHORS TITLE

JOURNAL MEDLINE REFERENCE AUTHORS

JOURNAL MEDLINE FEATURES

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DLTLDGNRDNLSAKVDGWFNGYIPGQDGADRDVTLERVEIREMSGYGFDPHEQTINL
IRDSVAHDNSLDGFVADYQVGGVFENNVSYNNDRHGFNIVTSTNDFVLSNNVAYGNG
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RFEVALDGDHTGDLSAANVVFAATGTTTELEVLGDSGTQAGAIV"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /GGDTDDQLQGGSGADRLDGGAGDD1LDGGAGRDRLSGGAGADTFVFSAREDSYRTD
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                                                                                                                                                                                                                                                                                                                                                                                                                         A family of modular type mannuronan C-5-epimerase genes controls alginate structure in Azotobacter vinelandii Mol. Murcobiol. 16 (4), 719-731 (1995) 96065700
gene; algE2 gene; algE3 gene; algE4 gene; mannuronan C-5
                                                                                                                                                                     1 (sites)
Ertesyag,H., Doseth,B., Larsen,B., Skjak-Braek,G. and Valla,S.
Cloning and expression of an Azotobacter vinelandil mannuronan
                                                                                                          Bacteria; Proteobacteria; gamma subdivision; Azotobacteraceae;
                                                                                                                                                                                                                                                                                                                                        2 (bases 1 to 15759)
Siresvag, H., Holdal, H.K., Hals, I.K., Rian, A., Doseth, B. and
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protein_id="AAA87310.1"
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protein_id="AAA87311.1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /organism="Azotobacter vinelandii"
/strain="E"
                                                                                                                                                                                                                                                        C-5-epimerase gene
J. Bacteriol. 176 (10), 2846-2853 (1994)
                                                        Azotobacter vinelandii (strain E) DNA.
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1: .15759
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transl_table=11
                                                                                  Azotobacter vinelandii
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'gene="algE4"
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gene="algE1"
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'gene="algEl"
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                                                                                                                                           Azotobacter.
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gene

CDS

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NNVAYNDRHGFNIYTETYDFYYMNNYAYGGGGGLTLDS YGADGGGGFYTLDGGGAY
YDALGGYTEKMTNYTLGNAEIYGNGSGGGLTLDGGGAY
LLQARDGGYTEKMTNYTLIGNAEIYGNGSGGYELYGTEDYOILDNOIHDNSQNGTYPEY
LLQARDGGYTGELYETLNYRIEGNIDASDNANYAYRERDGGSYTLYDNDISGGG
VASYQLGGAHSSLAGGGTYEVPQGATDGNDYLYGSDANDQLYGGAGDDRLDGGAGDDLLD
                                                                                                                                                                                       LSGGTVEVPQGTDGNDVLVGSDANDQLYGGAGDDRLDGGAGDDLLD
                                                                                                                                                                                                                 GGAGRDDLTGGTGADTEVFAARTDSYRTDAGVFNDLILDFDASEDRIDLSALGFSGFG
DGYNGTLLVQLSSAGTRTYLKSYEEEDLEGRRFEVALDGDHTGDLSAANVVFADDGSAA
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TIRDSVAHDNGLDGFVADFQIGGVFENNVSYNNDRHGFNIVTSNNDFVLSNNVAYGNG
GAGLVVQRGSSDVAHPYDILIDGGAYYDNGLEGVQIRMAHDVTLQNAEIYGNGLYGVF
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NSTYGIQERDDGTDYSSLYANSYSNYQNGSVRLYGANSYVSDLPGTGQQATLEGTAGN
DTLGGSDAHETLLGLDGNDRLNGGAGNDILDGGAGRDNITGGAGADLFRVSARTDSYR
GETVIKLIDGSDQKITGMVRSAYGEETSNFGMSDLTLDGNRDNTSGKVDGWFNGYIP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TDSASFNDLITDFDASQDRIDLSALGFTGLGDCYNGTLLLQVSADGSRTYLKSLEADA
EGRRFEIALDGNFAGLLGAGNLLFERTAIEGDAGDNALLGTSAAETLLGHAGNDTLDG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GAGDDILVGGAGRDSLTGGAGADVFRFDALSDSQRNYDIGDNQGDRIADFAVGEDKLD
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AGNDILDGGAGRDTLSGGSGSDIFRFGGALDSFRNYASGTNGTDSITDFTPGEDLIDL
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                                            ODGADRNVTIERVEIREMSGYGFDPHEQTINLTIRDSVAHDNGLDGFVADYLVDSVF
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DSASYADLITDFDASEDRIDLSGLGFSGLGNGYGGTLALQVNSAGTRTYLKSFETNAA
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/translation="MDFNVKDFGALGDGASDDTAAIQAAIDAAHAAGGGTVYLPAGEY
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QGRRFEIALDGNFVGQFNDGNLLFDAAPVTGTEGNDNLSGTDAGETLLGYGGNDTLNG
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protein_id="AAA87313.1"
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/gene="algE2"
6702. 9695
/gene="algE2"
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VAYNNDRHGFNVVTSTYDFTLSNNVAYGNGGAGLVIQRGAEDLAQPTDILIDGGAYYE

37GAGCGC 120 Oy 761 ggagccacccacagccgcctccactccccgcagt	861 Db 3794 180	RESULT 11 RESULT 11 PASSULT 11 PASSULT 11 PASSULT 11 PASSULT 11 PASSULT 11 PASSULT 240 PASSULT 2	981 NID VERSION S00 KEYWORDS	SOURCE unidentified. ORGANISM unidentified unclassified. REFERENCE 1 (bases 1 to 11832) AUTHORS NICOLA.N.A., Fabrit,L., Farley,A., AUTHORS NICOLA.J., Alexander,W., Hilton,D.	2 6 5 F	/db_xref="taxon:32644" BASE COUNT 2447 a 3367 c 3298 g 27 ORIGIN	Ouery Match Query Match Best Local Similarity 73.5%; Pred. No. 3e-28; Macda,M. and Matches 291; Conservative 0; Mismatches	cccgcccgac 	Oy 529 ctgagcgtgcgtggtgtcgccacccgccctcaaggatttccccgccctcaaggatttccccgccctcaaggatttccccbcccccccccc	6663; 68; Gaps 1; 68	528 Db 8784 3493 Qy 641	588 Db 8844 3553 Qy 701	626 Db 8904 3613 Qy 761	640 Db 8964 GGAGCCACCCACCGCTGCTCG	700 AVIALGEB 15759 bp LOCUS AVIALGEB 15759 bp DEFINITION Azotobacter vinelandil m	760 ACCESSION
	ccgggcccgggcgggcgtgcgaccgcgcggggcgggggcgggc	ggcgcgagctcaagctcctgggctggctcaagaagcacgcgtactgctccaacctc 	agcttccgcctctacgaccagtgcgagcctggatgcagaagtcgcacaagacccgcaacaclliiiiiiiiiiiiiiiiiii	cagcacaggacgagggg 998 	A70398 6663 bp DNA PAT Sequence 28 from Patent W09811225. A70398 A770308 G1 G1.4774676	ied.	unclassilleu 1 (bases 1 to 6663) Nicola,N.A., Fabri,L., Farley,A., Nash,A., Willson,T Zhang,J., Alexander,W., Hilton,D.J., Kojima,T., Maed Kikuchi,Y.	SNETIC	/organism="unidentified" /db_xref="taxon:32644" 1462 a 1852 c 1715 g 1634 t	Query Match 13.7%; Score 190.8; DB 5; Length Best Local Similarity 73.5%; Pred. No. 3.3e-28; Antches 291; Conservative 0; Mismatches 37; Indels	gtgaccacggacccccgcccgacgtgcacgtgagccgcgtcggggggcctggaggaccag	ctgagogtgcgctgggtgtcgccacccccaaggatttcctcttcaagccaaatac 	cagatccgctaccgatggaggacagtgtggactgga	COCCCCTGACCCCGCCCCCCGCATCTGACTCCTCCCTCACCGTGCAGGTGGTGGATGACG	tgagcaaccagacctcctgccgcctggcggcctgaaacccggcaccgtgtacttcgtgc 	aagtgcgctgcaacccctttggcatctatggctccaagaaagccgggatctggagtgagt

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1 (bases i to 11832)
Nicola,N.A., Fabri,L., Farley,A., Nash,A., Willson,T., Rakar,S.,
Nicola,N.A., Fabri,L., Farley,A., Nojima,T., Maeda,M. and
Kikuchi,Y.
A NOVEL HAEMOPOIETIN RECEPTOR AND GENETIC SEQUENCES ENCODING SAME
Patent: WO 9811225-A 19-MAR-1998;
NICOLA NICOS ANTONY (AU)
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AVIALGEB 15759 bp DNA BCT 22-FEB-1996 Azotobacter vinelandil mannuronan C-5-epimerase (algE4, algE1, algE2 and algE3) genes, complete cds. L39066 L29009 9790690 L390690 L39060 LG
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Pred. No. 3e-28;
0; Mismatches 37; Indels 68; Gaps
07-MAY-1999
    PAT
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A70408 11832 bp DNA
Sequence 38 from Patent W09811225.
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a 3367 c 3298 g 272(
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Pred. No. 1.4e-55; 0; Mismatches 0;

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aggiccigccagataagcigtaggggcicaggccaccicccigccacgiggagacgcag 1090
                               Best Local Similarity 99.4
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VERSION
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/rpt_family-"Alu"

complement(18270. 18438)

/note-"predicted exon, Program: grail2exons_human_1.3,
frame: 0, quality: excellent, score:
100.000--(18438. 18284) DDS similarity to W66776

mel7bil.ri Scares mouse embryo NDME13: 14.5 Mus musculus
cDNA clone 387741 5, similar to Pir: B38252 338252

granulocyte colony-stimulating factor receptor precursor
(157. 1); 824 identity. --(18438. 18406) DDS similarity to
|AA049280 mj45402.ri Scares mouse embryo NDME13: 514.5 Mus
musculus cDNA clone 479043 5' similar to SW:ILGB_MOUSE
Q00560 NNTERLEUKIN-6 RECEPTOR BETA PRECURSOSR (432. 464);
                                                                                                                                                                                                                                                                                                   / Arctamenty: Actual of the control 
clone 365523 5' (428. 496); 97% identity.--(13756. 13984)
DDS similarity to AA009693 ze82h02.si Soares fetal heart
NDH19W Home sapiens CDNA clone 365523 3' (227. 1); 98%
identity.--(13756. .13984) DDS similarity to AA450010
zx33f04.si Soares total fetus ND2HF8 9w Home sapiens CDNA
clone 788287 3' (228. .1); 99% identity.-"
complement(14100. .14672)
// fpt_family.*Alu.*
14885. .15317
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Anote-"DDS similarity to AA121532 zk89c11.s1 Soares Pregnant uterus NbHPU Homo sapiens cDNA clone 490004 3′ (389. 343); 99% identity.~-DDS similarity to AA127694 clone 490004 5′ (77. 125); 90% identity.~-(18735. 15713) DDS similarity to W46603 zc32h10.r1 Soares senescent fibroblasts NbHSF Homo sapiens cDNA clone 324067 5′ (351. 329); 100% identity.~-(18735. 324067 5′ (351. 329); 100% identity.~-(15735. 15713) DDS similarity to W46604 zc32h10.s1 Soares senescent fibroblasts NbHSF Homo sapiens cDNA clone 324067 3′ (299. 321); 100%
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gkloracvgrkgaberdpgdppphrliskhrtrgscpradgvrrevrgsg" 212 q 117 p
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A NOVEL HARMOPOLETIN RECEPTOR AND GENETIC SEQUENCES ENCODING SAME PATENT: WO 9811225-A 19-MAR-1998; NICOLA NICOS ANTONY (AU)
LOCATION/QUALIFIERS
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Zhang,J., Alexander,W., Hilton,D.J., Kojima,T., Maeda,M. and
Kikuchi,Y.
                                                                            1269 cctagaaccctgccagggctgggggtgagaagggggtcattactccccattacctag
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Pred. No. 1.5e-39;
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/protein_id="CAB42574.1"
/db_xref="PID:e1433693"
/db_xref="PID:g4774666"
/db_xref="GI:4774666"
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Sequence 16 from Patent W09811225.
A70386
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86.8%;
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23.8%; Score 331; DB 11; Length 40668,

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Query Match

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//rpt_family-*hlu"
complement(571. .640)
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Lamerdin, J.E., McCready, P.M., Adamson, A.W., Burkhart-Schultz, K.,
Gordon, L., Christensen, M., Kyle, A., Ramirez, M., Stilwagen, S.,
Garnes, J., Danganan, L., Bruce, R., Quan, G., Montgomery, M., Ow, D.,
Kobayashi, A., Olsen, A.O. and Carrano, A.V.
Sequence analysis of an ~1 Mb region containing the MEF2B gene in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      frame: 1, quality: good, score: 71.000"

complement(1383. .1444)

frame: 1, quality: good, score: 62.000"

2257. .8516
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Submitted (21-NOV-1997) Human Genome Center, Lawrence Livermore
National Laboratory, 7000 East Ave., Livermore, CA 94551, USA
Location/Qualifiers
                                                        568 ttcctctttcaagccaaataccagatccgctaccgagtggaggacagtgggactggaag 627
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Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                             21-NOV-1997
                                                                                                                                                                                                                                                                                                       AC003112 40668 bp DNA PRI 21-NOV-1997
Human DNA from chromosome 19 specific cosmid R30292, genomic
sequence, complete sequence.
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                                     gtcgggggcctggaggaccagctgagcgtgcgctgggtgtcgccacccgccctcaaggat
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/note="HERV9 retroviral sequence"
complement(3169. .3544)
/rpc_family="Alu"
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'cell_line="5HL2-B"
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/db_xref="taxon:9606"
/clone="R30292"
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Eutheria; Primates; Catarrhin;
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DLTCRWTPGAHGETFLHTNYSLKYKLRWYGQDNTCEEYHTVGPHSCHTPKDLLETPY
EIWYEATNRLGSARSDVLTLDVLDVVTTDPPPDVHVSRVGGLEDQLSVRWYSPPALKD
FLFQAKYQIRYRVEDSVDWKVVDDVSNQTSCRLAGLKPGTVYFVQVRCNPFGIYGSKK
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Nicola N.A., Fabri, L., Farley, A., Nash, A., Willson, T., Rakar, Shang, J., Alexander, W., Hilton, D.J., Kojima, T., Maeda, M. and Kikuchi, Y.
A NOVEL HARNPOIETIN RECEPTOR AND GENETIC SEQUENCES ENCODING (Patent: WO BWI225-A 19-MAR-1998)
NICOLA NICOS ANTONY (AU)
LOCALION/QUALIFIERS
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Pred. No. 2.2e-107;
0; Mismatches 92;
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/db_xref="PID:e1433696"
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A NOVEL HAEMOPOIETIN RECEPTOR AND GENETIC SEQUENCES ENCODING SAME PATENT: WO 9811225-A 19-MAR-1998; NICOLA NICOS ANTONY (AU)
LOCATION/QUALIFIERS
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Zhang,J., Alexander,W., Hilton,D.J., Kojima,T., Maeda,M. and
Kikuchi,Y.
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Pred. No. 3.4e-99;
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/db_xref="taxon:32644"
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Best Local Similarity 99.6%;
Matches 558; Conservative
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Nicola,N.A., Fabri,L., Farley,A., Nash,A., Willson,T., Rakar,S.,
Zhang,J., Alexander,W., Hilton,D.J., Kojima,T., Maeda,M. and
Kikuchi,Y.
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Pred. No. 2e-146;
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Db 1202 GAGCCCAGCTCQY 901 cacgogtactc	Qy 1021 gcacgacgage 1. Db 1377 GTGCGCGAGE	RESULT 4 A70392 LOCUS A70392	DEFINITION Sequence ACCESSION A70392 NID 94774670 VERSION A70392.1	S	REFERENCE 1 (bases AUTHORS NICOla,N. Zhang,J.,	TITLE A NOVEL B JOURNAL PAtent: W NICOLA NI FEATURES	Source BASE COUNT 375 a	tch	Best_Local Similari Matches: 874; Cons	362	422	QY 121 cacgcccgtga 	Oy 181 aaaccogtcaa 	Oy 241 ccaggggccca 	301		
SAME	1;		0 1	0 1	0 1								ਜ਼ _	.	1	1	
GENETIC SEQUENCES ENCODING	0B 5; Length 1673; 153; 124; Indels 5; Gaps	gtactcaacgcctccaccttg 60	tegggggacaacetegtgtge.120 	tatgttggcctgccccagag 180 	gacttgacctgccgctggacg 240 	tcctcaagtacaagcttagg 300 	9tggggccccactcctgccac 360 	tgggtggaggccaccaaccgc 420 	ctggatgtggtgaccacggac 480 				STCAGCAACCAGACCTGC 1021 caagtgcgctgcaacccctt 720 	CAAGTGCGTTGTAACCCATTC 1081 tggagccacccacagccgcc 780		9cgtgcgaaccgcgggggggg 840 	
HAEMOPOIETIN RECEPTOR AND 40 9811225-A 19-MAR-1998, COS ANTONY (AU) Location/Qualifiers Location/Qualifiers //organism="unidentified" //db_xref="taxon:3264" a 550 c 474 g 305	60.1%; Score 836.6; DB 5; llarity 87.8%; Pred. No. 1.2e-153; Conservative 0; Mismatches 124;	acctcaacgggcgccgcctgcccctgagctctcccgtgtactcaacgcctccaccttg 	gctctggccctggccaacctcaatgggtccaggcagcggtcgggggacaacctcgtgtgc. 	cacgcccgtgacgcagcatcctggctgctctatgttggctgccccagag	aaacccgtcaacatcagctgctggtccaagaacatgaaggacttgacctgccgctggacg 	ccaggggcccacggggagacttcctccacaccactactcctcaagtacaagcttagg 	tggtatggccaggacaacatgtgaggagtaccacacagtggggcccactcctgccac 	atccccaaggactggctcttttacgccctatgagatctgggtggaggccaccaacgc 	ctgggctctgccgctccgatgtactcacgctggtatatctggatgtggtgaccacggac 		tgggtgtcgccaccgcctcaaggatttcctctttcaagccaaataccagatccgctac 	Cgagtggaggacagtgtggactggaaggtggtggtggacgatgtgagaaccagacctcctgc	COCCIOCARCARCARCAGACIGGAAGGIGGAIGATGACGICAGCAACCAGCCACCTGC CGCCtggccggcctgaaacccggcaccgtgtacttcgtgcaagtgcgctgcaaccccttt	GGGCCTGAAGCCGGCACCGTTTACTTCGTC tggctccaagaaagccgggatctggagtgag	GGGATCTATGGGTCGAAAAAGGCGGGAATCTGGAGCGAGTGGAGCCACCCCACCACCGCTGCC	tccactcccgcagtgagcgcccgggcccgggcgggggggg	gagccgagctcgggggccggtgcggcgagctcaagcagttcctgggctggct
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Ja.N.A., Fabriller, Farley, A., Nash, A., Willson, T., Rakar, S., Ja, V. Alexander, W., Hilton, D.J., Kojima, T., Maeda, M. and Johl, Y. Merander, W., Hilton, D.J., Kojima, T., Maeda, M. and Johl, Y. Nashing Receptor and Generic Sequences encoding same ent: WO 9811225-A 19-MAR-1998;
OLA NICOS ANTONY (AU)
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/organism="unidentified"
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Nlcolah,N.A., Fabri,L., Farley,A., Nash,A., Willson,T., Rakar,S.
Zhang,J., Alexander,W., Hilton,D.J., Kojima,T., Maeda,M. and
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/protein_id="AAC28335.1"
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Eutheria; Primates; Catarrhini; Hominidae; Homo.

El (Asassa Ito 1716)

ElSon,G.C.A., Graber,P., Losberger,P., Herren,S., Gretener,D., Menoud,L.N., Wells,T.N.C., Kosco-Vilbois,M.H. and Gauchat,J.F. Cytokine Type-I. Receptor Family

J. Immunol. (1998) In press

E (Asses I to 1716)

Elson,G.C.A., Graber,P., Losberger,P., Herren,S., Gretener,D., Menoud,L.N., Wells,T.N.C., Kosco-Vilbois,M.H. and Gauchat,J.F.

Direct Submitssion

Submitted (14-APR-1998) Dept. of Immunology, Serono Pharmaceutical Research Institute, 14, Chemin des Aulx, Plan-les-Ouates, GE 1228, Switzerland
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Homo sapiens cytokine-like factor-1 precursor (CLF-1) mRNA,
Ar059293
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A70384 Sequence 14 A70392 Sequence 22 A70382 Sequence 18 A70383 Sequence 18 AC03112 Human DNA AC0312 Human DNA A70386 Sequence 28 A70408 Sequence 28 E39996 Azotobacter

ALG31848 Human DNA
AF680247 Tilapia m
U86634 Rhodobacter
030510 Rabbit prol
M34083 Rat lactoge
M39304 Rat prolact
M5766 Rat prolact
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L48060 Rat (clone

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AL035636 Streptomy M86351 Streptomyce Y07955 O.sativa mR

S.cereale m Oreochromis AL023797 Streptomy 017391 Human mRNA AL031350 Streptomy AL034355 Streptomy 139268 Streptômyce NF027403 Bos tauru L02549 Bos taurus X14753 Cervus ela X94953 C.elaphus

07-MAY-1999

Result No.

AL009204 Streptomy Y11548 S.pristinae X96690 S.pristinae M31661 Human prola AF017434 Methyloba S78505 prolactin r Y17736 Streptomyce

Database :

Searched:

Sequence:

Run on:

AL035707 Streptomy AC007391 Homo sapi

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A NOVEL HAEMOPOIETIN RECEPTOR AND GENETIC SEQUENCES ENCODING SAME PALENT: WO 98111255.4 19-MAR-1998; NICOLA NICOS ANTONY (40)
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Alexander, W., Hilton, D.J., Kojima, T., Maeda, M. and
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1267.586 Million cell updates/sec
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6210. .6215 /gene="SC9B10.04"

ö 0; Gaps 3.4%; Score 47.8; DB 1; Length 33320; Stmilarity 43.9%; Pred. No. 1.6; Conservative 0; Micmath. Query Match Best Local S Matches 205

14709 casacascrassicarcascrassicarcascrassicarcas de 14768 cgtgcacgtgagccgcgtcggggcctggaggaccagctgagcgtgcgctgggtgtcgcc 551

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Search completed: September 28, 1999, 16:40:47 Job time: 7034 sec

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     cancer;
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                                                                                    cccccgccgacgtgcacgtgagccgcgtggaggcctggaggaccagctgagcgtgcgc
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Pred. No. 1e-108;
0; Mismatches 2; Indels
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Kojima T, Maeda M, Nash A, Nicola NA, Rakar S, Willson T,
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99.6%;
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Best Local Similarity 99.6
Matches 558, Conservative
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WO9811225-A2.
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WPI; 98-2
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Novel haemopoietin receptor NR6.3 gene.
Haemopoietin receptor; cell proliferation; cell differentiation; cancer.
cell survival; therapeutic; neuronal proliferation; drug screening; ss;
                                                                                                                                                                                                                                                                                                                                     567
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New isolated haemopoietin receptor - used for developing products
for modulating proliferation, differentiation and survival of cells,
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aagaacatgaaggacttgacctgccgctggacgccagggggcccacggggagaccttcctc
                                                                                                                                          121 AAGAACATGAAGGACTTGACCTGCCGCTGGACGCCCAGGGGCCCACGGGGAACCTTCCTC
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11-SEP-1997; G02479.
11-SEP-1996; AU-002246.
(AMRA-) AMRAD OPERATIONS PTY LTD.
(DZIE/) DZLEGLEWSKA H E.
Alexander W, Fabri L, Farley A, Hilton DJ, Kikuchi Y,
Rojima T, Maeda M, Nash A, Nicola NA, Rakar S, Willson
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/product= "Haemopoietin receptor NR6.
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V27142;
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WPI; 98-260970/23.
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standard; cDNA; 834
                                                   WO9811225-A2
          V27143
V27143;
                                  Mus sp.
                                                                                  WPI; 98
P-PSDB;
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  Length 1629;
Conservative
Query Match
Best Local Similarity
Matches 872; Conserv
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For any angulation of celebration of developing products for modulating proliferation, differentiation and survival of cells, For modulating proliferation, differentiation and survival of cells, For e.g. neuronal cells

Claim 7: Page 93-95; 182pp; English.

The nucleotide sequence was generated by a SN RACE of brain CDNA using CC Interaction between the novel Haemopoletin receptor (HR) and ifferentiation and survival of a wide variety of cells. The HR and it's darivatives can be used for modulating the activity of the receptors e.g. to regulate development, maintenance or regeneration in an array of differentiation and issues in vitro and in vivo. They can be present in therapeutics used for modulating neuronal proliferation, differentiation come survival. The products can also be used for detection and diagnosis, e.g. for cancers or predisposition to cancers, or for drug screening.

Sequence 834 BP; 167 A; 274 C; 225 G; 168 T;
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29-SEP-1998 (first entry)
Nucleotide sequence of products generated by 5N race of brain cDNA.
Haemopoletin receptor; cell proliferation; cell differentiation; cancer
cell survival; therapeutic; neuronal proliferation; drug screening; ss;
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(DZIE/) DZIEGLEWSKA.H.E.
Alexander W. Fabri L., Farley A. Hilton DJ, Kikuchi Y.
Kojima.T., Maeda M., Nash A., Nicola NA, Rakar S., Willson
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43.0%; Score 598.8; DB 1;
Best Local Similarity 87.7%; Pred. No. 1.7e-117;
Matches 654; Conservative 0; Mismatches 92;
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/product= !Haemopoietin receptor'
                                                                                                                                                             Location/Qualifiers
1..834
/*tag= a
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11-SEP-1996; AU-002
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29-SEP-1998 (first entry)
Unspliced murine NR6 nucleotide sequence.
Haemopoletin receptor; cell proliferation; cell differentiation; cancell survival; therapeutic; neuronal proliferation; drug screening;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  57.5%; Score 799.6; DB 1; Length 1930; 87.6%; Pred. No. 1.3e-159; 1ve 0; Mismatches 124; Indels 0;
                                                                                                                                   11.-SEP-1996; AU-002246.
(AMRA-) AMRAD OPERATIONS PTY LTD.
(DZIE-) DZIEDWSKA H & A
ALEXANDER W, FADYI L, FATIEY A, Hilton DJ, Kikuchi Y,
Kojima T, Maeda M, Nash A, Nicola NA, Rakar S, Willson
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Best Local Similarity 87.6
Matches 874; Conservative
                                                                                                                      11-SEP-1997; G02479
11-SEP-1996; AU-0022
                                                                                                                                                                                                            Zhang J;
mpr: 98-260970/23
                                                                                          WO9811225-A2
                                                                                                           19-MAR-1998
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Tor mountains, received the instance of the movel HR NR6.

Claim 4, Page 77.81; 182pp; English.

The haemopoietin receptor (HR) NR6.1 is a form of the novel HR NR6.

Interaction between the novel HR and a ligand facilitates proliferation, differentiation and survival of a wide variety of cells. The HR and it's derivatives can be used for modulating the activity of the receptors e.g. to requiate development, maintenance or regeneration in an array of different cells and tissues in vitro and in vivo. They can be present in therapeutics used for modulating neuronal proliferation, differentiation and survival. The products can also be used for detection and diagnosis, e.g. for cancers or predisposition to cancers, or for drug screening.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            v27140;
29-SEP-1998 (first entry)
Novel hemopoietin receptor NR6.1 gene.
Haemopoietin receptor; cell proliferation; cell differentiation; cancer;
cell survival; therapeutic; neuronal proliferation; drug screening; ss;
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(DZIEZ) DZIEGLEWSKA H E.
Alexander W, Fabri L, Farley A, Hilton DJ, Kikuchi Y,
Kojima T, Maeda M, Nash A, Nicola NA, Rakar S, Willson
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/product= "Haemopoletin receptor
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113. .1355
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11-SEP-1996; AU-002246.
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P-PSDB; W55011.
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New nucleic acid encoding U4 haematopoietin receptor superfamily chain - potentially useful, e.g. for modulating call proliferation or immune response, for treating cancer and auto:immune disease Claim 1; pages 25-26; 38pp; English.

This is the nucleotide sequence encoding the murine U4 protein from the haematopoietin receptor superfamily, used in the method of the invention for the modulation of call proliferation, or the immune response. Transformed mammalian calls are used to produce recombinant U4 protein. The U4 protein is used to screen for specific binding agents, raise antibodies. It is also used as reagents for assays and as tissue markers for isolation of cognate ligands and receptors, and in pharmaceutical compositions which may modulate cell proliferation, cell differentiation, and the immune system (e.g. for treating immune cell differentiation).
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26-OCT-1998 (first entry)
Nucleotide sequence of the murine U4 gene.
Murine; U4 protein; haematopoietin receptor superfamily;
cell proliferation; immune response; antibody; cell differentiation; autoimmune disease; cancer; allergy; ds.
               478 G;
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(GEMY ) GENETICS INST INC.
Collins M, Donaldson DD, Neben T, Whitters M;
WPI; 98-414109/35.
P-PSDB; W59804.
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V27158 standard; DNA; 1930 BP V27158;

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RESULT V27158 ID V2' AC V2'

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Novel haemopoletin receptor NR6.2 gene.
Haemopoletin receptor; cell proliferation; cell differentiation; cell survival; therapeutic; neuronal proliferation; drug screenin Mouse.
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ctgggctctgcccgctccgatgtactcacgctggatatcctggatgtggtgaccacggac
          CTGGGTTCAGCGAGATCTGACGTGCTCACACTGGATGTCCTGGACGTGGTGACCACGGAC
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19-MAR-1998.
11-SEP-1997; G02479.
11-SEP-1996; AU-002246.
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WITT, 98.260970/23.

PPEDBS W55012.

New isolated hemopoletin receptor - used for developing products

for modulating proliferation, differentiation and survival of cells,

e.g. neuronal cells

Claim 5; Page 84-87; 182pp; English.

The haemopoletin receptor (HR) NR6.2 is a form of the novel HR NR6.

Interaction between the novel HR and a ligand facilitates proliferation,

Interaction between the novel HR and a ligand facilitates proliferation,

Claim 5; Page 84-87; 182pp; English.

The haemopoletin receptor (HR) NR6.2 is a form of the novel HR NR6.

Interaction between the novel HR and a ligand facilitates proliferation,

Claim 5; Page 84-87; Page 84-87; Page 8-99;

Corgulate development, maintenance or regeneration in an array of

different cells and tissues in vitro and in vivo. They can be present in

Claim 5: The HR and tissues in vitro and in vivo. They can be present in

Claim 5: The HR and tissues in vitro and in vivo. They can be present in

Claim 5: The HR and tissues in vitro and in vivo. They can be present in

Claim 5: The HR and tissues in vitro and in vivo. They can be present in

Claim 5: The HR and tissues in vitro and in vivo. They can be present in

Claim 5: The HR and tissues in vitro and in vivo. They can also be used for detection and diagnosis,

Claim 5: The HR and tissues in vitro ancers, or for drug screening.

Claim 5: The HR and tissues the tissues the vitro and tissues the vitro and diagnosis,

Claim 5: The HR and tissues the vitro and to drug screening.
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Best Local Similarity 87.8%;
Matches 926; Conservative
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V70896 ID V70896 standard; cDNA; 1724 BP.

RESULT

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Disclosure, Page 72-75; 55pp; English.

The present sequence encodes a protein designated Zcytor5, which is a cytokinin-like receptor. Soluble Zcytor5 may be administered to down-regulate the effects of a growth and/or maintenance factor in thyroid, heart, and skeletal muscle for example to lessen the effect of cardiotrophin-1 on cardlac pathologies, so preventing heart enlargement. Zcytor5 could be used to detect cardiotrophin-1 in the blood, and to discover other possible Zcytor5 ligands. A probe and integrity of the Zcytor5 gene on chromosome 19. Antibodies and therapeutically to modify Zcytor5 ligand to purify Zcytor5 and therapeutically to modify Zcytor5 ligand effects.

Sequence 1724 BP; 550 C; 500 C; 324 T;
17-MAR-1999 (first entry)

CDNA encoding rat Zoytor5.

Zoytor5; cytokinin-like receptor; down-regulation; growth factor;
maintenance factor; thyroid; heart; skeletal muscle; cardiotrophin-1;
cardiac pathology; heart enlargement; Zcytor5 ligand; ss.
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down-regulating Zcytor5 natural ligands or detecting cardiotrophin-1
in blood
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01-MAY-1997; US-85030.
01-MAY-1999; US-045287.
01-MAY-1999; US-033890.
(ZYMO.) ZYMOGENETICS INC.
Adams RL, Foster DC, Glibert T, Jelmberg AC, Lehner WPI; 99-034662.
P-PSDB; W70862.
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60.9%; Score 847.4; DB 1;
Best Local Similarity 84.9%; Pred. No. 1.1e-169;
Matches 987; Conservative 0; Mismatches 166;
                                                                                                                                      Location/Qualifiers
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/*tag= a
/product= Zcytor5
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01-MAY-1998;
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TGGTATGGCCAGGACAACACATGTGAGGAGTACCACACAGTGGGGCCCCACTCCTGCCAC

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standard; cDNA; 1579
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V41689;
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1655 AAAAAAAAAAA 1667

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the heamatopoletin receptor superiamily used in the method of the invention for the modulation of cell proliferation, or the immune response. Transformed mammalian cells are used to produce recombinant U4 protein. The U4 protein is used to screen for specific binding agents, raise antibodies. It is also used as reagents for assays and as tissue markers for isolation of cognate ligands and receptors, and in pharmaceutical compositions which may modulate cell proliferation, cell differentiation, and the immune system (e.g. for treating immune deficiency, inherited or the result of infection, autoimmune diseases, sequence 1579 BP; 304 A; 535 C; 473 G; 267 T;
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                                                                                          Human; U4 protein; haematopoietin receptor superfamily; cell proliferation; immune response; antibody; cell differentiation; autoimmune disease; cancer; allergy; ds.
                                                                                                                                                                                                                                                                                                                        15-JUL-1998.
15-JUL-1998.
16-JAN-1999; U00334.
16-JAN-1999; U00334.
16-JAN-1997; US-784863.
16-JAN-1997; US-784863.
Collins M, Donaldson DD, Neben T, Whitters M;
WPI; 98-414109/35.
P-PSDB; W59805.
New nucleic acid encoding U4 haematopoietin receptor superfamily chain - potentially useful, e.g. for modulating call proliferation chain - potentially useful, English.
This is the nucleotide sequence encoding the human U4 protein from
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99.2%; Pred. No. 8.3e-276;
ive 0; Mismatches 4;
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Disclosure; Page 63-66; 55pp; English.

Disclosure; Page 63-66; 55pp; English.

The present sequence encodes a protein designated Zcytor5, which is a cytokinhi-like receptor. Soluble Zcytor5 may be administered to down-regulate the effects of a growth and/or maintenance factor in thyroid, heart, and skeletal muscle for example to lessen the effect of cardiotrophin-1 on cardiac pathologies, so preventing heart of andiotrophin-1 in the blood, and to discover other possible Zcytor5 ligands. A probe comprising Zcytor5 punk or RNA can be used to determine the presence and integrity of the Zcytor5 gene on chromosome 19. Antibodies and the therapeutically to modify Zcytor5 ligand effects.

C sequence 1690 BP; 319 A; 592 C; 505 G; 274 T;
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13-FEB-1998; US-033890.

(ZYMO ) ZYMOGENETICS INC.

Adams RL, Foster DC, Gilbert T, Jelmberg AC, Lehner JM,

LOK S, Presnell SR, Whitmore TE;

P-PSDB; W70860.
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Disclosure: Page 68-70; 55pp; English.

The present sequence encodes an allelic varaint of protein designated

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CC Zoytor5, which is a cytokinin-like receptor. Soluble Zoytor5 may be

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CC dactor in thyroid, heart, and skeletal muscle for example to lessen the

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CC blood, and to discover other possible Zoytor5 ligands. A probe

CC comprising Zoytor5 DNA or RNA can be used to determine the presence

CC and integrity of the Zoytor5 gene on chromosome 19. Antibodies and the

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CC anti-idiotypic antibody could be used to purify Zoytor5 and

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CC charapeutically to modify Zoytor5 ligand effects.
                               V70895 standard; cDNA; 1813 br.
V70895;
17.MAR-1999 (first entry)
cDNA encoding an allellc varaint of human 2cytor5.
2cytor5; cytokinin-like receptor; down-regulation; growth factor; maintenance factor; thyroid; heart; skeletal muscle; cardiotrophin-1; cardiac pathology; heart enlargement; 2cytor5 ligand; allelic varaint;
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13-FEB-1998; US-023890.
Adams RL, Foster DC, Gilbert T. Jelmberg AC, Lehner LoK S, Fresnell SR, Whitmore TE;
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Human granulocyte Comamonas sp. N-Ac

ALIGNMENTS

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GenCore version 4.5
Copyright (c) 1993 - 1998 Compugen Ltd.
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OM nucleic - nucleic search, using sw model

Run on:

September 28, 1999, 16:45:58; Search time 303.81 Seconds (without alignments).
1145.509 Million cell updates/sec

Title: Perfect score: Sequence:

US-09-037-657-24 1391 1 accetcaaegggegegeget.....geaaaaaaaaaaaaaa 1391

IDENTITY_NUC Scoring table:

311585 seqs, 125096042 residues Searched:

N_Geneseq_36:* Database: Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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Length 259;

223.6; DB 1; No. 9.1e+39;

Score Pred.

16.1%; 92.2%;

Query Match Best Local Similarity

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Claim 9; Fig 3; 182pp; English.

The NR6 protein is a novel Haemopoietin receptor (HR). Interaction between the novel HR and a ligand facilitates proliferation, differentiation and survival of a wide variety of cells. The HR and it's derivatives can be used for modulating the activity of the receptors e.g. to regulate development, maintenance or regeneration in an array of different cells and tissues in vitro and in vivo. They can be present in therapeutics used for modulating neuronal proliferation, differentiation and survival. The products can also be used for detection and diagnosis, e.g. for cancers or predisposition to cancers, or for drug screening.

Sequence 11832 BP; 2447 A; 3367 C; 3298 G; 2720 T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ä
                                                                                                                                                                                                                                                                                                                                                                               29-58P-1998 (first entry)
Nucleotide sequence for murine NR6 containing additional SN sequence.
Haemopoletin receptor; cell proliferation; cell differentiation; cancer; cell survival; therapeutic; neuronal proliferation; drug screening; ss;
                                                                                  aggatttcctcttcaagccaaataccagatccgctaccgagtggaggacagtgtggact 622
                                                                                                                                                                                               743 ccgggatctggagtgagtgagcacccacagccgctccactcccgcagtgagcgcc 802
                                                                                                                                                                                                               Gaps
                                          529 ctgagogtgogctgggtgtcgccaccgccctcaaggatttcctcttcaagccaaatac 588
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WPI: 98-260970/23.
New isolated haemopoletin receptor - used for developing products
for modulating proliferation, differentiation and survival of cells,
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Alexander W, Fabrí L, Farley A, Hilton DJ, Kikuchi Y,
Kojíma T, Maeda M, Nash A, Nicola NA, Rakar S, Willson
     19;
  0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                     V27148 standard; -DNA; 11832 BP.
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 237; Conservative
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Best Local Similarity 73.5
Matches 291; Conservative
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11-SEP-1997; G02479.
11-SEP-1996; AU-002246.
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New Jobated heemopoletin receptor - used for developing products for modulating proliferation, differentiation and survival of cells, e.g. neuronal cells

cig. neuronal cells

cig. neuronal cells

the neuronal cells

The NR6 gene encodes a novel Haemopoletin receptor (HR). Interaction

between the novel HR and a ligand facilitates proliferation,

differentiation and survival of a wide variety of cells. The HR and it's products can be used for modulating the activity of the receptors e.g. to requirate development, maintenance or regeneration in an array of aliferent cells and tissues in vitro and in vivo. They can be present in therapeutics used for modulating neuronal proliferation, differentiation and survival. The products can also be used for detection and diagnosis, e.g. for cancers or predisposition to cancers, or for drug screening.

Sequence 6663 BP; 1462 A; 1852 C; 1715 G; 1634 T;
                                                                                                       8784 CGCCCTGACCCCGCCCCCGCATCTGACTCCTCCCTCACCGTGCAGGTGGATGACG 8843
8724 CAGATCCGCTACCGCGTGGAGGACAGCGTGGACTGGAAGGTGCCCGTCCCGCCCCGGACC 8783
                                                                                                                                                                                                                     8904 AAGTGCGTTGTAACCCATTCGGGTCTATGGGTCGAAAAAGGCGGGAATCTGGAGCGAGT 8963
                                                                                                                                                                                  --aggtggtggacgatg
                                                                                                                                                                                                                                                                                                                                                                                                                                            Nucleotide sequence of Murine NR6.
Haemopoietin receptor; cell proliferation; cell differentiation;
cancer; cell survival; therapeutic; neuronal proliferation; drug;
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Pred. No. 1.2e-31;
0; Mismatches 37; Indels 68:
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11-SEP-1997; G02479.
11-SEP-1996; AU-002246.
(AMRA-) AMRAD DERTIONS PTY LTD.
(D21E) DZIEGLEWSKA H E.
Alexander W, Fabri L, Farley A, Hilton DJ, Kikuchi Y,
Kolima T, Maeda M, Nash A, Nicola NA, Rakar S, Willson T,
WPI; 98-260970/23.
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                     3554 CAGAICCGCIACCGCGIGGAGGACAGCGIGGACIGGAAGGIGCCCGTCCCGCCCCGGACC 3613
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completed: September 28, 1999, 16:46:31 ne: 7376 sec Search com

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MOLECULE TYPE: CDNA HYPOTHETICAL: NO
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/cgn2_6/ptodata/2/ina/5D_COMB.seq:*
/cgn2_6/ptodata/2/ina/5D_COMB.seq:*
/cgn2_6/ptodata/2/ina/PCTUS9_COMB.seq:*
/cgn2_6/ptodata/2/ina/PCTUS9_COMB.seq:*
GenCore version 4.5
Copyright (c) 1993 - 1998 Compugen Ltd.
                                                                                                                                                                                                                               176461 segs, 45838279 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                          SUMMARIES
                                                    nucleic search, using sw model
                                                                                                                                        US-09-037-657-24
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Pred. No. 0.16;
0; Mismatches 144; Indels 0
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CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/845,998
                                                                                                                                                                                                                                                                                                                                     APPLICANT: De Smet, Charles
APPLICANT: Lucas, Sophie
APPLICANT: BOON, Thierry
TILE OF THE FOR THE TO SEQUENCES: 16
CORRESPONDENCE ADDRESS:
US-08-456-837-6
US-08-457-342-6
US-08-457-646A-6
US-08-458-076A-6
US-08-764-233A-1
US-08-764-233A-4
                                                                                                                    US-08-729-214-6
                                                                                                                                                                                                                                                                                                                                                                                                                                                3: Wolf, Greenfield & Sacks, P.C.
600 Atlantic Avenue
                                                                                                                                                                        ALIGNMENTS
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                                                                                                                                                                                                                                                      Sequence 7, Application US/08845998
Patent No. 5879892
                                                                                                                                                                                                                                                                                                         Van Baren, Nicolas
Coulle, Pierre G.
De Smet, Charles
Lucas, Sophie
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Van Amsterdam, John R.
REGISTRATION NUMBER: 40,212
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Conservative
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TYPE: nucleic acid
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ggcggggggtgcgaaccgcggggggggagagccgagctcggggccggtgcgggggctc 873
                                                                                                                                                 754 agtgagtggagccacccacagccgcctccactcccgcagtgagcgcccgggcccgggc
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                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: DELLAPORTA, STEPHEN L. TITLE OF INVENTION: MATERIALS AND METHODS FOR PRODUCING TITLE OF INVENTION: PLANTS WITH SINGLE-SEX FLOWERS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Patentin Release #1.0, Version #1.25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Pred. No. 0.13;
; Mismatches 209;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DB 3;
                                                                                                                                                                                                                              753 ATGCACAGCCTGGGCCACCTGTCGCACCCGCG 785
                                                                                                                                                                                        874 aagcagttcctgggctggctcaagaagcacgcg 906
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STREET: 2000 PENNSYLVANIA AVE. N.W. CITY: WASHINGTON
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/440,856A
FILIGO DATE: 15-MAY-1995
CLASSIFICATION: 800
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                     Sequence 9, Application US/08440856A Patent No. 5750873 GENERAL INFORMATION: APPLICANT: DELLAPORTA, STEPHEN L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0.0%; Sc.
Best Local Similarity 39.3%; Pr.
Matches 152; Conservative 26;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ATTORNEY/AGENT INFORMATION:
NAME: MILLMAN, ROBERT A.
REGISTRATION NUMBER: 36,217
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          REFERENCE/DOCKET NUMBER: 05
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        INFORMATION FOR SEQ ID NO: 9: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (202) 887-1517
(202) 887-0763
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1288 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                           NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
ADDRESSEE: MORRISON
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STRANDEDNESS:
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US-08-440-856A-9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELEPHONE:
                                                                                                                                                                                                                                                                                                          08-440-856A-9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SOFTWARE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ENGTH:
                                                                                                               814
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422 tgggctctgcccgctccgatgtactcacgctggatatcctggatgtggtgaccacggacc 481
                                                                                                                                                                                                                                                                                                                                                                                            542 gggtgtcgccacccgccctcaaggatttcctctttcaagccaaataccagatccgctacc
                                                                                                                                                                                                                                                                                    924 AGGAGGIGGAGAAGAIGGAGGAGGIGGICAGGGGCCISGCCACGCICAAGGGCSCSACGC
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APPLICANT: BARR, PHILIP J
APPLICANT: KIEFER, MICHAEL C
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR PACE 4 AND
TITLE OF INVENTION: PACE 4.1 GENE AND POLYPEPTIDES IN CELLS
NUMBER OF SEQUENCES: 16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              68; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           E: COOLEY GODWARD CASTRO HUDDLESON & TATUM FIVE PALO ALTO SQUARE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 40.2; DB Pred. No. 0.57;
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REFERENCE/DOCKET NUMBER: CHIR-009/01US
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1044 IWTCSGGCCACACCTYGTCGTSGACG 1070
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APPLICATION NUMBER: US/08/284,941
FILING DATE: 2 August 1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              602 gagtggaggacagtgtggactggaagg 628
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 1, Application US/08284941
Patent No. 5863756
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TELEFAX: (415) 857-0663
TELEX: 380816 COCLEY PA
INFORMATION FOR SEQ ID NO: 1:
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Best Local Similarity 54.4%;
Matches 81; Conservative
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LENGTH: 4403 base pairs
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CORRESPONDENCE ADDRESS:
ADDRESSEE: COOLEY GO
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MOLECULE TYPE:
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; LOCATION:
US-08-284-941-1
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US-08-284-941-1/c
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; NAME/KEY;
; LOCATION;
US-07-923-976-3
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                                     824 gcgaaccgcgggggggggagaccgagctcggggccggtgcggcggagctcaagcagttcc 883
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APPLICANT: KIEFER, MICHAEL C
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR PACE 4 AND
TITLE OF INVENTION: PACE 4.1 GENE AND POLYPEPTIDES IN CELLS
CORRESPONDENCE ADDRESS:
ADDRESSEE: COOLEY GODWARD CASTRO HUDDLESON & TATUM
STREET: FIVE PALO ALTO SQUARE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US93/02147A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 40.2; DB 5;
Pred. No. 0.57;
0; Mismatches 68;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER: US 07/848,629
FILING DATE: 09 PAR-10992
ATTORNEY/AGENT INFORMATION:
NAME: NEELEY PH.D., RICHARD L
REGISTRATION NUMBER: 30092
REFERENCE/DOCKET NUMBER: CHIR-009/00US
                                                                          884 tgggctggctcaagaagcacgcgtactgc 912
                                                                                                             165 GCGACAGGCTCGCGCGGCGCCCGAGCTGC 137
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                                                                                                                                                              RESULT 4
PCT-US93-02147A-1/C
; Sequence 1, Application PC/TUS9302147A
; GENERAL INFORMATION:
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (415) 494-7622
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 2.9%;
Best Local Similarity 54.4%;
Matches 81; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELEFAX: (415) 857-0663
TELEX: 380816 COOLEY PA.
INFORMATION FOR SEQ ID NO: SEQUENCE CHARATTERISTICS:
LENGTH: 4403 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TOPOLOGY: linear
MOLECULE TYPE: DNA (cDNA)
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STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         OMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NAME/KEY: CDS
LOCATION: 170..3077
                                                                                                                                                                                                                                                                                                                                                                                                   PALO ALTO
CALIFORNIA
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PCT-US93-02147A-1
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348 ccactcctgccacatccccaaggacctggctctctttacgccctatgagatctgggtgga 407
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                                                       APPLICANT: Nagata, Shigekazu
APPLICANT: Fukunaga, Rikiro
TITLE OF INVENTION: DNA Encoding Granulocyte
TITLE OF INVENTION: Colony-Stimulating Factor Receptor
NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
ADDRESSEE: Jones, Tullar & Cooper, P.C.
STREET: P.O. Box 2266 Eads Station
                                                                                                                                                                                                                                                                                                                                                                                                      Patentin Release #1.0, Version #1.25
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Pred. No. 1.1;
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FILING DATE: 22-MAR-1991
ATTORNEY/AGENT INFORMATION:
NAME: Hellwege, James W.
REFESTATION NUMBER: 28,808
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FILING DATE: 03-JUL-1990
PRIOR APPLICATION DATA:
RAPLICATION NUMBER: PCT/TD01 ....FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION DATA:
FILING DATE: 23-MAR-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 176629/1990
                                                                                                                                                                                                                                                                                                                                                                                                                  CUCREENT APPLICATION DATA:
APPLICATION NUMBER: US/07/923,976
FILING DATE: 19920922
                                                                                                                                                                                                                                                                                                                                     MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
Sequence 3, Application US/07923976
Patent No. 5574136
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match 2.8%;
Best Local Similarity 55.1%;
Matches 76; Conservative
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PORMATION FOR SEC ID NO.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  linear
                                                                                                                                                                                                                                                                    STATE: Virginia
ZIP: 22202
                                                                                                                                                                                                                                               CITY: Arlington
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APPLICANT: Nagata, Shigekazu
APPLICANT: Fukunaga, Rikiro
TITLE OF INVENTION: DA Eccoding Granulocyte
TITLE OF INVENTION: Colony-Stimulating Factor Receptor
                                                                                                                                                                                                                                                                                                                                                                            PatentIn Release #1.0, Version #1.25
                                                                                                                                                                                   5: Jones, Tullar & Cooper, P.C. P.O. Box 2266 Eads Station
                                                                                                                                                                                                                                                                                                                                                                                                                                                        CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 74539/1990
FILING DATE: 23-MAR-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 176629/1990
FILING DATE: 03-JUL-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCI/JP91/00375
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICATION NUMBER: PCT/JP91/00375
FILING DATE: 22-MAR-1991
ATTORNET/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                             OPERAL
CUGRESMT APPLICATION DATA:
APPLICATION NUMBER: US/07/923,976
                                                                                                                                                                                                                                                                                                                              COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
Application US/07923976
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NAME: Hellwege, James W.
REGISTRATION NUMBER: 28,808
REFERENCE/DOCKET NUMBER: 51.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TELECOMMUNICATION INFORMATION TELEPHONE: 703-415-1500
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MOLECULE TYPE: CDNA to mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 2.8%;
Best Local Similarity 55.1%;
Matches 76; Conservative
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                                                                       APPLICANT: NOGERCA, SILIGE
APPLICANT: PUKUNAGA, RIK
TITLE OF INVENTION: COLO
NUMBER OF SECURNCES: 8
CORRESPONDENCE ADDRESS:
ADDRESSEE: Once, Tull
STREET: P.O. Box 2266
CITY: Arlington
STREET: P.O. Box 2266
CITY: Arlington
STREET: Virginia
ZIP: RAZADABLE FORM:
MEDIUM TYPE: Floppy dis
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STRANDEDNESS: single
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US-07-923-976-7
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                                                                                                        APPLICANT: Nagata, Shigekazu
APPLICANT: Fukunaga, Rikiro
TITLE OF INVENTION: DNA Encoding Granulocyte
TITLE OF INVENTION: Colony-Stimulating Factor Receptor
NUMBER OF SQUENCES: 8
CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                                                    SSEE: Jones, Tullar & Cooper, P.C. :: P.O. Box 2266 Eads Station Arlington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 74539/1990
FILING DATE: 23-MAR-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 176629/1990
FILING DATE: 03-JUL-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCI/JP91/00375
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER: PCT/JP91/00375
FILING DATE: 22-MAR-1991
ATTORNEY/AGENT INFORMATION:
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APPLICATION NUMBER: US/07/923,976
FILING DATE: 19920922
                                                                                                                                                                                                                                                                                                                                                          MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                               Application US/07923976
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NAME: Hellwege, James W. REGIGSTRATION NUMBER: 28,80 REFERENCE/DOCKET NUMBER: 5 TELECOMMUNICATION INFORMATION TELEPHONE: 703-415-1500
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2.88;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       841 TGTGAAACTGGAGCCCCC 858
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Best Local Similarity 55.1'
Matches 76; Conservative
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170..2482
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                                                                                                                                                                                                                                                                                                      Virginia
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CLASSIFICATION:
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                                                                                                                                                                                                                                     ADDRESSEE:
STREET: P.
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US-07-923-976-5
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US-07-923-976-7
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                                                                                          348 ccactcotgccacatccccaaggacotggctctttacgccctatgagatctgggtgga 407
DB 1; Length 3024;
                                               Indels
                          Pred. No. 1.1;
0; Mismatches
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Patent No. 5728523
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RESULT
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APPLICANT: KINZLET, Kenneth W.
TITLE OF INVENTION: POLYMERASE DELTA MUTATIONS IN COLORECTAL
TITLE OF INVENTION: TUMORS WITH REPLICATION ERRORS
NUMBER OF SEQUENCES:
ADDRESSPONDENCE ADDRESS:
ADDRESSEE: Banner, Birch, McKie & Beckett
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Indels
                                                                                                                                                                                                                                                                                                                            SOFTWARE: Patentin Release #1.0, Version #1.25
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Pred. No. 1.4;
0; Mismatches
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APPLICANT: Hillman, Jennifer L.
APPLICANT: G011, Surya K.
TITLE OF INVENTION: NOVEL CALCIUM-BINDING
TITLE OF INVENTION: PROTEIN
                                                                                                                                                                                                                                                                                                                                         CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/366,577
FILING DATE: 12-DEC-1994
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: Kagan, Sarah A.
REGISTRATION NUMBER: 32,141
REFERENCE/DOCKET NUMBER: 01107,48554
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 38.4;
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Patent No. 5871970
                                                                                                                                                                                                                                                                               IBM PC compatible SYSTEM: PC-DOS/MS
                                                                                                                                1001 G Street N.W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity 51.1%;
Matches 90; Conservative (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TELEFAX: 202-508-9299
TELEX: 197430 BBMB UT
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     nucleic acid
EDNESS: double
                                                                                                                                                                                                                                        COMPUTER READABLE FORM:
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                                                                                                                                               Washington
                                                                                                                                                                                                                                                                             COMPUTER: IBM PC
OPERATING SYSTEM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 linear
                                                                                                                                                                                              U.S.A.
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450 gotggatatoctggatgtggtgaccacggacccccgccgacgtgcacgtgagccgcgt 509
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GENERAL INFORMATION:
APPLICANT: Vogelstein, Bert
APPLICANT: Kinzler, Kenneth W.
TITLE OF INVENTION: POLYMERASE DELTA MUTATIONS IN COLORECTAL
TITLE OF INVENTION: TUMORS WITH REPLICATION ERRORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 1055
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DB 4;
                                                                                                                                                                             CURRENT APPLICATION DOS
CURRENT APPLICATION DATA:
APPLICATION NUMBER: 05/08/82,242
FILING DATE: Filed Herewith
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3: Incyte Pharmaceuticals, Inc. 3174 Porter Drive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 38.4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       E: Banner & Allegretti, Ltd
1001 G Street N.W.
                                                                                                         ZIP: >430.4
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM COMPATIDLE
                                                                                                                                                                                                                                                                                                                                                                                                     NAME: Billings, Lucy J.
REGISTRATION NUMBER: 36,7
REFERENCE/DOCKET NUMBER:
TELECOMMUNICATION INFORMATIO
TELEPHONE: 415-855-0555
                                                                                                                                                                                                                                                                                                                                                                                  ATTORNEY/AGENT INFORMATION
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APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELEFAX: 415-845-416
INFORMATION FOR SEQ ID NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NUMBER OF SEQUENCES: 1
CORRESPONDENCE ADDRESS:
ADDRESSEE: Banner &
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE CHARACTERISTI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: nucleic acid
STRANDEDNESS: singl
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Best Local Similarity
Matches 108; Conserv
                                         Palo Alto
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IMMEDIATE SOURCE
                                                                                   USA
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                                                                                                    94304
                                                                                   COUNTRY:
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                                         CITY:
STATE:
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MOLECULE TYPE:
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APPLICANT: Matsuhlsa, Akio.
APPLICANT: Wehara, Hirotsugu
APPLICANT: Eda, Soji
TITLE OF INVENTION: Probe for Diagnosing Infectious Disease
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              3: Marshall, O'Toole, Gerstein, Murray & Borun 6300 Sears Tower, 233 South Wacker Drive
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                                                                                     PatentIn Release #1.0, Version #1.25
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Pred. No. 1.4;
0; Mismatches
                                                     COMPUTER. THE SYSTEM: COMPUTER. CONTROL OF SOPTWARE: PATENTIN Release #1.0, VeCURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US96/00005 FILING DATE: 2-JAN-96
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      XY: United States of America 60606-6402
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                                                                                                                                                                                             ATTORNEY/AGENT INFORMATION:
NAME: Kagan, Sarah A.
REGISTRATION NUMBER: 32.141
REFERENCE/DOCKET NUMBER: 011
TELECOMMUNICATION: INFORMATION:
TELEPHONE: 202-508-9100
                                                                                                                                                                                                                                         32,141
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Best Local Similarity 51.1%;
Matches 90; Conservative
                                                                                                                                                                                                                                                                                                                              TELEFAX: 202568-9299
TELEX: 197430 BBMB UT
INFORMATION FOR SEQ ID NO: 15
SEQUENCE CHARACTERICS:
LENGTH: 3435 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: nucleic acid
STRANDEDNESS: double
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COMPUTER READABLE FORM:
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43..3364
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                                                                                                                                                                             CLASSIFICATION:
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5296 GTCGGCAGGCCCCGGCGGAGGATGAAGTCGAGCAGCGGCAACTGCCGGTAGAACAGCGCG 6355
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APPLICANT: Tibbot, Brian K
TILLE OF INVENTION: Cloned Alpha-Glucosidase from Barley
NUMBER OF SEQUENCES: 7
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  . 0; Mismatches 143; Indels
SUFTWARE: Patentin Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
PITTIN NUMBER: US/08/920.817
                                  29-AUG-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1006 cctcgggcagacgggggcgagag 1032
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                                                                                                 FILING DATE: 29-AUG-1997
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/362,577
FILING DATE: 27-MAR-1995
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ORGANISM: Pseudomonas aeruginosa,
STRAIN: Clinical Isolate P2-2
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STREET: 1 South Pinckney Street
CITY: Madison
                                                                                                                                                                                                                                                       NAME: Rin-Laures, Li-Hsien
REGISTRATION NUMBER: 33,54
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 2.7%;
Best Local Similarity 46.4%;
Matches 124; Conservative
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LENGTH: 9515 base pairs
                                                                                                                                                                                                                                                                                                                                                        : 312/474-6300
312/474-0448
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STRANDEDNESS: double
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us-09-037-657-24.rni

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TYPE: nucleic acid STRANDEDNESS: double
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MEDIUM TYPE: Floppy
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Best Local Similarity
Matches 124; Conserva
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                                                                                                                                  60606-6402
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APPLICANT:
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                                                                                 PatentIn Release #1.0, Version #1.30
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Pred. No. 1.5;
0; Mismatches 208;
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                                                                                                                                                                               ATTORNEY/AGENT INFORMATION:
NAME: Seay, Nicholas J
REGISTRATION NUMBER: 27,386
REFERENCE/DOCKET NUMBER: 960296.93171
TELECOMMUNICATION INFORMATION:
TELEPHONE: 608-251-5000
                                                                                                                       APPLICATION NUMBER: US/08/430,925/
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Patent No. 5770375
                                      IBM PC compatible
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APPLICANT: Uchara, Hirotsugu
APPLICANT: Eda, Soji
TITLE OF INVENTION: Probe for
NUMBER OF SEQUENCES: 25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity 45.5%;
Matches 179; Conservative
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                  CURRENT APPLICATION DATA
                                                                                                                                                                                                                                                                                                                                                                                            TYPE: nucleic acid
STRANDEDNESS: double
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                CLASSIFICATION: 435
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                                                         OPERATING SYSTEM
SOFTWARE: Patent
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                                                                                                                                        FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NAME/KEY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; LOCATION:
US-08-430-925A-3
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6296 GTCGGCAGGCCCCGGCGGAGGATGAAGTCGAGCAGCGGCAACTGCCGGTAGAACAGCGCG 6355
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;: Marshall, O'Toole, Gerstein, Murray & Borun 6300 Sears Tower, 233 South Wacker Drive
                                                                                                                                                                                                                                                   Version #1.25
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46.4%; Pred. No. 2.2;
tive 0; Mismatches 143;
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                                                                      STATE: Illinois
COUNTRY: United States of America
                                                                                                                                                                                                                                                                                                                                 CLASSIFFCATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/362,577
FILING DATE: 27-MAR-1995
ATTORNEY/AGENT INFORMATION:
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                                                                                                                                                                                                                                      SOFTWARE: Patentin Release #1.0, CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/920,827
FILING DATE: 29-AUG-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ORGANISM: Pseudomonas aeruginosa
STRAIN: Clinical Isolate P2-2
                                                                                                                                                                   MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
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Patent No. 5798211
                                                                                                                                                                                                                                                                                                                                                                                                                                                              NAME: Rin-Laures, Li-Hsien
REGISTRATION NUMBER: 33,54
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INFORMATION FOR SEQ ID NO:
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Eda, Soji
/ENTION: Probe for Diagnosing Infectious Disease
                                                                                       S: Marshall, O'Toole, Gerstein, Murray & Borun 6300 Sears Tower, 233 South Wacker Drive
                                                                                                                                                                                                                           COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0; Mismatches 143;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NAME: Rin-Laures, Li-Hsien
REGIESTRATION NUMBER: 33,547
REFERENCE/DOCKET NUMBER: 19036/32420
ELECOMMUNICATION INFORMATION:
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FILING DATE: 29-AUG-1997
CLASSIFICATION: 435
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APPLICATION NUMBER: US 08/362,577
FILING DATE: 27-MRR-1995
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                  COUNTRY: United States of America
ZIP: 60606-6402
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STRAIN: Clinical Isolate P2-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELEX: 25-3856
INFORMATION FOR SEQ ID NO: 13:
SEQUENCE CHARACTERISTICS:
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STRANDEDNESS: double
                                                                 CORRESPONDENCE ADDRESS:
ADDRESSEE: Marshall,
                   TITLE OF INVENTION:
NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Best Local Similarity
                                                                                                                                    Chicago
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Sequence 13, Application US/08362577C Patent No. 5807673 GENERAL INFORMATION:

RESULT 15 US-08-362-577C-13

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6176 caececagererrecaacaaccerecagaracegacageceregrarecagecerec 6235
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         886 ggctggctcaagaagcacgcgtactgctccaacctcagcttccgcctctacgaccagtgg 945
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             5296 GICGGCAGGCCCCGGGGGAGGAIGAAGICGAGCAGCGGCAACIGCCGGIAGAACAGCGCG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 9515;
APPLICANT: Matsuhisa, Akio
APPLICANT: Uchara, Hirotsugu
APPLICANT: Eda, Sol,
TITLE OF INVENTION: Probe for Diagnosing Infectious Disease
NUMBER OF SEQUENCES: 25
CORRESPONDENCE ADDRESS:
ADDRESSEE: Marshall ~.-
                                                                                                                                                                          3: Marshall, O'Toole, Gerstein, Murray & Borun 6300 Sears Tower, 233 South Wacker Drive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0; Mismatches 143; Indels
                                                                                                                                                                                                                                                                                                                                                               SOFTWARE: Patentin Release #1.0, Version #1.25 CURRENT APPLICATION DATA: APPLICATION NUMBER: US/08/362.5777
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Search completed: September 28, 1999, 16:40:56
Job time: 7042 sec
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Pred. No. 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1006 cctcgggcagacggggcacggcgagag 1032
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                                                                                                                                                                                                                                                                                                                                                                                                       ELLING DATE: 27-MAR-1995
CLASSIFICATION: 536
                                                                                                                                                                                                                                 STATE: Illinois
COUNTRY: United States of America
ZIP: 60606-6402
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       υκGANISM: Pseudomonas aeruginosa
;
US-08-362-577C-13
                                                                                                                                                                                                                                                                                                                     MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ATTORNEY/AGENT INFORMATION:
NAME: Rin-Laures, Li-Hsien
REGISTRATION NUMBER: 33,547
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELECOMMUNICATION INFORMATION TELEPHONE: 312/474-6300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 2.7%;
Best Local Similarity 46.4%;
Matches 124; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELEX: 25-3856
INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         312/474-0448
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         nucleic acid
EDNESS: double
                                                                                                                                                                                                                                                                                                COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      linear
                                                                                                                                                                                  STREET: bocc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MOLECULE TYPE: CORIGINAL SOURCE:
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EST

FEATURES

COMMENT

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qe50c05.x1 Soares_fetal_lung_NbHL19W Homo sapiens cDNA clone
INAGE:1742408 3' similar to TR:Q16354 Q16354 PROLACTIN RECEPTOR ;,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        normalization to a Cot = 5. Library constructed by Bento Soares and M.Fatima Bonaldo. This library was constructed from the same fetus as the fetal heart library, Soares fetal heart NbH119W ... 83 t 1 others
                                                                                                                                                                                                                           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalla; Eutherla; Primates; Catarrhini; Hominidae; Homo.
1. (bases 1 to 477)
NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
                                                                                                                                                                                                                                                                                                                                                                         Contact: Robert Strausberg, Ph.D.
Tel: (301) 496-1550
Email: Robert_Strausbergenih.gov
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image:llnl.gov) for further information.
Insert Length: 1552 Std Error: 0.00
Seg primer: -400P from Gibco
High quality sequence stop: 467.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       61 getetggecetggecaaceteaatgggteeaggeageggtegggggaeaacetegtgtge 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           181 aaacccgtcaacatcagctgctggtccaagaacatgaaggacttgacctgccgctggacg
                                                                                                                                                                                                                                                                                                                                          On Feb 17, 1998 this sequence version replaced gi:2150926
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          22.1%; Score 307; DB 43;
99.7%; Pred. No. 9.5e-55;
tive 0; Mismatches 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /organism="Homo sapiens"
/db_xref="taxon:9606"
                                                                                                                                               93736562
A1185924.1 GI:3736562
                                                                                                                                                                                                                                                                                                             Tumor Gene Index
Unpublished (1997)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity 99.77
Matches 307; Conservative
                                                                                                                  mRNA sequence.
AI185924
                                                                                                                                                                                                               Homo sapiens
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                                                                                                                                                                                              human,
                                                                          DEFINITION
                                                                                                                                                                                                         ORGANISM
                                                                                                                                                                                                                                                          REFERENCE
AUTHORS
TITLE
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COMMENT
                            RESULT 1
AI185924
LOCUS
                                                                                                                              ACCESSION
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                                                                                                                                                           VERSION
KEYWORDS
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                                                                                                                                                                                                                                                                                                                                                        /Glone="IMAGE:1665990"
/clone="IMAGE:1665990"
/clone_lib="Soares_senescent_fibroblasts_NbHSF"
/tissue_type="senescent fibroblast"
/lab_host="DH10B (ampicillin resistant)"
/note="Vector: pT7T3D (Pharmacia) with a modified
polylinker V_TYPE: phagemid; Site_1: Not I: Site_2: Eco
RI: lst strand cDNA was primed with a Not I - oligo(dT)
             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Primates; Catarrhin; Hominidae; Homo.

1 (bases 1 to 364)

NCI-GAP http://www.ncbl.nlm.nih.gov/ncicgap.

National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
                                                                                                                                                            Contact: Robert Strausberg, Ph.D.
Tel: (301) 496-1550
Email: Robert_Strausberg@hih.gov
This clone is available royalty-free through LLNL; contact the
INAGE Consortium (info@image.llnl.gov) for further information.
Insert Length: 1197 Std Exror: 0.00
Seq primer: -40ml3 fred. ET from Amersham
High quality sequence stop: 353.
Localin/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           gggcacctgagccctcagcaggagctgggctggccctgagctccaacggccataacag 1192
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1253 agggttggttgagttgcctagaacccctgccagggctgggggtgagaagggagtcatta 1312
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                                                                                                                               On Jan 19, 1998 this sequence version replaced gi:2285562
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ,;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     42; Length 364;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 313.2; DB 42; Length
Pred. No. 4.6e-56;
0; Mismatches 18; Indels
                                                                                                                                                                                                                                                                                                               1. .364
/organism="Homo sapiens"
/db_xref="taxon:9606"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
22.5%;
Best Local Similarity 94.5%;
Matches 346; Conservative
                                                                                                  Tumor Gene Index
Unpublished (1997)
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ORGANISM
                                              REFERENCE
AUTHORS
TITLE
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ORIGIN
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Gaps

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Length 477; Indels us-09-037-657-24.rst

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LOCUS
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AI085207/c
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           JOURNAL
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                                                                                                                       NCI-CGAP http://www.ncbi.nlm.nlh.gov/nclcgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
                                                                                                                                                                                                                                                   normalization to a cot - 5. Library constructed by M.Fatima Bonaldo. This library was constructed from the same fetus as the fetal lung library, Soares fetal lung
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 356 bp mRNA EST 16-FEB-1999 Soares_pregnant_uterus_NbHPU Homo saplens cDNA clone 50 3', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                      1270 ctagaacccctgccagggctgggggtgagaagggggggtcattactccccattacctaggg 1329
                                                                                                                                                                                                                                                                                                                                                                                                                                                        aggoogaacccaaactggggccacctctgtaccctcacttcagggcacctgagc.cctc 1149
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         agcaggagctggggtggcccctgagctccaacggccataacagctctgactcccacgtga 1209
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      225 AGCAGGAGCTGGGGTGGCCCCTGAGCTCCAACGGCCATAACAGCTCTGACTCCCACGTGA 166
                                                                                                                                                                                                                                                                                                                                                                               Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         105 CIAGAACCCCTGCCAGGGTGAGAGGGGAGTCATIACTCCCCATIACCTAGGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DB 37; Length 394;
                                                                                                                                                                                                                                                                                                                                                     Score 326.6; DB 37; Length Pred. No. 7.5e-59; 0; Mismatches 4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota; Metazoa; Chordata; Cranlata; Vertebra
Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 356)
                                                                                             clone_lib="Soares_fetal_heart_NDHH19W"
'sex="unknown"
 primer: -40m13 fwd. ET from Amersham
                                                  organism-"Homo sapiens"
/db_xref="GDB:1288024"
/db_xref="taxon:9606"
/clone="IMAGE:379768"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GI:4175774
                                                                                                                                                                                                                                                                                                                                                     Query Match 23.5%;
Best Local Similarity 98.6%;
Matches 340; Conservative (
                                                                                                                                                                                                                                                                                          NDHL19W."
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IMAGE:2042750 3'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Homo sapiens
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AI375784/C
LOCUS
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AUTHORS
TITLE
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oyl6c04.sl Soares_senescent_flbroblasts_NbHSF Homo sapiens CDNA clone IMAGE:1665990 3', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the No and Eco RI sites of the modified pT/T3 vector. Library went through one round of normalization. Library constructed by M. Fatima Bonaldo."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      coccaging grater grater grange grant grant transition can a same second con 1286
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1049 tgtaggggeteaggeeaceteeetgeeacgtggagacgeagaggeegaacecaaaetgg 1108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ggccacctctgtaccctcacttcagggcacctgagc.-ccctcagcaggagctggggtgg 1166
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                occetgagetecaacggecataacagetetgaeteceacgtgaggecacetttgggtgca 1226
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /note="Organ: uterus; Vector: pT7T3-Pac; Site_1: Not I
Site_2: Eco RI: 1st strand cDNA was primed with a Not
Oligo(dT) primer [5'
AACTGGAAGAATTGGGGGCGGCTTTTTTTTTTTTTT 3'],
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               356 TGTAGGGGCTCAGGCCACCTCCCTGCCACGTGGAGACGCAAAGGCCCGAACCCAAACTGG 297
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   236 cccrigacrccaacgccaraacacrrrgacrcccacgrgagccaccrrrgggrgca 177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    57
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Tumor Gene Index
Unpublished (1997)
On Apr 3, 1998 this sequence version replaced gi:3017967
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 356;
                                                                                             Contact: Robert Strausberg, Ph.D.
Tel: (301) 496-1550
Email: Robert_Strausberg@hih.gov
Email: Robert_Strausberg@hih.gov
Ints clone is available royalty-free through LLNL
INAGE Consortium (info@image.llnl.gov) for further
Insert Length: 1238 Std Error: 0.00
Seg primer: -40UP from Gibco
High quality sequence stop: 307.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                 /clone="IMAGE:2042750"
/clone_lib="Soares_pregnant_uterus_NbHPU"
/sex="female"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 321.4; DB 45; Length
Pred. No. 8.9e-58;
0; Mismatches 6; Indels
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/organism="Homo sapiens"
                                                                                                                                                                                                                                                                                                                                                                                                     /db_xref="taxon:960
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /dev_stage="adult"
/lab_host="DH10B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GI:3423630
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 23.1%;
Best Local Similarity 97.7%;
Matches 337; Conservative
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human.
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AA706010/c
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AUTHORS
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JOURNAL
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                                                                                                                                                                                                                                                                                                                                                                                                                                              AA4U6406 433 bp mRNA EST 17-MAY-1997
2V11e07.s1 Soares_NhHMPu_S1 Homo sapiens cDNA clone IMAGE:753348
3', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /clone="IMAGE:753348"
/clone_11b="Soares_NhHMPu_S1"
/tissue_type="Pooled human melanocyte, fetal heart, and
pregnant uterus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 433)

Hiller, L., Allen, M., Bowles, L., Dubuque, T., Geisel, G., Jost, S., Kucaba, T., Lacy, M., Le, N., Lennon, G., Marra, M., Martin, J., Moore, B., Schellenberg, K., Steptoe, M., Tan, F., Theising, B., White, Y., Wille, T., Waterston; R. and Wilson, R. WashU-Merck EST project 1997

Unpublished (1997)

On Nov 29, 1993 this sequence version replaced g1:430306.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
7el: 314 286 1810
Fax: 314 286 1810
Email: est@watson.wustl.edu
This clone is available royalty-free through LLNL; contact the IMAGE Consortium (info@image.llnl.gov) for further information.
High quality sequence stop: 422.
                                                                                                                  caggacaacacatgtgaggagtaccacacagtggggccccactcctgccacatccccaag 369
                                                          gacciggcictctttacgccctatgagatctgggtggaggccaccaaccgcctgggctct 429
                                                                        /lab_host="DH10B"
/note="Organ: mixed (see below); Vector: pI7T3D-Pac

    433
    /organism="Homo sapiens'
/db_xref="GDB:5976201"
    /db_xref="taxon:9606"

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AA406406.1 GI:2064592
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AA406406/c
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VERSION
KEYWORDS
SOURCE
ORGANISM
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310
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JOURNAL
COMMENT
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FEATURES

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(Pharmacia) with a modified polylinker; Site_1: Not I; Site_2: Eco RI: Equal amounts of plasmid DNA from three normalized libraries (melanocyte ZNBHW, pregnant uterus NDHPU, and fetal heart NDHH19W) were mixed, and ss circles wer made in vitro. Following HAP purification, this DNA was used as tracer in a subtractive hybridization as saccing and as tracer. The diriver was PCR-amplified cDNAs from pols of 5,000 clones made from the same 3 libraries. The pools of consisted of I.M.A.G.E. clones 260232-265223, and 484488 489479."
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Tel: 314 286 1800
Fax: 314 286 1810
Email: esfewatson.wustl.edu
This clone is available royalty-free through LLNL; contact the IMAGE Consortium (info@image.llnl.gov) for further infommation.
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1 (bases 1 to 394)

Hiller,L. Allen,M., Bowles,L., Dubuque,T., Geisel,G., Jost,S., Krizman,D., Kucaba,T., Lacy,M., Le,N., Lennon,G., Marra,M., Martin,J., Moore,B., Schellenberg,K., Steptoe,M., Tan,F., Theising,B., Wilte,Y., Wylie,T., Waterston,R. and Wilson,R. WashGrNCI human BST Project
Unpublished (1997)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            286
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1091 aggoogaacocaaactggggccacetotgtaccetcacttcagggcacctgage--cect
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1149 cagcaggagctgggtggccctgagctccaacggccataacagctctgactcccacgtg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   cctagaacccctgccagggctgggggtgagggggggggtcattactccccattacctagg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 327.8; DB 33; Length 433;
Pred. No. 4.3e-59;
0; Mismatches 2; Indels 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             On May 8, 1995 this sequence version replaced g1:801325
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Washington University School of Medicine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AA706010 394 bp mRNA EST zf44a09.sl Soares_fetal_heart_NbHH19W Homo IMAGE:379768 3', mRNA sequence.
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AA706010.1 GI:2715928
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ilarity 98.8%;
Conservative
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us-09-037-657-24.rst

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AA866388.1 GI:4230568
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Best Local Similarity 87.7%;
Matches 365; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                             Contact: Soares, MB
                                                                                                                                                                                                                                                                      Norway rat.
Rattus norvegicus
                                                                                                                                                                                                                                                                                                                                                                                        97044477
                                                                                                                                     AA866388
LOCUS
DEFINITION
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KEYWORDS
SOURCE
ORGANISM
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TITLE
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COMMENT
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                                                                                                                           Homo sapiens
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalla;
Butheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 415)
NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
                                                                                                                                                                                                                                                                                           This clone is available royalty free through LLNL; contact the IMAGE Consortium (info@image.llnl.gov) for further information. Insert Length: 1466 Std Error: 0.00 Seq primer: -40ml3 fwd. Er from Amersham High quality sequence stop: 403.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AA992638 415 bp mRNA EST 27-AUG-1998 ot81b10.s1 Soares_total_fetus_Nb2HF8_9w Homo sapiens cDNA clone IMAGE:1623163313', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                 On Sep 12, 1996 this sequence version replaced g1:1406852
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Pred. No. 1.2e-65;
0; Mismatches 8; Indels 3;
                                                                                                                                                                                                                                                                                                                                                                                       /organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:1623163"
/clone_lib="Soares_total_fetus_Nb2HF8_9w"
/dev_stage="8-9 weeks"
/lab_host="DH108"
                                                                                                                                                                                                                                                         Contact: Robert Strausberg, Ph.D.
Tel: (301) 496-1550
Email: Robert_Strausberg@nih.gov
                                                                                       AA992638.1 GI:3178372
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity 97.2%;
Matches 387; Conservative
                                                                                                                                                                                                        Tumor Gene Index
Unpublished (1997)
                                                                                                                                                                                                                                                                                                                                                                             1. .415
                                                                AA992638
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                                                                                                                 human.
RESULT 9
AA992638/c
LOCUS
DEFINITION
                                                                            NID
VERSION
KEYWORDS
SOURCE
ORGANISM
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ORIGIN
                                                                                                                                                                  REFERENCE
AUTHORS
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/strain="sprague-basiey"
/strain="sprague-basiey"
/db_xref="taxon:10116"
/map="between D118176.8 and UGB"
/clone=lub="tu-R-A0-1f-604-0-ful"
/dev_stage="dault"
/dev_stage="dault"
/lab_host="bH108 (life Technologies)"
/note="vector: pT73D-Pac (Pharmacia) with a modified
polyplinker; Site_1: Not I; Site_2: ECO RI; This library
consists of a mixture of individually tagged normalized
libraries constructed from rat placenta, adult lung,
brain, liver, kidney, heart, spleen, ovary, and muscle.
The tag is a string of 3.5 nucleotides present between the
Not I site and the oligo-dT track which allows
identification of the library of origin of a clone within
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           451 Eckstein Medical Research Building Iowa City, IA 52242, USA Tel: 319 335 8250
Fax: 319 335 9565
Fax: 319 335 9565
Fax: 319 335 9565
Fax: 319 335 9665
Fax: 319 335 9666
Fax: 319 326 971
Fax: 319 335 9666
Fax: 319 5066
Fax: 319 
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota: Metazoa, Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
I (bases 1 to 428)
Bonaldo, M.F., Lennon, G, and Soares, M.B.
Normalization and subtraction: two approaches to facilitate gene
                                                                                                                       1279 ctgccagggctgggggtgagaaggggagtcattactccccattacctagggcccctccaa 1338
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0; Gaps
                                                                                                                                                                                                      98 CIGCCAGGGCTGGGGGTGAGATAGGGAGTCATTACTCCCCATTACCTAGGGCCCCTCCAA 39
158 regerecaccccagregererererererereserreserreserreceracaaacc
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Pred. No. 1.8e-60;
0; Mismatches 51; Indels 0;
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    .428
    /organism="Rattus norvegicus"

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source

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/note="Organ: 1909 | Vector: p1773D-Pac (Pharmacia) with a modified polylinker; Site_1: Not I; Site_2: Eco RI; Equal amounts of plasmid DNA from three normalized libraries (fetal lung NbHL19W, testis NHT, and B-cell NCI_CGAP_GCBI) were mixed, and ss circles were made in vitro. Following HAP purification, this DNA was used as tracer in a subtractive hybridization reaction. The driver was PCR-amplified CDNAs from pools of 5,000 clones made from the same 3 libraries. The pools consisted of I.M.A.G.E. clones 297480-302087, 682632-687239, 726408-72871, and 729096-731399. Subtraction by Bento
                                                                                                                                                                                      Contact: Robert Strausberg, Ph.D.
Tel: (301) 496-1550
Email: Robert_Strausbergeinh.gov
Email: Robert_Strausbergeinh.gov
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
Insert Length: 117 Std Error: 0.00
Seg primer: -40ml3 fwd. ET from Amersham
High quality sequence stop: 358.
Location/Qualifiers
                    Dubaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.

1 (Dases 1 to 394)

NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP).
Tumor Gene Index
Unpublished (1997)

On Jan 17, 1998 this sequence version replaced gi:2044794.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             cacctctgtaccctcacttcagggcacctgagc--cctcagcagagctggggtggcc 1169
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 cgagggatectgecetegggeagaeggggeaeggegagaggteetgeeagataagetgt 1051
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ctgagctccaacggccataacagctctgactcccacgtgaggccacctttgggtgcaccc 1229
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          334 CGAGGGGATCTTG-CCTCGGGCAGACGGGCCACGGCGAGAGGTCCTGCCAGATAAGCTGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 365.8; DB 40; Length 394;
Pred. No. 5.1e-67;
0; Mismatches 2; Indels 3;
                                                                                                                                                                                                                                                                                                                                                                                                                                 /clone_11b="Soares_NFL_T_GBC_S1"
/lab_host="DH10B"
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                                                                                                                                                                                                                                                                                                                                                         1. .394
/organ1sm="Homo saplens"
/db_xref="taxon:9606"
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                                                                                                                                                                                                                                                                                                                                                                                                                  /clone="IMAGE:1542230"
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           Homo saptens
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          364 occaaggacotggotototttacgcoctatgagatotgggtggaggocaccaacgcotg 423
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       424 ggctctgcccgctccgatgtactcacgctggatatcctggatgtggtgaccacggacccc 483
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  722
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ;;
                                                 /map-"10 pter-cen"
/clone="IMAGE:387741"
/clone_11b="Soares mouse embryo NbME13.5 14.5"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DB 26; Length 482;
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                                                                                                    /sex="unknown"
/issue_type="embryo"
/dev_stage="13.5.14.5dpc total fetus"
/lab_host="DH109"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    tch 26.5%; Score 368.4; DB 26; al Similarity 87.9%; Pred. No. 1.5e-67; 413; Conservative 0; Mismatches 56;
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/organism-"Mus musculus"
                                /db_xref-"taxon:10090"
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AA927378.1 GI:3076275
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BASE COUNT ORIGIN

Matches

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RESULT 8 AA927378/C

DEFINITION

ACCESSION VERSION KEYWORDS

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RESULT 7
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/note_notgan: mixed (see below); vector: p1713D-Pac
/the_notgan: mixed (see below); vector: site_1: Not I:
/the_notgan: sco RI; Equal amounts of plasmid DNA from three
normalized libraries (melanocyte 2NbHW, pregnant uterus
NbHPU, and fetal heart NbHH19W) were mixed, and ss circles
was used as tracer in a subtractive hybridization
reaction. The driver was PCR-amplified cDNAs from pools of
//off clones made from the same 3 libraries. The pools
340488-345479, and 484488-489479.
                                                                                                                                                                                                                                                                                                                                                                                                                  A1417616 389 bp mRNA EST · 30-MAR-1999
tg80c02.xl Soares_NhHMPu_S1 Homo sapiens cDNA clone IMAGE:2115074
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /clone="IMAGE:2115074"
/clone_lib="Soares_NhiMPu_S1"
/tissue_type="Pooled human melanocyte, fetal heart, and pregnant uterus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
                                                                                                                                                              Contact: Robert Strausberg, Ph.D.
Tel: (301) 496-1550
Email: Robert_Strausberg@inh.gov
This clone is available royalty free through LLNL; contact the
This clone is available royalty free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
Insert Length: 800 Std Error: 0.00
Seq primer: -40UP from Gibco
High quality sequence stop: 383.
Location/Qualifiers
                                                                                               1277 ccctgccagggctgggggtgagaaggggagtcattactccccattacctagggcccctcc 1336
                                338 CCAGATAAGCTGTAGGGGCTCAGGCCACCCTCCCTGCCACGTGGAGACGCAGAGGCCGAA 279
                                                                                                                                                                                                                                                   98 CCCTGCCAGGGCTGGGGGTGAGAGGGAAGTCATTACTCCCCATTACCTAGGGCCCCTCC 39
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 389)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         On May 7, 1998 this sequence version replaced gi:3120565.
                                                                                                                                                                                                                                                                                                /organism="Homo sapiens"
/db_xref="taxon:9606"
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A1417616.1 GI:4261120
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Unpublished (1997)
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AI417616
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A1417616/c
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AUTHORS
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BASE COUNT ORIGIN

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Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 482)
Marra, M., Hillier, L., Allen, M., Bowles, M., Dietrich, N., Dubuque, T., Geisel, S., Kucaba, T., Lacy, M., Le, M., Martin, J., Morris, M., Schellenberg, K., Steptoe, M., Tan, F., Underwood, K., Moore, B., Theising, B., Wylle, T., Lennon, G., Soares, B., Wilson, R. and
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                                                                                                                                                                                                                                                                           987 caggacgagggatcctgccctcgggcagacggggcacggcgagaggtcctgccagataa 1046
                                                                                                                                                                                    gotgtagggggtcaggccacctccctgccacgtggagacgcagaggccgaacccaaact 1106
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  gggctgggggtgagaaggggagtcattactcccattacctagggccctccaaaagagt 1344
                                                                                                                                                                                                                                                                                                                                                                         W66776 BST 14-JUN-1996 mRNA mel7blirl Soares mouse embryo NbME13.5 14.5 Mus musculus CDNA clone IMAGE:387741 5 similar to PIR:B38252 B38252 granulocyte colony-stimulating factor receptor precursor ; mRNA sequence.
                                                                                                                 89 GGGCTGGGGGTGAGAAGGGGAGTCATTACTCCCCATTACCTAGGGCCCCTCCAAAAGAGT 30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Waterston,R.
The WashU-HHMI Mouse EST Project
Unpublished (1996)
On Apr 14, 1993 this sequence version replaced g1:785250
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Length 389
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Contact: Marra M/Mouse EST Project
WashU-HHMI Mouse EST Project
WashIngton University School of Medicinep
4444 Forest Park Parkway, Box 8501, St. Louis, MO
Fax: 314 286 1810
Fax: 314 286 1810
Email: mouseest@watson.wustl.edu
                                                Indels
  DB 46;
                        Pred. No. 1.3e-68;
0; Mismatches 1
  26.8%; Score 373.4; 99.2%; Pred. No. 1.3
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W66776.1 GI:1375694
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  Query Match
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                                                Matches 386;
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301 ACGTGAGCCGCGTTGGGGGCCTGGAGGACCAGCTGAGTGTGCGCTGGGTCTCACCACCAG 360
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WashU-HMI Mouse EST Project
WashIngton University School of Medicinep
444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
7e1: 314 286 1800
Fax: 314 286 1810
Email: mousesetewatson.wustl.edu
Email: mousesetewatson.wustl.edu
IMAGE Consortium (info@image.llnl.gov) for further information.
MGI128978
Seq primer: -28M13 rev2 from Amersham
High quality sequence stop: 437.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            T 3'), on equal amounts of mRNA from 2 13.5dpc and 2 State Univ., from 2 1; double-stranded cDNA was lighted to Eco RI adaptors (Pharmacia), dispested with Not I and Cloned into the Not I and Eco RI sites of the modified pp773 vector. Library went through one round of M.Fatima Bonalido.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      257 agacettectecacaceaactaeteceteaagtacaagettaggtggtatggeeaggaea 316
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    317 acacatgtgaggagtaccacacagtggggcccactcctgccacatcccaaggacctgg 376
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      Gelsel,S., Kucaba,T., Lacy,M., Le,M., Martin,J., Morris,M.,
Schellenberg,K., Steptoe,M., Tan,F., Underwood,K., Moore,B.,
Theising,B., Wylie,T., Lennon,G., Soares,B., Wilson,R. and
                                                  Waterston, R.
The WashU-HHMI Mouse EST Project
Unpublished (1996)
On Dec 30, 1996 this sequence version replaced g1:1528951.
                                                                                                                                                                                                                                                                                                                                                                                                            /clone="IMAGE:479043"
/clone_lib="Soares mouse embryo NDME13.5 14.5"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 380.8; DB 29; Length 464;
Pred. No. 4e-70;
0; Mismatches 52; indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                             /tissue_type="embryo"
/dev_stage="13.5-14.5dpc total fetus"
/lab_host="DH10B"
Lacy, M., Le,...
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                88
t
                                                                                                                              Contact: Marra M/Mouse EST Project

    464
    /organism="Mus musculus"

                                                                                                                                                                                                                                                                                                                                                                                                'db_xref="taxon:10090"
   Kucaba, T., Lacy, M. rq, K., Steptoe, M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              130 g
                                                                                                                                                                                                                                                                                                                                                                               /strain="C57BL/6J
                                                                                                                                                                                                                                                                                                                                                                                                                                                   'sex≖"unknown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 27.4%;
Best Local Similarity 88.8%;
Matches 412; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            102
                                                                                                                                                                                                                                                                                                                                                 source
                                                                TITLE
JOURNAL
COMMENT
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ORIGIN
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/note="Organ: mixed (see below); vector: pT7T3D-Pac (Pharmacia) with a modified polylinker; Site_1: Not I; Site_2: Eco RI: Equal amounts of plasmid DNA from three normalized libraries (melanocyte 2NbHM, pregnant uterus NbHPU, and fetal heart NbHH19W) were mixed, and ss circles were made in vitro. Following HAP purification, this DNA was used as tracer in a subtractive hybridization reaction. The driver was PCR-amplified cDNAs from pools 5,000 clones made from the same 3 libraries. The pools consisted of I.M.A.G.E. clones 260232-265223, 340488-34849, and 484488-489479."
                                                                                                                                                                                                                                                                                       AI264328 398 bp mRNA EST 27-JAN-1999
q109c05.x1 Soares_NhHMPu_S1 Homo sapiens cDNA clone IMAGE:1855976
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap,
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /clone_lib="Soares_NhHWPu_si"
/tissue_type="Pooled human melanocyte, fetal heart, and
pregnant uterus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    This clone is available royalty-free through LLNL; contact the IMAGE Consortium (info@image.llnl.gov) for further information. Insert Length: 699 Std Error: 0.00
                                979 aaccagcacaggacgagggatcctgccctcgggcagacgggggcacggcgagagtcctg 1038
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ocagataagetgtaggggeteaggecaceeteeetgeeacgtggagacgeagggeegaa 1098
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Vertebrata; Mammalla;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
557 ccctcaaggatttcctctttcaagccaaataccagatccgctaccgagtggagggcagtg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      On Jan 14, 1998 this sequence version replaced g1:1797852.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ;;
7
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota; Metazoa; Chordata; Craniata; Vertebra
Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 398)
                                                                                                27.4%; Score 380.8; DB 4.99.0%; Pred. No. 3.9e-70; ive 0; Mismatches 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Contact: Robert Strausberg, Ph.D.
Tel: (301) 496-1550
Email: Robert_Strausberg@nlh.gov
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           organism="Homo sapiens"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Seq primer: -400p rrow 559 High quality sequence stop: 397 Location/Qualifiers 1.398 Location saplen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /db_xref="taxon:9606"
/clone="IMAGE:1855976"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /lab_host="DH10B"
                                                                                                                                                                                                                                                                                                                                                                                                                     ĀI264328.1 GI:3872531
                                                                                                                                                                                                                                                                                                                                            3', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Tumor Gene Index
Unpublished (1997)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Matches 394; Conservative
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BASE COUNT ORIGIN

943

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Matches

1063

1123

1242

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72

12

ACCESSION

JOURNAL

COMMENT

FEATURES

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AA049280 464 bp mRNA EST 30-DEC-1996 mj45d02.rl Soares mouse embryo NbME13.5 14.5 Mus musculus CDNA clone IMAGE:479043 5' similar to SW:ILGB_MOUSE Q00560 INTERLEUKIN-6 RECEPTOR BETA CHAIN PRECURSOR ;, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Allen, M., Bowles, M., Dietrich, N., Dubuque, T.,
                                                                         Anotes Organ: pooled; vector: pT713D-Pac (Pharmacia) with modified polylinker; Sites 1: Not I: Sites 2: ECO R; Equal amounts of plasmid DNA from three normalized libraries (fetal lung NbHL19W, testis NHT, and B-cell NCI_CGAP_GCB1) were mixed, and ss circles were made in vitro. Following HAP purification, this DNA was used as tracer in a subtractive hypridization reaction. The driver was PCR-amplified cDNAs from pools of 5,000 clones made Ifm the Area of Since and Since an
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       agacgcagaggccgaacccaaactggggccacctctgtaccctcagtgggca--cct 1140
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      gagccctcagcaggagctggggtggccctgagctccaacggccataacagctctgact 1200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       963 giogoacaagaccogcaaccagcacaggacgaggggatccigccciogggcagacggggc 1022
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      295 AGACGCAGAGGCCGAACCCAAACTGGGGCCACCTCTGTACCCTCACTTCAGGGCACTCTG 236
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    235 NACACCTCAGCAGGAGCT-GGGTGGCCCCTGAGCTCCAACGGCCATAACAGCTCTGACT 177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         469 cecenacrecrecaaccreae-rrececereraceaecagegegegegegeagecregarecagaa 411
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota; Metazoa; Chordata; Cranlata; Vertebrata; Mammalla;
Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 464)
Marra,M., Hillier,L., Allen,M., Bowles,M., Dietrich,N., Dubuq
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      cgcgtactgctccaacctcagcttccgcctctacgaccagtggcgagcctggatgcagaa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    410 GICGCACAAGACCCGCAAC----CAGGACGAGGGGATICCICCCICGGGCAGAGGGGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 469;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 394.8; DB 40;
Pred. No. 4.9e-73;
0; Mismatches 8;
                            /clone_lib="Soares_NFL_T_GBC_S1"
/lab_host="DH10B"
                                                                                                                                                                                                                                                                                                                                                     Soares and M. Fatima Bonaldo.
139 c 142 g 100 t
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                             28.4%;
illarity 96.2%;
Conservative 0
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Best Local Similarity
Matches 459; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AA049280
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SOURCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1083
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     903
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Email: Robert_Strausberg@nih.gov
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
Insert Length: 763 Std Error: 0.00
Seq primer: -40ml3 fvd. Ef from Amersham
High quality sequence stop: 448.
Location/Qualiflers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NCI-CGAP http://www.ncbl.nlm.nlh.gov/nclogap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1062
                                                                                                                                                                                                                                                                                                                                                                                   ccacctccctgccacgtggagacgcagaggccgaacccaaactggggccacctctgtac 1122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1182 ggccataacagctctgactcccacgtgaggccacctttgggtgcaccccagtgggtgtt 1241
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 192 GGCCATAACAGCTCTGACTCCCACGTGAGGCCACCTTTGGGTGCACCCCAGTGGGTGTGT 133
                                                                                                                                                                                                                     Eukaryota; Metazoa; Chordata; Cranlata; Vertebrata; Mammalla;
Eutheria; Primates; Catarrhin1; Hominidae; Homo.
1 (bases 1 to 469)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AA922128 469 bp mRNA EST 23-JUN-1998
om45e12.s1 Soares_NPL_T_GBC_S1 Homo sapiens cDNA clone
IMAGE:1544014 3', mRNA sequence.
                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   tggcgagcctggatgcagaagtcgcacaagacccgcaaccagcacaggacgaggggtcc
                                                                                                                                                                                                                                                                                             1003 tgccctcgggcagacggggcacggcgagaggtcctgccagataagctgtaggggctcagg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              On May 8, 1995 this sequence version replaced gi:800381.
                                                                                                                                         .;
?
                                                                                           Length 431;
                                                                                           Score 406.4; DB 28; Length
Pred. No. 1.8e-75;
0; Mismatches 1; Indels
16
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/db_xref="taxon:9606"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Contact: Robert Strausberg, Ph.D.
     Б
  129
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                                                                                                29.2%;
99.3%;
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Unpublished (1997)
     O
                                                                                                                                              429; Conservative
  134
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                                                                                                                            Similarity
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  77
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                                                                                                   Query Match
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KEYWORDS
SOURCE
ORGANISM
                                                                                                                               Local
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AA922128/c
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DEFINITION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           REFERENCE
AUTHORS
TITLE
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3

us-09-037-657-24.rst

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db_xref="taxon:9606"
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lab_host="DH10B"
                                                                                                                                                                                                                                                                                                                                                                                                              AA121532.1 GI:1679146
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eutheria; Primates;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Contact: Wilson RK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    and Marra, M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    97044478
                                                                                                                                                                                                                                                                                                RESULT 2
AA121532/c
                                                                                                                                                                                                                                                                                                                                               DEFINITION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      source
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JOURNAL
MEDLINE
COMMENT
                                                                                                                                                                                                                                                                                                                                                                              ACCESSION
                                                                                                                                                                                                                                                                                                                                                                                                           VERSION
KEYWORDS
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                                                            Generation and analysis of 280,000 human expressed sequence tags Genome Res. 6 (9), 807-828 (1996)
97044478
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further information
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                                                                                                                                                                                                                                                                On Sep 12, 1996 this sequence version replaced gi:1393691
                                                                                                                                                                                                                                                                                                                  Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louls, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
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Pred. No. 2.1e-79;
0; Mismatches 4; Indels 4;
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The vector to vector length is 468
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Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                 Email: est@watson.wustl.edu
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Best Local Similarity 98.3%;
Matches 460; Conservative
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                                    Homo sapiens
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1 (bases 1 to 431)
Hillier,L., Lennon,G., Becker,M., Bonaldo,M.F., Chiapelli,B.,
Chissoe,S., Dietrich,N., DuBuque,T., Favello,A., Gish,W.,
Hawkins,M., Hultman,M., Kucaba,T., Lacy,M., Le,M., Le,M., Le,M.
Mardis,E., Moore,B., Morris,M., Parsons,J., Prange,C., Rifkin,L.,
Rohlfing,T., Schellenberg,K., Soares,M.B., Tan,F., Thierry-Meg,J.
Trevaskis,E., Underwood,K., Wohldmann,P., Waterston,R., Wilson,R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EST 11-MAY-1997 IMAGE: 490004 3', mRNA sequence. 11AAC: 1537 AA121537
1146 cctcagcaggagctggggtggccctgagctccaacggccataacagctctgactcccac 1205
                                                                                              1206 gigaggocacctitgggigcacccagigggigigigigigigigigggggitggitgag 1265
                                                                                                                                                                                                 1266 ttgcctagaacccctgccagggctgggggtgagaaggggagtcattactcccattact 1325
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This clone is available royalty-free through LLNL; contact the
This clone is available royalty-free through LLNL; contact the
TMAGE Consortium (info@imge.llnl.gov) for further information.
Insert Length: 542
Seq primer: -40M13 fwd. from Amersham
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Location/Qualifiers
                                                                                                                                                                                                                                /note-"Organ: uterus; Vector: pT7T3-Pac; Site_1: Not I
Site_2: Eco RI; 1st strand cDNA was primed with a Not
oligo(dT) primer [5'
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalla;
                                            241 CCTCAGCAGGAGCTGGGGTGGCCCCTGAGCTCCAACGGCCATAACAGCTCTGACTCCCAC
                                                                                                                             Generation and analysis of 280,000 human expressed sequence
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4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1810
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                                         Database :
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                                                                    2546578 seqs, 986266752 residues
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SUMMARIES

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 | AI187 | W3717 | AI333 | W4660 | AI394 | AI126
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ID Description 1 |

ALIGNMENTS

ACCESSION NID VERSION	RESULT 1 AA127694 LOCUS DEFINITION
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	EST
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Search completed: September 28, 1999, 15:38:23 Job time: 3291 sec

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(bases 1 to 179436)

Zhang,G., Lao,V., Zhan,M. and Roe,B.A.

Direct Submission

Submitted (06-NOV-1997) Department Of Chemistry And Blochemistry,

The University Of Oklahoma, 620 Parrington Oval, Room 208, Norman,
                                                                                                                                                  337 tatttgattttatgaaaatatacctgtttgtatttggtttggtttggtttgagttttgtt 396
                                                                                                                                                                                                  457 aggotggoottgaactcagaaatccgcotgottgtgttcccaagtgottagattaaagg 516
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Mus musculus chromosome 16 clone tbx1, WORKING DRAFT SEQUENCE,
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Zhang, G. and Roe, B. M.
Mouse Chromosome 16 BAC Clone tbx1
Onpublished (1997)
2 (bases 1 to 179436)
Emanuel, B. and Budarf, M.
Mouse Chromosome 16 BAC Clone tbx1
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* NOTE: This is a 'working draft' sequence. It currently 'consists of 5 contigs. The true order of the pieces 'is not known and their order in this sequence record is
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                                                             Length 91638;
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                                                       Score 123; DB 34;
Pred. No. 1.2e-19;
                                                                                            0; Mismatches
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Unpublished (1997)

E 3 (bases 1 to 39061)

S Zhang,G., LaO., L., Zhan,M. and Roe,B.A.

S Zhang,G., LaO., L., Zhan,M. and Roe,B.A.

Direct Submission

L Direct Submission

L Submitted (06-NOV-1997) Department of Chemistry And Biochemistry,

The University of Oklahoma, 620 Parrington Oval, Room 208, Norman,

OK 73019, USA

ON C4 31, 1998 this sequence version replaced gi:3132482.

* NOTE: This is a 'working draft' sequence. It currently

consists of 7 contigs. The true order of the pieces

consists of 7 contigs. The true order of the pieces

to snot known and their order in this sequence record is

* arbitrary. Gaps between the contigs are represented as

runs of N, but the exact sizes of the gaps are unknown.

This record will be updated with the finished sequence

* as soon as it is available and the accession number will
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                                                                                                                                                                   HTG 31-OCT-1998 clone tbx3, WORKING DRAFT SEQUENCE,
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Butheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 39061)
                                                                                                        Score 122; DB 35; Length 179436;
Pred. No. 2.1e-19;
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Chases 1 to 39061)
Emanuel, B. and Budarf,M.
Mouse Chromosome 16 BAC Clone tbx3
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Hawkins, T.L., Birren, B.W., Fasman, K.H., Nussbaum, C., Lander, E.S., McKernan, K., Murro, C., Richardson, P., Barna, N., Chang, A., Cooke, P., Dally, M.J., Devon, K., Dewar, K., Forrest, C., Gage, D., Geraigery, K., Hagos, B., Huang, J., Hang, L., Jacottot, L., Kirby, A., Lane, M., Mackenzie, J., Marquis, N., McDermott, J., Molla, M., Morrow, J., Nathanan, A., Naylor, N., Noberts, D., Connor, T., Olotu, A., Stone, C., Strickland, C., Sydney, K., Tang, L., Wilmer, F., Zemtseva, I.
AC002489 91638 bp DNA HTG 20-JAN-1998
Homo sapiens chromosome X clone 592 map X, WORKING DRAFT SEQUENCE,
8 unordered pieces.
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Submitted (22-AUG-1997) Whitehead Institute/MIT Center for Genome Submitted (22-AUG-1997) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA On Jan 20, 1998 this sequence version replaced 91:2772532.

The Staden databases, finishing information, and all chromatographic files used in the assembly of this clone are available from our anonymous ftp site.
                                                                                                                                                                                                                                                                                                                                                      irren, B., Fasman, K., McKernan, K., Nusbaum, C., Richardson, P. and
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http://ftp.genome.washington.edu/RM/RepeatMasker.html.

* NOTE: This is a 'working draft' sequence. It currently

* consists of 8 contigs. The true order of the pieces

* is not known and their order in this sequence record is

* arbitrary. Gaps between the contigs are represented as

* runs of N. but the exact sizes of the gaps are unknown.

* This record will be updated with the finished sequence

* as soon as it is available and the accession number will

* be preserved.
                                                                                                                                                                                                                                                                  Vertebrata; Mammalia;
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Homosapiens

Bukaryota; Metazoa; Chordata; Craniata; ...

Eutheria; Primates; Catarrhini; Hominidae; Homo.

Frases 1 to 91638)

McKernan,K., Nusbaum,C.,
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Unpublished
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/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="592"
/clone=1ib="unknown"
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GSILAGGCLYVGLPPERKYNISCWSRNKDIJCRWTPGAHGEFFLHTWYSLKYKLRWY
GODNYCEEYHTVGPHECHIPKDLALFTPYEIWVEATNRLGSARSDVLTLDILDVYTTD
PPPDVHVSRVGGLEDQLSVRWYSPPALKDFLPQAKYOTYRYWEDSYDKKVVDDYSTOP
PCRAGLEYGTYYFVQYYRCVPGIYGSKRAGIWSEWSHPTAASTPRSERPGFGGGCE
PRGGFPSSGPVRRELKQFLGWLKKHAYCSNLSFRLYDQWRAWMQKSHKTRNGHRTRGS
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NICOLA NICOS ANTONY (AU)
LOCATION/QUALIFIERS
1. 5560
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Nicola,N.A., Fabri,L., Farley,A., Nash,A., Willson,T., Rakar,S.,
Zhang,J., Alexander,W., Hilton,D.J., Kojima,T., Maeda,M. and
Kikuchi,Y.
                                                                                                                                                                                                                                                                                                                        3494 ctgagtgtgcgctgggtctcaccaccagctctcaaggatttcctcttccaagccaagtac 3553
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                                                                                                                                                                                                                                                                                                       68;
                                                                                                                                                                                                                                                                   Ouery Match 2.9%; Score 190.8; DB.5; Length 1391; Best Local Similarity 73.5%; Pred. No. 3e-36; Matches 291; Conservative 0; Mismatches 37; Indels 68;
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                                     /note="unnamed protein product"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /protein_id="CAB42576.1"
/db_xref="PID:e1433703"
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/db_xref="GI:4774673"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 23 from Patent WO9811225. 94774671
/organism="unidentified"
        /db_xref="taxon:32644"
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                                                    /codon_start=1
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Dupublished

2 (bases 1 to 170965)

3 Hua,A and Roce,B.A.

Direct Submission

3 University of Oklahoma, 620 Parrington Oval, Room 208, Norman, Ok 73019, USA

ON 73019, USA

ON Jun 4, 1999 this sequence version replaced gl:4895262.

* NOTE: This is a 'working draft' sequence. It currently consists of 33 configs. The true order of the pieces

* is not known and their order in this sequence record is

* arbitrary. Gaps between the contigs are represented as

* runs of N, but the exact sizes of the gaps are unknown.

* This record will be updated with the finished sequence

* as soon as it is available and the accession number will
                                                                                                                                                                                                                                                    3494 ctgagtgtgcgċtgggtctcaccaccagctctcaaggatttcctctccaagccaagtac 3553
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Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases I to 170965)
Hua, A. and Roe, B.A.
Mus musculus Clone p481n4
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Mus musculus, WORKING DRAFT SEQUENCE, 33 unordered pleces
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                                                                                                                 DB 5; Length 560;
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Pred. No. 4.1e-24;
0; Mismatches 13
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/organism="unidentified"
/db_xref="taxon:32644"
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HTG; HTGS_PHASE1.
                                                                                                       Query Match 2.1%;
Best Local Similarity 92.0%;
Matches 149; Conservative
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Location/Qualifiers
1. .1391
                                                                                                                                                                                                                                                   /note="putative"
                                                                                                                                                                                                                                                                                          /note="putative"
                                   Number AC003112"
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/gene="CLF-1"
                                                                                                                                                                                                                                                                230. .1384
/gene="CLF-1"
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ilarity 86.5%;
Conservative 0
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                      /db_xref="61:4774668"
//db_xref="61:4774668"
/translation="PTLLIGSSLQATCSIHGDTPGATAEGLYWTLNGRRLPSELSRLL
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ELFQARYGIRYRANGYLDVYTTDPPDDVHYSRVGGLEDQLSVRWYSPALKD
FLFQARYGIRYRVEDSYDWRVVDDVSNQTSCRLAGGLKPGTVFVQVRCNPFGIXGSKR
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                                                                                                                                                                                                                                                                            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eukheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 1716)

Elson, G.C.A., Graber, P., Losberger, P., Herren, S., Gretener, D., Menoud, L. N., Wells, T. N. C., Kosco-Vilbols, M. H. and Gauchat, J. F. CIF-1, a Novel Soluble Protein Shares Homology With Members of Cytokine Type-I Receptor Family
J. Immunol. (1998) In press
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Menoud,L.N., Wells,T.N.C., Kosco-Vilbois,M.H. and Gauchat,J.F.
Direct Submission
                                                                                                                                                                                                   Gaps
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                                                                                                                                                                                                                                         (CLF-1) mRNA
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Homo sapiens cytokine-like factor-1 precursor
complete cds.
                                                                                                                                                                      Score 254.4; DB 5;
Pred. No. 7.9e-52;
0; Mismatches 1;
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/organism="Homo sapiens'
/db_xref="taxon:9606"
/db_xref="PID:e1433696"
/db_xref="PID:g4774668"
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119. .1387
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Best Local Similarity 99.6
Matches 255; Conservative
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/note="similar to cytokine type-1 receptor family members; similar to the sequence presented in GenBank Accession
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popptlligssllatcsvhgdppgataeglywtingrrlppelsrvlnastlalalan
                                                                                                                                                                                                                                                                        LNGSRQRSGDNLVCHARDGSILAGSCLYVGLPPEKPVNISCWSKNMKDLTCRWTPGAH
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Nicola,N.A., Fabri,L., Farley,A., Nash,A., Willson,T., Rakar,
Zhang,J., Alexander,W., Hilton,D.J., Kojima,T., Maeda,M. and
Kikuchi,Y.
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                                                                                                     /product="cytokine-like factor-l precursor"
/protein_id="AAC28335.1"
/db_xref="PID:93372627"
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Pred. No. 1.9e-43;
0; Mismatches ,38
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Matches 281; Conservative
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NICOLA NICOS ANTONY (AU)
Location/Qualiflers
1. 1629
                         1 (bases 1 to 1629)
Nicola,N.A., Fabri,L., Farley,A., Nash,A., Willson,T., Rakar,S.,
Zhang,J., Alexander,W., Hilton,D.J., Kojima,T., Maeda,M. and
Kikuchi,Y.
                                                 acctectgecgtetegegggetgaageeeggeaeegtttaettegteeaagtgegttgt 3744
                                                                                            aacccattcgggatctatgggtcgaaaaaggcgggaatctggagcgagtggagccaccc 3804
      ccgcccccgcatctgactcctccctcaccgtgcaggtggtggtgatgacgtcagcaaccag 3684
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Best Local Similarity 99.6%; Pred. No. 3.4e-58;
Matches 281; Conservative 0; Mismatches 1
                                                                                                                                                                                                            A70382 1629 bp DNA
Sequence 12 from Patent W09811225.
A70382
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/db_xref="taxon:32644"
| 541 c 453 g 299
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Sequence 14 from Patent W09811225.
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11. (bases 1 to 1673)
NICOLA, NA., Fabri, L., Farley, A., Nash, A., Willson, T., Rakar, S., Nacola, V., A., Eabri, L., Hilton, D.J., Kojima, T., Maeda, M. and Kikuchi, Y.
A NOVEL HARDOPOLETIN RECEPTOR AND GENETIC SEQUENCES ENCODING SAME PATENT. WO 9811225-A 19-MAR-1998;
NICOLA NICOS ANTONY (AU)
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2hang, J., Alexander, W., Hilton, D.J., Kojima, T., Maeda, M. and
Kikuchi, Y.
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99.6%; Pred. No. 3.4e-58;
ative 0; Mismatches 1;
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/codon_start=1
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A70388
94774667
A70388.1 GI:A7177
                                                                                                                                                                                                         305
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550 c 474 g 30
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/db_xref="taxon:32644"
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SW:IL6B_MOUSE Q00560 INTERLEUKIN-6 RECEPTOR BETA CHAIN PRECURSOR (274. .431); 93% identity.--"
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                                                                                  teettgtagtgeeeettgagaageeetttaaeateagetgetggteeeggaaeatgaagg 1705
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                                                                                                                                                                                                                                                                                    ----tatgaactcaaaagggactctcgca
                                                           137;
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                                %; Score 484.6; DB 11;
%; Pred. No. 3.6e-108;
0; Mismatches 904;
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                                   7.3%;
                                               Best_Local Similarity 55.49
Matches 1294; Conservative
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18475 18655 18595 18767 19007 18715 18535 19305 GATCGAGACCATCCCGGCTAAAAACGGTGAAACCCCGTCTCTACTAAAAATACAAAAA 19246 19245 TTTAGCCGGGCGTAGTGGCGGGGGCGCCTGTAGTCCCAGCTACTTGGGAGGCTGAGGCAGGA 19186 GAATGGCGTGAACCCGGGAGGCGGAGCTTGCAGTGAGCCGAGATCCCGCCACTGCACTCC 19126 19006 GGCCTCCTAAGCATGATAATAATAATATCATCAACCCCGCAATGGCTGCTTTCCCATAGT 18947 3477 19603 GGGGAGAGGCCAGCTCACCCTGCTGCCCCTCAGGGGCCCCCAGAAGGATCCTCAGAACCCC 19544 3357 3417 3537 3597 3624 agcaactgctgctggctgtttctggaatattaaatgacagtaatctatcaggcctgggtg 3117 gcagcctagattacaccactgggtgttctgtcactaggccattctcaccaagcagtcctc 3237 tegecteactecetgittagagagatetetgegetaatetecaceceagetgggtggget 2997 cttccaagccaagtaccagatccgctaccgcgtggaggacagcgtggactggaaggtgcc getetgteceettgaggggaaggaatgtgtgtetteeatcagagataggaceegtggtage gcagaggcagaaggatctctcgagttcaaggccatcctgaatttacataaagagctcca GGCCACACTGCTGGGGGGAGTTAAAC-----CCAGACAGTCCCAGGCTGAGAGGGTC gcttgctccacccccagtgaccacggaccccccacccgacgtgcacgtgagccgcgttgg 18534 CCTCCCCTTCCCTGACTCCGCCCCTGTTCCTTCCAGGCCCCGCCCCCGCTCCTAGGC ttaagagtcagcttgtgacttaatactggaactcagggcctaataggtgctgggtgatgc 19065 IGTGAGTGGGGA-GGGGTGGCAGGAGGTTCCCAGAAGGCTGACGGCCTGACAGCCTT agtagetaacaggggtggggggggggtgggaaaacgcagatagggtcataggagccact CAGTIGAAGATAGGATTATGTTTCTCCCGTCACAGATAATAATGGTGATAACAGCTAACA agaactgggagcactgttgccagcatttaatgccagcatttaatgccagcattagggggag GTGGGGGCAGAGAGAAGAAGAAAACAGAGGCAGGTTCCATCTAGGCCAAGTGCCCTG gggcctggaggaccagctgagtgtgcgctgggtctcaccaccagctctcaaggatttcct CTITCAAGCCAAAIACCAGATCCGCTACCGAGIGGAGGACAGIGIGGACIGGAAGGIGAC tetgtggetggeacagetgeecegtggaggetettggtaatgtacaaggeatcagaggtg gacatgggatggggatacatagggatggagccaaatagcacctcaaggtggggtgatata ctggctcattcccacatccagaggttttgtgtcttcctggcatctaaccctcagttgtgc CTTCCCCACATCCTAACGCTACAGTG - - GGAAAGTTCTAAGCCTCAGTTGCTTCTCTGCA caataaagcttgtcaccctgacgctcagaaagcctactcatgatgatcac-3418 3538 18594 3598 2647 2818 2938 3118 3178 3298 3358 18654 2707 2767 2878 18766 19543 19483 19185 18946 18826 18714 2587 g ద òγ 셤 ö g ö g 음 ద 셤 ò ద ò - 염 à à 셤 ö g 8 õ ò 셤 ద a ద ö g ö ö ö ò ò à à

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/rpt_family="Alu"

complement(18270. .18438)

/note="predicted exon, program: grail2exons_human_1.3,
frame: 0, quality: excellent, score:
100.000--(18438. .18284) DDS.similarity to W66776
mel7bll.rl Scares mouse embryo NDME13.5 14.5 Mus musculus
cDNA clone 387741 5' similar to PIR:B3825 283825
granulocyte colony-stimulating factor receptor precursor
(157. .1); 82% identity.--(18438. .18406) DDS similarity to
Musculus cDNA clone 479043 5' similar to SW:IL6B_MOUSE
Q00560 INTERLEUKIN-6 RECEPTOR BETA PRECURSOSR (432. .464);
88% identity."
                              frame: 2, quality; good, regressing intercellations, frame: 2, quality; good, regressing intercellations, and accessing accessing accessing the matches: (13756. 13845) DDS similarity to AA009403 caglons clone 36523 5' (428. 496); 97% identity.—(13756. 13984) DDS similarity to AA009693 caglone 36523 3' (227. 11); 98% identity.—(13756. 13984) DDS similarity to AA460010 caglone 788287 3' (228. 11); 99% identity.—(13756. 13984) DDS similarity to AA460010 caglone 788287 3' (228. 11); 99% identity.—"

Crpt_family="Alu" | 199% identity.—"

In the sapiens cDNA clone 753348 3' (1. 433); Score: 858 identity: 43143 (99%).—--(14884. 15237) DDS similarity to MA406100 caglone cDNA clone 753348 3' (1. 433); Score: 858 identity: 43143 (99%).—--(14884. 15237) DDS similarity to MA121532 caglone cDNA clone 30266 5' (1. 355); 94% identity.—(15227. 14885) DDS similarity to AA121532 caglone cDNA clone 30266 5' (1. 355); 94% identity.—(15227. 14885) DDS similarity to M46603 caglone clone 490004 3' (32. 1); 99% identity.—(15227. 14885) DDS similarity to W46603 caglone cDNA clone 304067 5' (326. 467); 99% identity.—(15227. 14887) DDS similarity to W46603 caglone cDNA clone 324067 5' (328. 11); 99% identity.—(15227. 14887) DDS similarity to W46603 caglone cDNA clone 324067 5' (328. 11); 99% identity.—(15227. 14887) DDS similarity to W46603 caglone cDNA clone 324067 5' (328. 11); 99% identity.—(15227. 14897) DDS similarity to W46603 caglone cDNA clone 324067 5' (328. 13); 96% identity.—(15227. 14897) DDS similarity to W46603 caglone cDNA clone 324067 3' (322. 465); 96% identity.—(15227. 14897) DDS similarity to W46603 caglone cDNA clone 324067 3' (322. 465); 96% identity.—(15227. 15227. 15227. 15227. 15227. 15227. 15227. 15227. 15227. 15227. 15227. 15227. 15227. 15227. 15227. 15227. 15227. 15227. 15227. 15227. 15227. 15227. 15227. 15227. 15227. 15227. 15227. 15227. 15227. 15227. 15227. 15227. 15227. 15227. 15227. 15227. 15227. 15227. 15227. 15227. 15227. 15227. 15227. 15227. 15227. 15227. 15227. 15227. 15227. 15227. 15227. 15227. 15227. 
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/note="DDS similarity to AA121532 zk89c11.s1 Soares
pregnant uterus NbHPU Homo sapiens cDNA clone 490004 3'
2890.343); 99% identity.--DDS similarity to AA127694
zk89c11.r1 Soares pregnant uterus NbHPU Homo sapiens cDNA
clone 490004 5' (77. 125); 90% identity.--(15735. 15713)
DDS similarity to W46603 zc32h10.r1 Soares senescent
fibroblasts NbHSF Homo sapiens cDNA clone 324067 5'
(351. 329); 100% identity.--(15735. 15713) DDS similarity
to W46604 zc32h10.s1 Soares senescent fibroblasts NbHSF
Homo sapiens cDNA clone 324067 3' (299. 321); 100%
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similarity to W66705 mellonis Score: 100.000--DDS
similarity to W66705 mellonis Score: 100.000--DDS
NDME13.5 14.5 Mus musculus cDNA clone 387741 5' similar treceptor precursor (316. 158); 928.1dentity.-DDS
similarity to AA049280 mj45402.rl Scares mouse embryo
NDME13.5 14.5 Mus musculus cDNA clone 479043 5' similar t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      .16082)
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frame: 1, quality: excellent, score: 100,000--DDS
similarity to AA047548 zf15e0z.rl Soares fetal heart
NDHH19W Homo sapiens CDNA clone 377018 5' (139. '221); 100%
identity. --DDS similarity to AA136115 zk90b04.rl Soares
pregnant uterus NDHPU Homo sapiens CDNA clone 490663 5'
(111. 192); 99% identity. --DDS similarity to AA452628
zx33f04.rl Soares total fetus ND2HF8 by Homo sapiens CDNA
clone 788287 5' (83. .165); 100% identity. --DDS similarity
to AA009412 ze82h02.rl Soares fetal heart NDHH19W Homo
sapiens cDNA clone 365523 5' (62. .144); 100% identity."
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/note="DDS similarity to AA136115 zk90b04.rl Soares
pregnant uterus NbHPU Homo sapiens cDNA clone 490063 5'
(193. 1944); 944 identity.--DDS similarity to AA009412
ze62h02.rl Soares fetal heart NbHH19W Homo sapiens cDNA
clone 365523 5' (145. 146); 96% identity.--(1121. 11331)
DDS similarity to AA009693 ze62h02.sl Soares fetal heart
NbH19W Homo sapiens cDNA clone 365523 3' (429. 307); 95%
identity.--(1127. 11246) DDS similarity to AA047548
zf15e02.rl Soares fetal heart NbHH19W Homo sapiens cDNA
clone 377018 5' (222. 341); 97% identity.--(11061. 11331)
predicted exon, program: graallzexons_human.3, frame: 0,
quality; good, score: 73.000--(11061. 11209) DDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   heart NDHH19W Homo sapiens cDNA clone 377018 5' (1. .138); 96% identity. --Other overlapping matches: -(10435, .10548) DDS similarity to AA136115 zk90b04.r1 soares pregnant uterus NDHPU Homo sapiens cDNA clone 490063 5' (1. .110); 93% identity. --(10466, .10548) DDS similarity to AA452628 zx33f04.r1 soares total fetus ND2HF8 9W Homo sapiens cDNA clone 78287 5' (1. .82); 95% identity. --(10486, .10548) DDS similarity to AA009412 ze82h02.r1 soares fetal heart NDHH19W Homo sapiens cDNA clone 385523 5' (1. .61); 97%
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Anote-"DDS similarity to AA136115 zk90b04.rl Soares pregnant uterus NbHPU Homo sapiens cDNA clone 490063 5/ (395. 477); 92% identity. --DDS similarity to AA009412 cB20400.rl Soares fetal heart NbHH19W Homo sapiens cDNA to AA009693 ze82h02.sl Soares fetal heart hbH19W Homo sapiens cDNA clone 36523 5/ (347. 427); 94% identity. --DDS similarity canologogo ze82h02.sl Soares fetal heart NbHH19W Homo sapiens cDNA clone 365523 3' (306. 228); 99% identity. --DDS similarity to AA450010 zx33f04.sl Soares
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NDZHEW 9W HOMO sapiens CDNA clone 788287 5' (167. 313);
98% identity
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                                                                                                                                                                                                                                                                                         frame: 1, quality: good, score: 63.000"
complement(9629. .9672)
                                                                                                                                                                                                                                                                                                                                                                                                                                  /note="predicted exon, program: grail2exons_human_1.3,
frame: 1, quality: excellent, score: 75.000"
/rpt_family="Alu"
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complement(12966. .13240)
/rpt_family="Alu"
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complement(11869. 12161)
/rpt_family="Alu"
12502. 12581
rpt_family="Alu"
951, .925"
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/note="predicted exon,
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9358. 9535
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                                                                                                                                                          1 (bases 1 to 1930)
Nicola,N.A., Fabri,L., Farley,A., Nash,A., Willson,T., Rakar,S.,
Zhang,J., Alexander,W., Hilton,D.J., Kojima,T., Maeda,M. and
Kikuchi,Y.
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Pred. No. 2e-170;
0; Mismatches 27;
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/db_xref="taxon:32644"
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ilarity 96.3%;
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Best Local Similarity
Matches 778; Conserva
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                                                                                 Sequence 22
                                                                                                    94774670
A70392.1
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complement(1833. .1444)
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Lamerdin, J.E., McCready, P.M., Adamson, A.W., Burkhart-Schultz, K.,
Gordon, L., Christensen, M., Kyle, A., Ramirez, M., Stilwagen, S.,
Garnes, J., Danganan, L., Bruce, R., Quan, G., Montgomery, M., Ow, D.,
Kobayashi, A., Olsen, A.O. and Carrano, A.V.
Sequence analysis of an -1 Mb region containing the MEF2B gene in
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Direct Submission
Submitted (21-NOV-1997) Human Genome Center, Lawrence Livermore National Laboratory, 7000 East Ave., Livermore, CA 94551, USA Location/Qualifiers
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Eutheria, Primates, Catarrhini, Hominidae, Homo.
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Location/Qualifiers
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Nicola, N.A., Fabri, L., Farley, A., Nash, A., Willson, T., Rakar, Zhang, J., Alexander, W., Hilton, D.J., Kojima, T., Maeda, M. and
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Sequence 16 from Patent WO9811225.
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	ογ	3312	gagttcaaggccatcctgaatttacataaagagctccaggccagcgggt
	g	8482	TCTCTCTGAGTTCAAGGCCATCCTGAATTTACATAAAGAGCTCCAGGCCAGCCA
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	δ	3492	tgtgcgctgggtctcaccagctctcaaggatttcctcttccaagccaag
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* 13136 24191: contig of 11056 bp in length

* 24192 24261: gap of unknown length

* 24262 39061: contig of 14800 bp in length.

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* 24061: contig of 14800 bp in length.

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* 1 39061: contig of 14800 bp in length.

/ Organism="Mus musculus"

/ Adp_aref="taxon:10090"

/ Clone="taxon:10090"

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/ Chromosome="16"

BASE COUNT 11103 a 8839 c 8427 g 10272 t 420 others

ORIGIN
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Query Match
1.8%; Score 120.2; DB 34; Length 39061;
Best Local Similarity 75.1%; Pred. No. 5.8e-19;
Matches 163; Conservative 0; Mismatches 53; Indels 1; Gaps 1;
Oy 312 titatgactgatgttttaaaatttttatttgatttatgaaaatatacctgtttgtattt 371

Search completed: September 28, 1999, 16:46:12 Job time: 7359 sec

Truncated upstream Upstream region of

1 V34386 1 V34385

1.3

89.6 89.6

44

ALIGNMENTS

GenCore version 4.5 Copyright (c) 1993 - 1998 Compugen Ltd.

OM nucleic - nucleic search, using sw model

n: September 28, 1999, 16:46:31 ; Search time 303.81 Seconds (without alignments) 5487.080 Million cell updates/sec

Run on:

Title: US-09-037-657-28
Perfect score: 6663
Sequence: 1 cccagaactcttggacqctq...

ect score: bbb3 ence: 1 cccagaactcttggacgctg.......tatgtgctggggggggg 6663

Scoring table: IDENTITY_NUC

Searched: 311585 segs, 125096042 residues

Database : N_Geneseq_36:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Description	cadamaa afitoolom	otide sequ	iced murin	Novel haemopoietin	Novel haemopoietin	haemopo1	eotide s	otide sequ	encodin	encoding h	cDNA encoding an a	Nucleotide sequenc	Nucleotide sequenc	broduct for h	Mouse 1-alpha-OHas	Mouse 1-alpha-OHas	Expressed section	Mus musculus EPCR	se butvron	lar endothel	sed	IL-5 CDNA	spomic		A antigen pre	genomic DNA	protein	SM22 protein gene	protein g	M22 protein g	tide	Sequence encoding	:1ally	ednence en	ce encodin	e creatine	Mouse ESX transcri	e encod1	otide seque	se n	F recep	us SOCS	T2L gene.
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K>HK	RESULT 1 V27145 . ID V27145 standard; DNA; 6663 BP.
រំណ័សសស	Mus Sp. Key Location/Qualifiers CDS 11821744 /*tag= a /product= "Murine NR6"
PP PP PA PP PP PP	MO9811225-A2. 19-MAR-1998. 11-SEP-1997; G02. 11-SEP-1996; AU-(AMRA-) AMRD OF (DZIE/) DZIEGLEW Alexander W, Fab. Kojima T, Maeda J, Zhang J;
######################################	DR WPI: 98-260970/23. BR P-PSDB; W55016. The New isolated haemopoietin receptor - used for developing products PT New isolated haemopoietin receptor - used for developing products PT for modulating proliferation, differentiation and survival of cells, Claim 8: Page 108-114; 182pp; English. CLAIM 8: Page 108-114; 182pp; English. CC The NR6 gene encodes a novel Haemopoietin receptor (HR). Interaction concerned the novel HR and a ligand facilitates proliferation, differentiation and survival of a wide variety of cells. The HR and it's products can be used for modulating the activity of the receptors e.g. to requiate development, maintenance or regeneration in an array of different cells and tissues in vitro and in vivo. They can be present in the products can also be used for detection and diagnosis, and survival. The products can also be used for detection and diagnosis, cells or cancers or predisposition to cancers, or for drug screening: Sequence 6663 BP; 1462 A; 1852 C; 1715 G; 1634 T;
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                                                                                                 New isolated haemopoletin receptor - used for developing products

Tor modulating proliferation, differentiation and survival of cells,

For modulating proliferation, differentiation and survival of cells,

Claim 9: F19 3: 182pp; English.

Claim 9: F19 3: 182pp; English.

Claim 9: F10 3: 182pp; English.

Claim 9: F10 3: 182pp; English.

Claim 9: F10 3: 182pp; English.

Claim 9: F10 3: 182pp; English.

Claim 9: F10 3: 182pp; English.

Claim 9: F10 3: 182pp; English.

Claim 9: F10 3: 182pp; English.

Claim 9: F10 3: 182pp; English.

Claim 9: F10 3: 182pp; English.

Claim 9: F10 3: 182pp; English.

Consideration in an array of an intenance or regeneration in an array of therapeutics used for modulating neuronal proliferation, differentiation and survival. The products can also be used for detection and diagnosis,

Claim 9: F10 3: 182pp; English 2: 2447 A; 3367 C; 3298 G; 2720 T;
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Best Local Similarity 99.6%; Pred, No. 0;
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tggtaccagccagcci TGIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIII	SCCCTCTTCACTCCCT tctgatgtcctcacac		cottgagetgggggg 	99a99ttcctgggtg(ctcaaggtgggtgat
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δy	8	gtcagctt 289
셤	8002	CTGGGACATGTAGTGAGACCCTAGCTCAAAACACAGACAG
δ	2892	cctaataggtgctgggtgatgctcgcc
q	8062	TGACTTAATACTGGAACTCAGGGCCTAATAGGTGCTGGGTGATGCTCGCCTCACTCCC
ογ	2952	cccagctgggtgggctgctct
QQ	8122	TTTAGTGAGATCTCTGCGCTAATCTCCACCCCAGCTGGGTGGG
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δŷ	3072	ctgtttctggaatattaaatgacagtaatctatcaggcctgggtgagtagctaacaggg 3
q	8242	TCTGGAATATTAAATGACAGTAATCTATCAGGCCTG
δλ	3132	ogcagatagggtcataggagccactgcagcctag
QQ .	8302	TGGGGGCGTCTGGAAAACGCAGATAGGGTCATAGGAGCCACTGCAGCTAGATTA
οy	3192	gtcactaggccattctcaccaagcagtcctcagaact
Op	8362	CCACTGGGTGTTCTGTCACTAGGCCATTCTCAAGCAGCAGTCCTCAGAACTGGGAGCA
οy	3252	atgccagcatttaatgccagcattaggggaggcag
g	8422	GTTGCCAGCATTAATGCCAGCATTTAATGCCAGCATTAGGGGAGGCAGAGGCAGAAG
δ.	3312	ttcaaggccatcctgaatttacataaagagctccaggccaggccagg
QQ	8482	TCTCTCTGAGTTCAAGGCCATCCTGAATTTACATAAAGAGCTCCAGGCCAGCCA
ογ	3372	cttgtctcaaaaacaaagcatctttagtgaccaggcttgctccacc
q	8542	GCAGTAAAACCTTGTCTCAAAAAACAAAGCATCTTTAGTGACCAGGCT
δy	3432	ccccacccgacgtgcacgtgagccgcgttggggggcctggaggac
đ.	8602	AGTGACCACGGACCCCCACCCGACGTGCACGTGAGCCGCGTTGGGGGCCCTGGAGGACC 86
ον	3492	ctgagtgtgcgctgggtctcaccaccagctctcaaggatttcctcttccaagccaagt 35
q	8662	GCTGAGTGTGCCTCACCACCACCTCTCAAGGATTTCCTCTTCCAAGCCAAG
QY	3552	cagatecgctaccgcgtggaggacagcgtggactggaaggtgcccgtcccgc
q	8722	CAGATCCGCTACCGCGTGGAGGACAGCGTGGACTGGAAGGTGCCCGTCCCGCCCG
ογ	3612	cgcccctgaccccgcccccgcatctgactcctccctcaccgtgcaggtggtggatg
Q	8782	CGCCCCTGACCCGCCCCCCCGCATCTGACTCCTCCCTCACCGTGCAGTGGTGGA
δλ	3672	gtcagcaaccagacttctgccgtctcgcgggcctgaagcccggcaccgtttacttc
qq	8842	CAGCAACCAGACCTCCTGCCGTTTTCTTCGCGGCCTGAAGCCCGGCACCGTTTACTTCT
ογ	3732	Caagtgcgttgtaacccattcgggatctatgggtcgaaaaggcgggaatctggagcg
qq	8902	GCGTTGTAACCCATTCGGGATCTATGGGTCGAAAAGGCGGGAATCTGGAGCGG 89
ογ	3792	agccacccacgctgctccaccctcgaagtggtgagcacctctccagggctgg 385
Q O	8962	TGGAGCCACCCACCGCTGCTCCACCCTCGAAGTGGTGAGCACCTCTCCAGGGCTG
οy	3852	cccatggaatccccaatccatcctgttccttco
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. G	10162	TTATTTATGGCGTGAGGCCGATGTCCTTATCCGCTGGCCTGCTGGGGGATGGCTGCGGCT	10221
ά	5052	ggggattggacccaagggctggcttcccactcagtcctccagcccactccatqtcacac	-
្ត ដ	10222	GGGGAITGGACCCAAGGGTGGCTTCCCACTCAGTCCTCCAGCCCACTCCATGTCACACC	02
δλ	5112	cgtgcattctctgaggcttatcttgggaaccggccttgttctgtgctgtctgt	5171
a	10282	CGTGCATTCTCTGAGGCTTA	10341
ò	17	ttctgtcattcactttcccagagcctttttttatgcttttaataactacgttttaaa	5231
a :		CTGTCATTCACTTTCCCAGAGCCTTTTTTTATGCTTTTAATATAACTACGTTTT	04
දි දි	5232 10402	altgetttgfataatgftgfgeettegtgacgfgegtgcecacacacacacgggaa 	5291
ò	5292	gitagagaacttigitgagtaggctccitccaccaigiggactagggctggcgaca	351
<u>පි</u>	10462	GGTTAGAGAACTTTGTTGAGTAGGCTCCTTCCACCATGTGGGACTAGGGCTGGCGAGAAG	05
ŏ	5352	caattactgagtcatctcgccagcccctcacccctcacttcccatctgata	5411
ପ୍ର	10522	GCAATTAC	10581
δ	41	tcataggtaatcgaaggtaaatcgctggctttaatttcgtagctatcctgcctcagccta	5471
g G	r)	CATAGGTAATCGAAGGTAAATCGCTGGCTTTAATTTCGTAGCTATCCTGCCTCAGCCT	10641
දී දි	5472	ccaagtgctgtgctaccacgtttgtgggagggctctcctcccagtgtctgggggtgaca	531
3 8	, ,	CANGE GLIGIGGT ACCACGTTIGT GGGGGGCTCTCCTCCCAGTGTCTGGGGGGT-AC	03
S 8	10701	cag.cccaaga.cccgct.cctagg.cct.ggtcttagt.tgccccttgctttgt.ccgtg 	5591
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: 음	16	TCCCTAGAGICTCCGCCCCACCTTAGTTTCCTTTCTCTCCGAATACTCC	10820
δλ	5652	tttacctcccactgatttgactccctcttgcttgtctccatcgccatggcattgca	; ;
qq	10821		. 8
δy	5712	cotctgggtgactctgggtccacacctgacacctttcccaacttccccagccgaagc	5771
đ	10881	TCTCTGGGTGACTCTGGGTCCACCTGACACCTTTCCCAACTTTCCCCAGCCGAAGC	10940
Oγ	5772	aggccgccgccgcgcgcgcccccaacact	5831
6	10941	GGTCTGGTATGGGAGGCCGCCGTCCCGCGCGCGCCTCCTGCTGGCCGCCCCCAACACT	11000
δλ	5832	tttagagcgcccgggcccgggcggcgggtgtgcgagccgcggggc	5891
<u>ප</u>	11001	CCGCTCCATTCTCTTTAGAGCGCCCGGGCCGGGCGGGGGGGTGTGCGGGCGG	11060
ογ	5892	ccggtgcggcgagctcaagcagttcctcggctggctcaag	5951
අ	11061	GGGAGCCCAGCTGGGGCCGGGTGCGGCGCGGGGTCAAGCAGTTCCTCGGCTGGCT	11120
οχ	5952	gcacgcatactgctcgaaccttagtttccgcctgtacgaccagtggcgtgcttggatg	6011
d d		SCACGCATACTGCTCGAACCTTAGTTTCCGCCTGTACG	11180
ď	6012	cgaaaccaggtaggaaagttgggggaggcttgcgtgggggt	6071
셤 .	18	SAAGTCACACAAGACCCGAAACCAGGTAGGAAAGTTGGGGGGAGGCTTGCGTGGGGGGT	11240
ογ	6072	agagaccogggtgagcagctccacaaacaccgcactcttctt	6131
g -	11241	GGAGCAGAGGAAGAGAGACCCGGGTGAGCAGCCCCCCCACAACACCGCACTCTTCTT	11300

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                                                                                           TGCTCAAAGGGATCTCTTAGTGCTCATTTCACCCACTGCAAAGAGCCCCAGGTTTTACTG 11480
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Haemopoletin receptor; cell proliferation; cell differentiation; can
cell survival; therapeutic; neuronal proliferation; drug screening;
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Example 8; Page 99-100; 182pp; English,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       11541 GCCGCTAAACTCTAAGGATAGGCCATCCTCCTGCTGGGTCAGACCTGGAGGCTCACCTG
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                            tgctcaaagggatctcttagtgctcatttcacccactgcaagaggcccaggttttactg
                                                                                                                                                                                                                                                                                                   gccggctaaactctaaggataggccatcctcctgctggggtcagacctggaggctcacctg
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11-SEP-1996; AU-002246.
(AMRA) AMRAD OPERATIONS PTY LTD.
(DZIEC,) DZIEGEEWSKH E.
Alexander W. Fabri L., Farley A, Hilton DJ, Kikuchi Y,
Kojima T, Maeda M, Nash A, Nicola NA, Rakar S, Willson
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29-SEP-1998 (first entry)
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WPI; 98-260970/23.
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29-SEP-1998 (first entry)
Novel haemopoletin receptor NR6.3 gene.
Haemopoletin receptor; cell proliferation; cell differentiation; cancer;
cell survival; therapeutic; neuronal proliferation; drug screening; ss;
Mouse.
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96.3%;
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Location/Qualifiers

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Claim 6; Page 90-9: 182pp; English.

The haemopoletin receptor (RR) NR6; as a form of the novel HR NR6.

Interaction between the novel HR and a ligand facilitates proliferation, differentiation and survival of a wide variety of cells. The HR and 11/s derivatives can be used for modulating the activity of the receptors e.g. to regulate development, maintenance or regeneration in an array of different cells and tissues in vitro and in vivo. They can be present in therapeutics used for modulating neuronal proliferation, differentiation and survival. The products can also be used for detection and diagnosis, e.g. for cancers or predisposition to cancers, or for fary screening.

Sequence 938 BP; 243 A; 245 C; 272 G; 178 T;
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                                                                                                                                                                                                                                                          New isolated haemopoietin receptor - used for developing products for modulating proliferation, differentiation and survival of cells,
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                                                                                                      11-SEP-1996; AU-002246.
(AMRA-) AMRAD OPERATIONS PTY LTD.
(DZIEZ) DZIEGLEWSKA H.
Alexander W. Fabri L. Farley A, Hilton DJ, Kikuchi Y,
Kojima I, Maeda M, Nash A, Nicola NA, Rakar S, Willson
                                        "Haemopoietin receptor NR6.3"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 738.8; DB 1;
Pred. No. 8.7e-186;
0; Mismatches 27;
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   1. .468
/*tag= a
/product= '
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Best Local Similarity 96.3
Matches 778; Conservative
                                                                                            11-SEP-1997; G02479
                                                                                                                                                                                                                     WPI; 98-260970/23 P-PSDB; W55013.
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proliferation; cell differentiation; cancer;
neuronal proliferation; drug screening; ss;
                                                                                                                                                         6530
                                                                                                                                                                                                                                                                                         798
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(DZIE/) DZIEGLEWSKA H E.
Alexander W, Fabri L, Farley A, Hilton DJ, Kikuchi Y,
Kojima T, Maeda M, Nash A, Nicola NA, Rakar S, Willson
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Pred. No. 3e-64;
0; Mismatches 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                   Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    v27140;
29-SEP-1998 (first entry)
Novel haemopoietin receptor
Haemopoietin receptor; cell
cell survival; therapeutic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          4.2%;
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Best Local Similarity 99.6
Matches 281; Conservative
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11-SEP-1997; G02479.
11-SEP-1996; AU-002246.
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GAGACGCCAGCATTCTGGCTGGCTCCTGCCTCTATGTTGGCT 530
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V27143
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V41688
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              For mountarian, etc., and in mountains a form of the novel HR NR6. Claim 5; Page 84.87; 182pp; English.

The haemopoletin receptor (HR) NR6.2 is a form of the novel HR NR6. Interaction between the novel HR and a ligand facilitates proliferation, differentiation and survival of a wide variety of cells. The HR and it's derivatives can be used for modulating the activity of the receptors e.g. to regulate development, maintenance or regeneration in an array of different cells and tissues in vitro and in vivo. They can be present in therapeutics used for modulating neuronal proliferation, differentiation and survival. The products can also be used for detection and diagnosis, e.g. for cancers or predisposition to cancers, or for drug screening.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ö
                                                                                                                                                                                                                                                                  29-SEP-1998 (first entry)
Novel haemopoietin receptor NR6.2 gene.
Namenpoietin receptor: cell proliferation; cell differentiation; cancer; cell survival; therapeutic; neuronal proliferation drug screening; ss;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            atggtcgccgcctgccctctgagctgtcccgcctcttaacacctccaccctggccctgg 1338
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                                                    368 ATGGTCGCCCCCTCTCTGAGCTGTCCCGCCTCCTTAACACCTCCACCCTGGCCCTGG 427
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 P-PSDB, W55012.
New isolated haemopoletin receptor - used for developing products
for modulating proliferation, differentiation and survival of cells,
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                                     369 AIGGICGCCGCCTGCCCTCTGAGCTGTCCCGCCTCCTTAACACCCTCCACCCTGGCCCTGG
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11.SEP-1996; AU-002246.
(AMRA-) AMRAD DERATIONS PTY LTD.
(DZIE/) DZIEGLEWSKA H E.
Alexander W, Fabri L, Farley A, Hilton DJ, Kikuchi Y,
Kolima T, Maeda M, Nash A, Nicola NA, Rakar S, Willson T,
Zhang J;
WPI; 98-260970/23.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                  /product- "Haemopoietin receptor NR6.2"
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Pred. No. 3.1e-64;
0; Mismatches 1;
                                                                                                                                                                                                                                                                                                                                                                            Location/Qualifiers
1. .1278
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                / Match 4.2%;
Local Similarity 99.6%;
hes 281; Conservative C
                                                                                                                                                                                                                                  V27141 standard; cDNA; 1673
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                                                                                                                                                                                                                                                                                                                                             Mouse.
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15-JAN-1998; U00334.

16-JAN-1999; US-784863.

16-JAN-1999; US-784863.

16-JAN-1999; US-784863.

17-JAN-1999; US-784863.

18-JAN-1999; US-784863.

20-JAN-1999; US-784869.

20-JAN-1998; US-784869.

20-JAN-1998; US-784869.

20-JAN-1998; US-784869.

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                                                                                                                                                                   superfamily;
dy; cell differentiation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          306 CCTGCTCTAIACAIGGAGACACCTGGGGCCACCGCTGAGGGCTCTACTGGACCCCTCA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1279 atggtcgccgcctgccctctgagctgtcccgcctccttaacacctccacctggccctgg
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Indels
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Pred. No. 2.1e-63;
0; Mismatches 3;
                                                                                                                                                                                                          immune response; antibody;
                              741688, 26-0CT-1998 (first entry)
Nucleotide sequence of the murine U4 gene.
Murine; U4 protein; haematopoletin receptor cell proliferation; immune response; antibod autoimmune disease; cancer; allergy; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                           /product= "U4 protein"
                                                                                                                                                                                                                                                                                                                                  Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         V27143 standard; cDNA; 834 BP
V27143;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity 98.9%;
Matches 279; Conservative 0
V41688 standard; cDNA; 1656
                                                                                                                                                                                                                                                                                                                                                                         122. .1399
/*tag= a
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Best Local Similarity
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The nucleotide sequence was generated by a 5N RACE of brain cDNA using NR6 specific primers. NR6 is a novel Haemopoletin receptor (HR). Interaction between the novel HR and a ligand facilitates proliferation, differentiation and survival of a wide variety of cells. The HR and it's derivatives can be used for modulating the activity of the receptors e.g. to regulate development, maintenance or regeneration in an array of different cells and tissues in vitro and in vivo. They can be present in therapoutics used for modulating neuronal proliferation, differentiation and survival. The products can also be used for detection and diagnosis, e.g. for cancers or predisposition to cancers, or for drug screening.
29-SEP-1998 (first entry)
Nucleotide sequence of products generated by 5N race of brain cDNA.
Haemopoletin receptor; cell proliferation; cell differentiation; cancer; cell survival; therapeutic; neuronal proliferation; drug screening; ss;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       17-MAR-1999 (first entry)

CDNA encoding rat Zcytor5.

Zcytor5: cytckinin-like receptor; down-regulation; growth factor;
maintenance factor; thyroid; heart; skeletal muscle; cardiotrophin-1;
cardiac pathology; heart enlargement; Zcytor5 ligand; ss.

Rattus sp.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          New isolated haemopoietin receptor - used for developing products for modulating proliferation, differentiation and survival of cells.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (AMRA-) AMRAD OPERATIONS PTY LTD.
(DZIE/) DZIEGLEWSKA H E.
Alexander W, Fabri L, Farley A, Hilton DJ, Kikuchi Y,
Kojima T, Maeda M, Nash A, Nicola NA, Rakar S, Willson
                                                                                                                                                                                                                                                                          /*tag= a
/product= "Haemopoletin receptor"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           e.g. neuronal cells
Claim 7; Page 93-95; 182pp; English.
                                                                                                                                                                                                            Location/Qualiflers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Best Local Similarity 99.6
Matches 255; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                         11-SEP-1996; AU-002246
                                                                                                                                                                                                                                                                                                                                                                                                              .1-SEP-1997; G02479
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Zhang J;
WPI; 98-260970/23.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              P-PSDB; W55014
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
                                                                                                                                                                      Mus sp.
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V70896
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The present sequence encodes a protein designated Zcytor5, which is a cytokinin-like receptor. Soluble Zcytor5 may be administered to down-regulate the effects of a growth and/or maintenance factor in thyroid, heart, and skeletel muscle for example to lessen the effect of cardiotrophin-1 on cardiac pathologies, so preventing heart enlargement. Zcytor5 could be used to detect cardiotrophin-1 in the blood, and to discover other possible Zcytor5 ligands. A probe and integrity of the Zcytor5 gene on chromosome 19. Antibodies and the and integrity of the Zcytor5 gene on chromosome 19. Antibodies and the therapeutically to andidy Ccytor5 ligand effects. Sequence 1724 BP; 350 A; 550 C; 500 G; 324 T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1159 acacagetgtaateagececeaggaceceaecetteteateggeteetegeaageta 1218
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1219 cctgctctatacatggagacacacctggggccaccgctgaggggctctactggaccttca 1278
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1279 atggtcgccgcctgccctctgagctgtcccgcctcttaacacctccacctggcctgg 1338
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            283 ACACAGCIGIGAICAGICCCCAGGACCCCACTICITCATCGGATCCITCCTTCATGCTA 342
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        V70894;
17-MAR-1999 (first entry)
CDNA encoding human zcytor5.
CSYtor5; cytokinin-like receptor; down-regulation; growth factor;
maintenance factor; thyroid; heart; skeletal muscle; cardiotrophin-l;
cardiac pathology; heart enlargement; Zcytor5 ligand; ss.
                                                                                                                                                                                                                                                                                 New mammalian cytokinin-like receptor Zcytor5 - useful for, e.g.
down-regulating Zcytor5 natural ligands or detecting cardiotrophin-1
in blood
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    343 CGTGCTCTATACATGGAGACACACGGGGGCCACTGCTGAGGGCCTCTACTGGACCCTCA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           463 CCCTGGCTAACCTTAATGGGTCCAGGCAGCTCAGGGGACAATCTGGTGTGTCACGCCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 1724;
                                                                                                                                    01-MAY-1997; US-045287.
01-MAY-1997; US-850030.
13-FEB-1998; US-0218890.
(ZYMO) ZYMOGENETICS INC.
Adams RL, Foster DC, Gilbert T, Jelmberg AC, Lehner JM,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              3.7%; Score 248; DB 1;
92.9%; Pred. No. 1.2e-55;
ative 0; Mismatches 20;
                                                                                                                                                                                                                                                                                                                                  Disclosure; Page 72-75; 55pp; English
 Location/Qualifiers
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                                  /*tag= a
/product= Zcytor5
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/product= Zcytor5
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity 92.9
Matches 260; Conservative
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                                                                                                                                                                                                                                              WPI; 99-034662/03
P-PSDB; W70862.
                                                                                                   01-MAY-1998;
13-FEB-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RESULT 10
В
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Provent to blood

PS Disclosure; Page 68-70; 55pp; English.

Disclosure; Page 68-70; 55pp; English.

Disclosure; Page 68-70; 55pp; English.

CC Zcytor5, which is a cytokinin-like receptor. Soluble Zcytor5 may be administered to down-regulate the effects of a growth and/or maintenance of actor in thyroid, heart, and skeletal muscle for example to lessen the ceffect of cardiotrophin-1 on cardiac pathologies, so preventing heart calculargement. Zcytor5 could be used to detect cardiotrophin-1 in the blood, and to discover other possible Zcytor5 ligands. A probe comprising Zcytor5 DNA or RNA can be used to determine the presence cand integrity of the Zcytor5 gene on chromosome 19. Antibodies and the anti-idiotypic antibody could be used to purify Zcytor5 and the countility to modify Zcytor5 ligand effects.

CC therapeutically to modify Zcytor5 ligand effects.

SQ Sequence 1813 BP; 415 A; 604 C; 519 G; 275 T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1219 cetgetetatacatggagacacacctggggccaccgctgaggggctctactggacettca 1278
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         200 ACACAGCTGTGATCAGTCCCCAGGATCCCACGCTCTCTCATCGGCTCCTCCCTGCTGGCGC 259
                                                                                                                                                                                                                                                                                               New mammalian cytokinin-like receptor Zcytor5 - useful for, e.g. down-regulating Zcytor5 natural ligands or detecting cardiotrophin-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Human; U4 protein; haematopoietin receptor superfamily; cell proliferation; immune response; antibody; cell differentiation; autoimmune disease; cancer; allergy; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             260 CCTGCTCAGTGCACGGAGACCCACCAGGAGCCACCGCGGGGGCCTCTACTGGACCCTCA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1279 atggtcgccgcctgccctctgagctgtccgcctccttaacacctccacctggcctgg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          37; Indels
13-FEB-1998; US-074721.
01-MAY-1997; US-045287.
01-MAY-1997; US-045287.
01-MAY-1997; US-025890.
(ZYMO ) ZYMOGENETICS INC.
Adams RL, Foster DC, Gilbert T, Jelmberg AC, Lehner JM, Lok S, Presnell SR, Whitmore TE;
P-PSDB; W70861.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DB 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    3.3%; Score 221.8; DB 1
86.8%; Pred. No. 1.1e-48;
ilve 0; Mismatches 37
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       23-JUL-1998.
15-JAN-1998; U00334.
16-JAN-1997; US-784863.
(GENI ). GENETICS INST INC.
CCOLLINS M, Donaldson DD, Neben T, Whitters in WPI; 98-414109/35.
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Nucleotide sequence of the human U4 gene.
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/product= "U4 protein"
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1. .1228
/*tag= a
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V41689;
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Matches 244; Conservative
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The present sequence encodes a protein designated Zcytor5, which is a cytokinin-like receptor: Soluble Zcytor5 may be administered to down-regulate the effects of a growth and/or maintenance factor in thyroid, heart, and skeletal muscle for example to lessen the effect of Cardiotrophin-l on cardiac pathologies, so preventing heart enlargement. Zcytor5 could be used to detect cardiotrophin-l in the blood, and to discover other possible Zcytor5 ligands. A probe comprising Zcytor5 DNA or RNA can be used to determine the presence and integrity of the Zcytor5 gene on chromosome 19. Antibodies and the anti-idiotypic antibody could be used to purify Zcytor5 and therapeutically to modify Zcytor5 ligand effects.

Sequence 1690 BP; 319 A; 592 C; 505 G; 274 T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1159 acacagetgtaatcagececcaggaececaecetteteateggeteetectgcaageta 1218
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Zcytor5; cytokinin-like receptor; down-regulation; growth factor; maintenance factor; thyroid; heart; skeletal muscle; cardiotrophin-1; cardiac pathology; heart enlargement; Zcytor5 ligand; allelic varaint;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        167 ACACAGCTGTGATCAGTCCCCAGGATCCCACGCTCTCATCGGCTCCTCCCTGCTGGCGA 226
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                                                                                                                                                                                                                                                                                                                                                                                       New mammalian cytokinin-like receptor Zcytor5 - useful for, e.g. down-regulating Zcytor5 natural ligands or detecting cardiotrophin-1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               37; Indels
                                                                                                                                                                                                                                                                    Jelmberg AC, Lehner
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88. .1365
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                                                                                                                                                                                                                        (ZYMO ) ZYMOGENETICS INC.
Adams R.L. FOSTER DC, Gilbert T,
ACK S, Presnell SR, Whitmore TE;
WPI; 99-034662/03.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Matches 244; Conservative
                                                         01-MAY-1998; U08865.
13-FEB-1998; US-074721.
01-MAY-1997; US-045287.
01-MAY-1997; US-856030.
13-FEB-1998; US-023890.
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01-MAY-1998; U08865
                                                                                                                                                                                                                                                                                                                                                        P-PSDB; W70860
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Query Match

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                   New nucleic acid encoding U4 haematopoietin receptor superfamily
The new nucleic acid encoding U4 haematopoietin receptor superfamily
This is chain - potentially useful, e.g. for modulating cell proliferation
Tor immune response, for treating cancer and auto:immune disease
This is the nucleotide sequence encoding the human U4 protein from
the haematopoietin receptor superfamily, used in the method of the
Invention for the modulation of cell proliferation, or the immune
response. Transformed mammalian cells are used to produce recombinant
U4 protein. The U4 protein is used to screen for specific binding
agents, raise antibodies. It is also used as reagents for assays and
in pharmaceutical compositions which may modulate cell proliferation,
cell differentiation, and the immune system (e.g. for treating immune
cancer, and allergy).
Sequence 1579 BP; 304 A; 535 C; 473 G; 267 T;
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Nucleotide sequence of clone HFK-66 encoding human NR6.
Haemopoietin receptor; cell proliferation; cell differentiation; cancer; cell survival; therapeutic; neuronal proliferation; drug screening; ss;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1219 cctgctctatacatggagacacacctggggccaccgctgaggggctctactggaccttca 1278
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 1579;
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Alexander W, Fabrí L, Farley A, Hilton DJ, Kikuchi Y,
Kojima T, Maeda M, Nash A, Nicola NA, Rakar S, Willson
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86.5%; Pred. No. 2.6e-48;
11ve 0; Mismatches 38;
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n 7; Page 102-104; 182pp; English.
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11-SEP-1996; AU-002246.
(AMRA-) AMRAD OPERATIONS PIY LTD.
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Best Local Similarity 86.5
Matches 243; Conservative
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The NR6 gene encodes a novel Haemopoietin receptor (HR). Interaction between the novel HR and a ligand facilitates proliferation, differentiation and survival of a wide variety of cells. The HR and it's derivatives can be used for modulating the activity of the receptors e.g. to regulate development, maintenance or regeneration in an array of different cells and tissues in vitro and in vivo. They can be present in therapeutics used for modulating neuronal proliferation, differentiation and survival. The products can also be used for detection and diagnosis, e.g. for cancers or predisposition to cancers, or for drug screening. Sequence 1391 BP; 281 A; 459 C; 417 G; 234 T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             e.g. neuronal cells
Disclosure; Page 101; 182pp; English.
NR6 is a novel haemopoietin receptor (HR). Interaction between the novel
HR and a ligand facilitates proliferation, differentiation and survival
of a wide variety of cells. The HR and it's derivatives can be used for
modulating the activity of the receptors e.g. to regulate development,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Haemopoletin receptor; cell proliferation; cell differentiation; cancer; cell survival; therapeutic; neuronal proliferation; drug screening; ss;
                                                                                                                                                                                                                                                                                                                                                                                       3434 gigaccacggacccccacccgacgigacgigagccgcgtiggggccigggaccag 3493
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 3554 cagatcogotacogogtggaggacagogtggactggaaggtgcccgtcccggacc 3613
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     3494 ctgagtgtgcgctgggtctcaccaccagctctcaaggatttcctcttccaagccaagtac 3553
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             aagtgcgttgtaacccattcgggatctatgggtcgaaaaggcgggaatctggagcgagt 3793
                                                                                                                                                                                                                                                                                                                                                                                                                641 TGAGCAACCAGCACCTCCTGCCGCCTGGCCTGAAACCCGGCACCGTGTACTTCGTGC 700
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          New isolated haemopoletin receptor - used for developing products for modulating proliferation, differentiation and survival of cells, e.g. neuronal cells
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 3614 egeceetgaeceegeeecegeatetgaetecteeeteaeegtgeaggtggtggtgaeg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ------AGGTGGTGGACGATG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            3674 tcagcaaccagacetectgecgtetegegggeetgaageeegggeacegtttaettegtee
                                                                                                                                                                                                                                                                                                                                                    68;
                                                                                                                                                                                                                                                                                                  DB 1; Length 1391;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (AMEA-) AMEAD OPERATIONS PTY LTD.
(DZIE/) DZIEGLEWSKA H E.
Alexander W, Fabri L, Farley A, Hilton DJ, Kikuchi Y,
Kojima I, Maeda M, Nash A, Nicola NA, Rakar S, Willson T,
                                                                                                                                                                                                                                                                                                                                                  Indels
                                                                                                                                                                                                                                                                                                                                               37;
                                                                                                                                                                                                                                                                                           Query Match 2.9%; Score 190.8; DB 1
Best Local Similarity 73.5%; Pred. No. 1.5e-40;
Matches 291; Conservative 0; Mismatches 37
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ggagccaccccaccgctgcctccacccctcgaagtg 3829
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         761 GGAGCCACCCCACAGCCGCCTCCACTCCCCGCAGTG 796
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   V27159;
29-SEP-1998 (first entry)
PCR product for human NR6.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             V27159 standard; DNA; 560
                                                                                                                                                                                                                                                                                                                                        Matches 291; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               11-SEP-1996; AU-002246.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         11-SEP-1997; G02479
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Zhang J;
WPI; 98-260970/23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Homo sapiens.
WO9811225-A2.
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New polynucleotides encoding 25-hydroxyvitamin D 1-^a-hydroxylase -
useful to detect and treat vitamin D-related disorders
Example 4; Page 79-81; SSpp; English.
This invention describes novel 25-hydroxyvitamin D 1-alpha-hydroxylase
(1-alpha-OHase), a renal cytochrome P450 enzyme of the vitamin D
pathway, and polynucleotides encoding the enzyme from human, mouse and
rat tissue. Molecules of the invention are used to diagnose and treat
rat tissue. Molecules of the invention are used to diagnose and treat
vitamin D-related disorders, to produce vitamin D metabolites, and to
identify modulators of the enzyme expression. The invention describes
an animal cell transformed with the enzyme promoter which is used to
identify compounds which modulate the production of vitamin D in
patients with vitamin D endocrine disorders in the vitamin D in
hydroxylation pathway, the enzyme catalyses conversion of
bydroxylation pathway, the enzyme catalyses
cuerce 4105 BP; 1063 A; 1032 C; 1063 G; 947 T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ä
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maintenance or regeneration in an array of different cells and tissues in vito and in vivo. They can be present in therapeutics used for
                 vitro and in vivo. They can be present in therapeutics used for modulating neuronal proliferation, differentiation and survival. The products can also be used for detection and diagnosis, e.g. for cancers or predisposition to cancers, or for drug screening.

Sequence 560 BP; 113 A; 182 C; 165 G; 100 T;
                                                                                                                                                                                                                                           3494 ctgagtgtgcgctgggtctcaccaccagctctcaaggatttcctcttccaagccaagtac 3553
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                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                    0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            11-JUN-1999 (first entry)
Mouse 1-alpha-OHase promoter region DNA #2.
1-alpha-OHase; vitamin D 1-alpha-hydroxylase; vitamin D pathway;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            renal cytochrome P450 enzyme; 25-hydroxyvitamin D; human; mouse;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ä
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                                                                                                                                                              Length 560;
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                                                                                                                                                                                                      Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  diagnosis; treatment; disorder; endocrine; promoter; ss
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                                                                                                                                                                                                                                                                                                                                                                                                                                  502 CAGATCCCCTACCGAGTGGAGGACAGTGTGGAATGGAAGGTG 543
                                                                                                                                                           Score 141.2; DB 1;
Pred. No. 1.2e-27;
0; Mismatches 13;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      X23316 standard; DNA; 4105 BP X23316;
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Matches 150; Conservation
                                                                                                                                                              2.1%;
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                                                                                                                                                                                                      Conservative
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06-AUG-1997; US-906791.
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Best Local Similarity
Matches 149; Conserv
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3520 GITITITGGITITCCCAGACAGGGITICICIGIGIAACCCIGGCIGITC-IGGAACICAC 3462

447 tctgtagaccaggctggccttgaactcagaaatccgcctgcttgtgcttcccaagtgctt 506

387 gagititgititatitgagacagggctictctgtgtagicctggctgiccttggaactcac 446

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Search completed: September 28, 1999, 16:50:24 Job time: 7609 sec

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1 (bases 1 to 447)
NCT-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    alggicgccgcttgccctctgagctgtcccgcctccttaacacctccaccctggccctgg 1338
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Tel: (301) 496-1550
Email: Robert_Strausberg@nih.gov
This clone is available royalty-free through LLNL; contact the
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  117 CCTGCTCAGTGCACGGAGACCCACAGGACCCACGCGGAGGGCCTCTACTGGACCCTCA 176
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                111111 | 11111 | 11111 | 111111 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            cctgctctatacatggagacacacctggggccaccgctgaggggctctactggaccttca
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 220.2; DB 43; Length 477;
Pred. No. 6.2e-44;
0; Mismatches 38; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebra
Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Tumor Gene Index
Unpublished (1997)
On Aug 21, 1998 this sequence version replaced
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Insert Length: 1667 Std Error: 0.00 Seg primer: -40ml3 fwd. ET from Amersham High quality sequence stop: 431.
Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /organism="Homo sapiens"
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86.5%;
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43; Conservative
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Matches 243;
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KEYWORDS
SOURCE
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ORIGIN
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TITLE
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AI187074
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normalization to a Cot = 5. Library constructed by Bento Soares and M.Fatima Bonaldo. This library was constructed from the same fetus as the fetal heart library, Soares
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q126b05.x1 Soares_NhHMPu_S1 Homo sapiens cDNA clone IMAGE:1857585
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Homo sapiens
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Butheria; Primates; Catarrhini; Hominidae; Homo.
1 (Dases 1 to 417)
NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
                                                                                                                                                                                                                                                                                                                                                                1159 acacagetgtaateageeeecaggaeeeecacetteteateggeteeteetgeaageta 1218
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Contact: Noted 1500
Tel: (301) 496-1550
Email: Robert_Strausberg@nih.gov
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1219 cctgctctatacatggagacacacctggggccaccgctgaggggctctactggacctca
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                                                                                                                                                                                                                                                                                                           Length 447;
                                                                                                                                                                                                                                                                                                     Score 220.2; DB 43; Length
Pred. No. 6e-44;
0; Mismatches 38; Indels
/clone_11D="Soares_fetal_lung_NbHL19W"
/dev_stage="19 weeks"
/lab_host="DH10B (ampicillin resistant)"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Contact: Robert Strausberg, Ph.D.
                                                                                                                                                                                                                         fetal heart NDHH19W.
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                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity 86.5%;
Matches 243; Conservative (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      3', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Tumor Gene Index
Unpublished (1997)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                VERSION
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SOURCE
ORGANISM
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AUTHORS
TITLE
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COMMENT
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of sequence

source

FEATURES

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/lab_host="Delta" audit.
/lab_host="Public Life Technologies)"
/lab_host="Public Life Technologies)"
/lab_host="Public Life Technologies)" with a modified
/note="Vector: pT7T3D-Pac (Pharmacia) with a modified
polylinker; Site_1: Not I; Site_2: Eco RI: The UI-R-G0
library is a normalized library constructed from a
mixture of rat tissues (nodose ganglia, dorsal root
ganglia, and trigeminal ganglia). The tag is a string of
6 nucleotides present between the Not I site and the
oligo-dr track. The library was constructed as described
by Bonaldo, Lennon and Soares, Genome Research 6:
791-806, 1996."
University of Iowa
451 Eckstein Medical Research Building Iowa City, IA 52242, USA
Tel: 319 315 8250
Fax: 319 335 8250
Email: msoares@blue.weeg.uiowa.edu
Oligo-dT track not found, Not I site shown in beginning of sequenc
011go-dT track not found, Not I site shown in beginning of sequenc
is likely internal to the message. cDNA Library Preparation: M.B.
Soares Lab Clone distribution: clones will be available through
Research Genetics (www.resgen.com)
Seq primer: M13 Forward.
Location/Qualifiers
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qp93e12.x1 Soares_fetal_lung_NbHL19W Homo sapiens CDNA clone
IMAGE:1930606 3' similar to TR:Q16354 Q16354 PROLACTIN RECEPTOR
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Catarrhini; Hominidae; Homo.
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Pred. No. 7.6e-44;
0; Mismatches 19;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /clone="UI-R-G0-ut-h-08-0-UI"
/clone_lib="UI-R-G0"
                                                                                                                                                                                                                                                                                                                                                                                                                                       /organism="Rattus norvegicus'
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Best Local Similarity 92.4%;
Matches 231; Conservative (
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AI333812
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                                                                                                                                                                                                                                                                                                                                                                 // Acad_mixed_mixed (see below); Vector: pT7T3D-Pac // Acad_mixed_mixed (see below); Vector: pT7T3D-Pac // Pharmacia) with a modified polylinker; Site_1: Not I; Site_2: Eco RI: Equal amounts of plasmid DNA from three normalized libraries (melanocyte 2NbHM, pregnant uterus NbHPU, and fetal heart NbHH19W) were mixed, and ss circles were made in vitro. Following HAP purification, this DNA was used as tracer in a subtractive hybridization reaction. The driver was PCR-amplified cDNAs from pools 5,000 clones made from the same 3 libraries. The pools consisted of I.M.A.G.E. clones 260232-265223, 340488-489479."
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Ratus norvegicus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;

Eukaryota; Metazoa; Chordata; Craniata; Murinae; Rattus.

I (bases 1 to 332)

Bonaldo, M.F. Lennon, G. and Soares, M.B.

Normalization and subtraction: two approaches to facilitate gene
                                                                                                                                                                                        /clone="INAGE: 857585"
/clone_lib="Soares_NhHMPu_S1"
/tissue_type="Pooled human melanocyte, fetal heart, and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1339 ccctggctaaccttaatgggtccaggcagcagtcaggagacaatctggtgtgtcacgcc 1398
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CDNA clone
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            3.3%; Score 220.2; DB 44; Length 417;
86.5%; Pred. No. 5.9e-44;
vative 0; Mismatches 38; Indels 0;
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UI-R-GO-ut-h-08-0-UI.s3 UI-R-GO Rattus norvegicus
UI-R-GO-ut-h-08-0-UI 3', mRNA sequence.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Genome Res. 6 (9), 791-806 (1996)
97044477
                                                                                                                                /organism="Homo sapiens"
/db_xref="taxon:9606"
                         ity sequence stop: 406.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                              pregnant uterus" /lab_host="DH108"
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                                 High quality
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discovery

JOURNAL MEDLINE COMMENT

REFERENCE AUTHORS . TITLE

A1579568

ACCESSION

LOCUS DEFINITION

RESULT AIS79568

VERSION , KEYWORDS SOURCE ORGANISM

us-09-037-657-28.rst

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double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not and Eco RI sites of the modified pT7T3 vector. Library went through one round of normalization. Library constructed by Bento Soares and M. Fatima Bonaldo. " 156 c 108 g 66 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /note="Organ: thymus, pooled; Vector: pr713D-Pac (Pharmacia) with a modified polylinker; Site_1: Not I; Site_2: Eco RI; 1st strand cDNA was primed with a Not I oligo(dT) primer [5'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutherla; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 385)
NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
                                                                                                                                                                                                                                                                                   Tel: (301) 496-1550
Email: Robert_Strausberg@nih.gov
This clone is available royalty.free through LLNL; contact the
TMAGE Consortium (info@image.llnl.gov) for further information.
Seq primer: -400P from glbco
High quality sequence stop: 372.
Location/Qualifiers
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Unpublished (1997)
On May 9, 1996 this sequence version replaced gi:1133091
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /clone="IMAGE:2345981"
/clone_llb="Soares_thymus_NHFTh"
/dev_stage="fetal"
/lab_host="DH10B (phage-resistant)"
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llarity 85.4%; Pred. No. 8.8e-43;
Conservative 0; Mismatches 41;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /organism="Homo sapiens"
/db_xref="taxon:9606"
                                                                                                                                                                                                                                                                     Contact: Robert Strausberg, Ph.D.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  double stranded cDNA was size selected, ligated to Eco RI adapters (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of a modified pT773 vector (Pharmacia). Library went through one round of normalization to a Cot = 5. Library constructed by Bento Soares and M.Fatina Bonaldo. This library was constructed from the same fetus as the fetal heart library, Soares fetal heart NDHH19W."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 National Cancer Institute, Cancer Genome Anatomy Project (CGAP), Tumor Gene Index Unpublished (1997)
On Jan 14, 1998 this sequence version replaced gi:1797892.
                                                                                                                                                                             This clone is available royalty free through LLNL; contact the IMAGE Consortium (info@image.llnl.gov) for further information. Insert Length: 1615 Std Error: 0.00 Seq primer: -400P from Gibco High quality sequence stop: 407.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1220 ctgototatacatggagacacacctggggccaccgctgaggggctctactggaccttcaa 1279
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1280 tggtcgccgcctgccctctgagctgtcccgcctccttaacacctccacctggcctggc 1339
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                                                                                                                                                                                                                                                                                                                                                                                                                              /clone_lib="Soares_feta'_lung_NbHL19w"
/dev_stage="19 weeks"
/lab_host="DH10B (ampicillin resistant)"
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                                                                                                               Contact: Robert Strausberg, Ph.D. Tel: (301) 496-1550
Email: Robert_Strausberg@nih.gov
                                                                                                                                                                                                                                                                                                                                           'organism="Homo sapiens"
'db_xref="taxon:9606"
                                                                                                                                                                                                                                                                                                                                                                                    /map="4p16.1-4pter"
/clone="IMAGE:1930606"
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                                                                      Eukaryota: Metazoa: Chordata: Craniata; Vertebrata; Mammalia; Eutheria; Rodentia; Sclurognathi; Muridae; Murinae; Mus.

1 (bases 1 to 482)

Amara,M., Hillier,L., Allen,M., Bowles,M., Dietrich,N., Dubuque,T., Geisel,S., Kucaba,T., Lacy,M., Le,M., Martin,J., Morris,M., Schellenberg,K., Steptoe,M., Tan,F., Underwood,K., Moore,B., Theising,B., Wylie,T., Lennon,G., Soares,B., Wilson,R. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    13:1, on equal amounts of mRNA from 2 13:50pc and 2
14.50pc embryos [total RNA provided by Minoru Ko, Wayne State Univ., from 2 ]; double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of the modified pT7T3 vector. Library went through one round of normalization, and was constructed by Bento Soares and M. Farima Bonaldo.
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                                                                                                                                                                                                                                                                                                                                                                                                               Email: mouseest@watson.wustl.edu
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       317 GTGACCACGGACCCCCACCCGACGTGCACGTGAGCCGCGTTGGGGGCCTGGAGGACCAG 258
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                                                                                                                                                                                                          Waterstön,R.
The WashD'HHMI Mouse EST Project
Unpublished (1996)
On Apr 14, 1993 this sequence version replaced gi:785250.
                                                                                                                                                                                                                                                                                                                       Washu-HHMI Mouse EST Project
Washington University School of MedicineP
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 482;
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Possible reversed clone: similarity on wrong strand
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /dev_stage="13.5-14.5dpc total fetus"
/lab_host="DH10B"
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                                                                                                                                                                                                                                                                                                       Contact: Marra M/Mouse EST Project
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          'organism-"Mus musculus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 High quality sequence stop: 359.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /strain="C57BL/6J"
/db_xref="taxon:10090"
/map="10 pter-cen"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         "sex="unknown"
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W66776.1 GI:1375694
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                                                         Mus musculus
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Email: genome-resertc.riken.go.jp
Thermostabilization and thermoactivation of thermolabile enzymes by
trehalose and its application for the synthesis of full length CDNA
(Proc. Natl. Acad. Sci. U.S.A. 95(2):520-524 (1998))
Transcriptional sequencing: A method for DNA sequencing using RNA
polymerase (Proc. Natl. Acad. Sci. U.S.A. 95(7):3455-3460 (1998))
Please visit our web site (http://genome.rtc.riken.go.jp) for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Oda, H.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Larding, P., Shibata, K., Ozawa, Y., Konno, H., Ito, M., Aizawa, K., Akahira, S., Akayama, J., Fukuda, S., Fukunishi, Y., Funayama, T., Hara, A., Hayatsu, N., Hori, F., Ishikawa, T., Itoh, M., Izawa, M., Kayina, Y., Kojina, Y., Matsuyama, T., Niitsuna, H., Oda, H., Kawai, J., Kikuchi, N., Kojina, Y., Matsuyama, T., Niitsuna, H., Oda, H., Sugahara, Y., Shipata, Y., Shipata, Y., Shipaki, T., Sogabe, Y., Sugahara, Y., Suzuki, H., Tateno, M., Tomaru, Y., Sogabe, Y., Tominaga, N., Matanabe, S., Yagame, M., Yamamura, T., Yokota, T., Yokhino, M., Muramatsu, M., Okazaki, Y. and Hayashizaki, Y. RIKEN Mouse ESTS
Unpublished (1999)
On Jun 22, 1998 this sequence version replaced gi:3246782.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AV032198 262 bp mRNA EST 03-JUN-1999
WA032198 Mus musculus adult C57BL/6J cerebellum Mus musculus CDNA
Clone 1500034F20, mRNA sequence.
AV032198
                                                              -----AGGTGGTGGATGAC 146
                                                                                                                                                                                                   86
                                                                                                                                                                                                                                                                            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 262)
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                                                                                                                                    gtcagcaaccagacctcctgcogtctcgcgggcctgaagcccggcaccgtttacttcgtc
cegeceetgaeceeegeeeeegeatetgaeteeteeeteaeegtgeaggtggtggatgae
                                                                                                                                                                                                          145 GTCAGCAACCAGACCTCCTGCCGTCTCGCGGGCCTGAAGCCCGGCACCGTTTACTTCGTC
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Tel: 81-298-36-9145
Fax: 81-298-36-9098
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/dev_stage="adult"
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/clone="1500034F20"
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Genome Science Laboratory
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116 c
                                                                                                                                Query Match 3.1
Best Local Similarity 92.0
Matches 218; Conservative
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W17583.1
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                                                                BASE COUNT
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Fax: 319 335 9565
Email: msoares@blue.weeg.uiowa.edu
Oligo-dr track not found, Not I site shown in beginning of sequence is likely internal to the message. cDNa Library Preparation: M.B. Soares.lab Clone distribution: clones will be available through Seq primer: Ml3 Forward.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /dev_stage="adult"
//dab_host="DH10B (Life Technologies)"
/note="Vector: pT713D-Pec (Pharmacia) with a modified
polylinker; Site_1: Not I; Site_2: Eco RI; The UI-R-G0
library is a normalized library constructed from a
mixture of rat tissues (nodose ganglia, dorsal root
ganglia, and trigeminal ganglia). The tag is a string
6 nucleotides present between the Not I site and the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Bonaldo,M.F., Lennon,G. and Soares,M.B.
Normalization and subtraction: two approaches to facilitate gene
                                                         6364 caggtcctgccggctaaactctaaggataggccatcctcct-gctgggtcagacctggag 6422
                                                                                                                                                                                            6423 gotcacotgaattggagococtotgtaccatotgggoaacaaagaaacotaccagaggot 6482
                                                                                                                                                                                                                                                            Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                               AI574687 319 bp mRNA EST · 30-MAR-1999
UI-R-GO-uc-b-11-0-UI.S1 UI-R-GO Rattus norvegicus cDNA clone
UI-R-GO-uc-b-11-0-UI 3', mRNA sequence.
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Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
                             Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    On May 18, 1998 this sequence version replaced
. 3e-42;
15;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Contact: Soares, MB Program for Rat Gene Discovery and Mapping University of Iowa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /clone="UI-R-G0-uc-b-11-0-UI"
/clone_lib="UI-R-G0"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /organism="Rattus norvegicus"
          Pred. No. 3e-42
); Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /db_xref="taxon:10116"
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                                                                                                                                                                                                                                                                                                                                                   242 AAAGGAGTTGTTCAGGTCCCG 262
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            93.58;
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        Best Local Similarity 93.5
Matches 244; Conservative
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s constructed as described
Genome Research 6:
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Eukaryota Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (Dases 1 to 390)
Marra,M., Hilliar,L., Allen,M., Bowles,M., Dietrich,N., Dubuque,T.,
Gelsel,S., Kucaba,T., Lacy,M., Le,M., Martin,J., Morris,M.,
Schellenberg,K., Steptoe,M., Tan,F., Underwood,K., Moore,B.,
Thelsing,B., Wylie,T., Lennon,G., Soares,B., Wilson,R. and
                                                                                                                                                                                                                                                             1159 acacagetgtaateagececeaggaececacetteteateggeteeteetgeaageta 1218
                                                                                                                                                                                                                                                                                                                                                            cctgctctatacatggagacacacctggggccaccgctgaggggctctactggaccttca 1278
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Email: mouseest@watson.wustl.edu
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
MGI:216609
                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           W17583 390 bp mRNA EST 10-SEP-1996 mb75b01.rl Soares mouse p3NMF19.5 Mus musculus cDNA clone IMAGE:335209 5', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        203 ACGGCCGCCTGCCCTCAGAGCTGTCNCGTCTCCTCAACACCTCCACCCTGGCCTTGG
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/dev_stage="19.5 dpc total fetus"
/lab_host="DH10B (ampicillin resistant)"
/note="Vector: pT773D (Pharmacia) with a modified
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                                                                                                                                                                     Length 319;
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                                                                        1 others
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WashU-HHMI Mouse EST Project
Washington University School of MedicineP
4444 Forest Park Parkway, Box 8501, St. Louis,
Fax: 314 286 1810
                                                                                                                                                                        DB 48;
ck. The library was Lennon and Soares, G
                                                                                                                                                                  Score 207.2; DB 48
Pred. No. 8.7e-41;
0; Mismatches 19;
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                                                                        δ
oligo-dī track.
by Bonaldo, Lenno
791-806, 1996."
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1st strand cDNA
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                     6425 tcacctgaattggagcccctctgtaccatctgggcaacaaagaaacctaccagaggct-g 6483
                                                                                                                                                                                                                                                                                                               6484 ggcacaatgageteceacaccacagetttggtecacatgatggteacaettggatatae 6543
                                                                                                                                                                                                                  6365 aggtcotgcoggctaaactctaaggataggccatcctcctgctgggtcagacctggaggc 6424
                                                                                                                                                                                                                               280 GGCACAATGAGCTCCCCACAACCACACTITGGTCCACATGATGGTCACATGGTATAC 339
                                                                                                                                                                                             Gaps
                                                                                                                                                                                            3;
                                                                                                                                                                Query Match
Best Local Similarity 97.4%; Pred. No. 5.1e-39;
Matches 225; Conservative 0; Mismatches 3; Indels 3;
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oligo(dT) primer
polylinker;
was primed w
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Search completed: September 28, 1999, 15:38:38 Job time: 3306 sec

Run on:

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AA039053 445 bp mRNA EST 29-AUG-1996
m199007.rl Soares mouse embryo NbMEl3.5 14.5 Mus musculus CDNA
clone IMAGE:474733 5', mRNA sequence.
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AA039053.1
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VERSION
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                                                                      3; Search time 2095.87 Seconds (without alignments) 6270.900 Million cell updates/sec
                                                                                                                 GenCore version 4.5
Copyright (c) 1993 - 1998 Compugen Ltd.
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                                                                     September 28, 1999, 15:38:23
                                            nucleic search, using sw model
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em_est19:
gb_est1:*
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em_est7:
em_est8:
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A1579568 UI-R-G0-u
A1333812 qp93e12.x
A1670108 we65f03.x
W66776 me17b11.rl
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AA04291 M.Z.56f01.8
RR7407 YM88609.81
AA049288 WI-R-A0-a
AV010798 AV010798
AA049278 M.S.2020.1.7
AA055924 WI-R-A1-e
AI0233311 EST229999
AV011309 AV011309
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AI574687 UI-R-GO-
W17583 mb75b01.rl
                                                                                                Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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em_est22:*
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Match Length
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GI:1514788

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                                        8
                                                      Eukaryota: Metazoa: Chordata; Craniata; Vertebrata; Mammalia; Eutheria: Rodentia; Sciurognathi; Muridae; Murinae; Mus.

1 (bases I to 445)
Marra,M., Hillier,L., Allen,M., Bowles,M., Dietrich,N., Dubuque,T., Gelseb,S., Kucaba,T., Lacy,M., Le,M., Martin,J., Morris,M., Schellenberg,K., Steptoe,M., Tan,F., Underwood,K., Moore,B., Theising,B., Wylle,T., Lennon,G., Soares,B., Wilson,R. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               T 3/), on equal amounts of mRNA from 2 i3.5dpc and 2
14.5dpc embryos [total RNA provided by Minoru Ko, Wayne
State Univ., from 2 ]; double-granded cDNA was ligated t
Eco RI adaptors (Pharmacia), digested with Not I and
cloned into the Not I and Eco RI sites of the modified
pT/T3 vector. Library went through one round of
normalization, and was constructed by Bento Soares and
M.Fatima Bonaldo.

129 c 124 g 107 t
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                                                                                                                                                                                                                                                                                                                                                                                                                  th LLNL; contact the further information
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ä
                                                                                                                                                                                                                                                                          Contact: Marra M/Mouse EST Project
WashU-HMI Mouse EST Project
WashIngton University School of MedicineP
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  embryo NbME13.5 14.5"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 248; DB 27; Length 445;
Pred. No. 8.1e-51;
0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    'tissue_type="embryo"
'dev_stage="13.5-14.5dpc total fetus"
'lab_host="DH10B"
                                                                                                                                                                                                                                                                                                                                                                                        Email: mouseest@watson.wustl.edu
This clone is available royalty-free through
IMAGE Consortium (info@image.llnl.gov) for fu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Seq primer: -28M13 rev2 from Amersham High quality sequence stop: 441. Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                clone_lib="Soares mouse
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    i. .445
organism="Mus musculus"
                                                                                                                                                                                                             The WashU-HHMI Mouse EST Project Unpublished (1996)
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Best Local Similarity 99.6
Matches 259; Conservative
                                                                                                                                                                                                                                                                                                                                                       rel: 314 286 1800
Fax: 314 286 1810
                                        Mus musculus
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JOURNAL
COMMENT
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KEYWORDS
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                                                                                                                 AUTHORS
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Contact: Robert Strausberg, Ph.D.
Tel: (301) 496-1550
Email: Robert_Strausberg@nih.gov
Tissue Procurement: David N. Louis, M.D., Myrna R. Rosenfeld M.D.,
                                                                                                                                                               AI394468 462 bp mRNA EST 30-MAR-1999
tf79d12.xl NCI_CGAP_Brn23 Homo sapiens cDNA clone IMAGE:2105495 3'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Bonaldo, Ph.D. cDNA ibrary Arrayed by: Greg Lennon, Ph.D. CDNA ibrary Arrayed by: Greg Lennon, Ph.D. DNA Sequencing by: Washington University Genome Sequencing Clone distribution: UCI-CGAP clone distribution information can I found through the I.M.A.G.E. Consortium/LLNL at: www-blo.llnl.gov/bbrp/image/image.html
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                                                                                                                                                                                                                                                                                                                                                       Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 46.2)
NCI/NINDS-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute / National Institute of Neurological Disorders and Stroke, Brain Tumor Genome Anatomy Project (CGAP/BTGAP), Tumor Gene Index Unpublished (1998)
On Feb 17, 1998 this sequence version replaced gi:2887603.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       cDNA Library Preparation: M. Bento Soares, Ph.D., M. Fatima
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /clone-"IMAGE:2105495"
/clone_Lib-"KGI_CGAP_Brn23"
/tissue_type-"Giloblastoma (pooled)"
/lab_hogt-"DH108"
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Pred. No. 2.5e-44;
0; Mismatches 37
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Seq primer: -400P from Gibco
High quallity sequence stop: 454.
Location/Qualifiers
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/map="10; 1"
6604 aggagttgttcaggtcccga 6623
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86.8%;
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AI394468
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Best Local Simi
Matches 244;
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Gaps

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Length 474; Indels

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/organism="Homo sapiens"
/db_xref="taxon:9606"
/map="8839C02; 821G11; 4; 4p15.33-4p16.1; 4p15.33-4p16.1"
/clone="IMAGE:1705398"
                                                                                                                           acacagotgtaatcagococcaggacoccacocttotcatoggotoctcoctgcaagota 1218
                                                                                                                                                                                                                                                                             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalla; Butheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 466)
NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
NSI-OGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP), Unpublished (1997)
                                                                                                                                                                                                   1219 cctgotctatacatggagacacacctggggccaccgctgaggggctctactggaccttca 1278
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                                                                                                                                                           54 ACACAGCTGTGATCAGTCCCCAGGATCCCACGCTTCTATCGCTCCTCCTGCTGCTGCCA 113
                                                                                                                                                                                                                           Al161002 466 bp mRNA EST 26-OCT-1998 qb69g04.xl Soares_fetal_heart_NbHH19W Homo sapiens cDNA clone IMAGE:1705398 3', mRNA sequence.
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/sex="unknown"
                                                                                                                                                                                                                                                                                                                                                                                                                                  1399 gagacggcagcattctggctggctcctgcctctatgttggc 1439
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Pred. No. 2.5e-44;
0; Mismatches 37;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Contact: Robert Strausberg, Ph.D.
Tel: (301) 496-1550
Email: Robert_Strausberg@nih.gov
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     g3694307
AI161002.1 GI:3694307
                                                 Query Match
3.3%;
Best Local Similarity 86.8%;
Matches 244; Conservative
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TITLE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A1421423 474 bp mRNA EST 30-MAR-1999
fif25h01.x1 NCI_CGAP_Brn23 Homo sapiens cDNA clone IMAGE:2097265 3'
similar to SW:IL6B_MOUSE Q00560 INTERLEUKIN-6 RECEPTOR BETA CHAIN
PRECURSOR;, mRNA sequence.
                                                         1339 ccctggctaaccttaatgggtccaggcagtcaggagacaatctggtgtgtcacgccc 1398
NCI/NINDS-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute / National Institute of Neurological
Disorders and Stroke, Brain Tumor Genome Anatomy Project
(CGAP/BTGAP), Tumor Gene Index
Unpublished (1998)
On Apr 7, 1998 this sequence Version replaced gi:3034955.
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Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Contact: Robert Strausberg, Ph.D.
Tel: (301) 496-1550
Email: Robert_Strausberg@nih.gov
Tissue Procurement: David N. Louis, M.D., Myrna
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/db_xref="taxon:9606"
/clone="IxMAE:3097265"
/clone_lib="NCI_CGAP_Brn23"
/tlssue_type="qlioblastoma (pooled)"
/lab_host="DH108"
                                                                                                                                                                                                           Insert Length: 1664 Std Error: 0.00
Seg primer: -400P from Glbco
High quality sequence stop: 450.
Location/Qualifiers
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BASE COUNT ORIGIN

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DEFINITION

A1421423 LOCUS

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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 466)
NCI-CGAP http://www.ncbi.nlm.nlh.gov/nclogap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Contact: Robert Strausberg, Ph.D.
Tel: (301) 496-1550
Email: Robert_Strausberg@inh.gov
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
Insert Length: 1622 Std Error: 0.00
Seq primer: -400P from Gibco
High quality sequence stop: 466.
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qe44h04.xl Soares_fetal_lung_NbHL19W Homo sapiens cDNA clone
IMAGE:1741879 3', mRNA sequence.
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Unpublished (1997)
On Jan 19, 1998 this sequence version replaced g1:2151491.
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                                                                                                                                           43; Length 466;
                                                                      1 others
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Pred. No. 6.1e-44;
0; Mismatches 38;
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AI185780.1 GI:3736418
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Best Local Similarity 86.5%;
Matches 243; Conservative
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double-stranded cDNA was size selected, ligated to Eco RI adapters (Pharmacia), digested with Not I and Eco RI sites of a modified pT7T3 vector (Pharmacia). Library went through one round of normalization to a Cot = 5. Library constructed by Bento Soares and M.Fatima Bonaldo. This library was constructed from the same fetus as the fetal heart library, Soares
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AI185924 477 bp mRNA EST 29-OCT-1998 qe50c05.xl Soares_fetal_lung_NDHL19W Homo sapiens cDNA clone IMAGE:1742408 3' similar to TR:Q16354 Q16354 PROLACTIN RECEPTOR ;,
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National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
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Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 477)
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Unpublished (1997)
On Feb 17, 1998 this sequence version replaced gi:2150926.
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                                                                                                                                                                                                                                                                        Length 466;
                                                                                                                                                                                     1 others
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Pred. No. 6.1e-44;
0; Mismatches 38; Indels
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/dev_stage="19 weeks"
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Tel: (301) 496-1550
Email: Robert_Strausberg@nih.gov
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/clone="IMAGE:1742408"
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A1185924.1 GI:3736562
                                                                                                                                                                                                                                                                      Query Match 3.3%;
Best Local Similarity 86.5%;
Matches 243; Conservative (
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AI185924
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AC005528 Mus musculus AC005528 Mus muscu L78823 Mycobacter L78823 Mycobacter L78823 Hycobacter L788242 H.saplens D X8752 H.saplens G AL008583 Human DNA E AL031317 Streptomy DB6087 Human DNA AC007226 Homo sapland AC005088 Homo saplacond B AC0468 Homo saplacond B AC06508 Homo saplacond B AC06508 Homo saplacond B AC06508 Homo saplacond B AC06508 Homo saplacond B AC064166 Homo saplacond B AC064166 Homo saplacond B AC064166 Homo saplacond B AC064166 Homo saplacond B AC064166 Homo saplacond B AC064166 Homo saplacond B AC064166 Homo saplacond B AC064166 Homo saplacond B AC064166 Homo saplacond B AC064166 Homo saplacond B AC064166 Homo saplacond B AC064166 Homo saplacond B AC064166 Homo saplacond B AC064166 Homo saplacond B AC064166 Homo saplacond B AC0641643 Homo saplacond B AC064164 Homo saplacond B AC064164 Homo saplacond B AC064164 Homo saplacond B AC064164 Homo Sapla

Title: Perfect score:

Run on:

Sequence:

Scoring table:

Database :

Searched:

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unclassified.

1 (bases 1 to 35)
Nicola,N.A., Fabri,L., Farley,A., Nash,A., Willson,T., Rakar,S., Zhang,J., Alexander,W., Hilton,D.J., Kojima,T., Maeda,M. and Kikuchi,Y.
A NOVEL HARMOPDIFIIN RECEPTOR AND GENETIC SEQUENCES ENCODING SAME Patent: WO 9811225-A 19-MAR-1998;
NICOLA NICOS ANTONY (AU)
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ALIGNMENTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 30 from Patent W09811225.
A70400

    .35
    /organism="unidentified"
    /db_xref="taxon:32644"
    14 c 14 g

MMBPRADPR
AC00528
MLCLG58
MSGB13GS
STWTLP
HSDNASGAT
HSNL2273D
HS327J16
HS294778
HSDNASTAO
PPPQQABCF
                                                                                                                                                                                                                                                                                                                                                                 RATBCCAPA
CNS0000H
AC002059
AB014348
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AC004463
MTCY164
AF126478
CTRIDITS1
HSA16521
HSEWSGAR
AC000026
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D86087801
B6087801
AC07226
AB015626
A70382
A70392
AC004867
AC005488
HS436C18
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ACO06014
RHMHSNAD
RMNODEFG
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AF127374
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                                                                September 28, 1999, 16:46:12; Search time 3489.95 Seconds (without alignments) 31.895 Million cell updates/sec
      GenCore version 4.5
Copyright (c) 1993 - 1998 Compugen Ltd.
                                                                                                                               1 agctggcgcgcctcccgggcggatcgggagcccac 35
                                                                                                                                                                        679419 seqs, 1590154680 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SUMMARIES
                                             nucleic - nucleic search, using sw model
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query
Match Length DB ID
                                                                                                         US-09-037-657-30
35
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gb_pr4:*
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Y07848 Homo sapien AC000026 Homo sapi M77245 R. norvegicu AL049836 Homo sapi AC002059 Homo sapi AB014348 Rhodococc U44891 Rhodococcus

AL031035 Streptomy M64859 S.lividans AF127374 Streptomy AF031612 Oryctolag

07-MAY-1999

PAT

BASE COUNT ORIGIN

A70400 Sequence 30

5 A70400

35

100.0

Score 35

Result No.

Description

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Gaps

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RESULT 2 MMBPRADPR/c

Matches

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ORGANISM

VERSION KEYWORDS SOURCE

REFERENCE

AUTHORS

TITLE

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ACOO5528 195923 bp DNA HTG 29-MAX-1999
Mus müsculus, WORKING DRAFT. SEQUENCE, 7 ordered pleces.
ACOO5528
                                                                                                                                                                                                                                                                                                                                                                Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 195923)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 195923;
     Length 3885;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Fang, F., Ying, F., Pan, H., Dumanski, J. and Roe, B.A. Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                     Fang, F., Ying, F., Pan, H., Dumanski, J. and Roe, B.A.
Mus musculus PAC Clone 493n6 In MDR Region
                                            Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        contig of 30014 bp in length
gap of unknown length
contig of 92336 bp in length
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     Score 22.2; DB 12;
Pred. No. 1.9e+02;
0; Mismatches 8;
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Pred. No. 69;
0; Mismatches 8;
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/db_xref="taxon:10090"
50392 a 48306 c 47825 g 48972 t
                                                                               1 agctggcgcgctcccgggcggatcgggagcccac 35
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HTG; HTGS_PHASE2.
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     Query Match 63.4%;
Best Local Similarity 77.1%;
Matches 27; Conservative
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Best Local Similarity 77.1%;
Matches 27; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Submitted (11-SEP-1996) C. Guilbaud, Dept. Of Molecular Medicine, Clinical Genetics Unit, Karolinska Hospital, Bullding L-6, S-171 76 Stockholm, SWEDEN
                                          ö
                                                                                                                                                                                                                                                                                                                                                                                                                                              Characterization of a mouse homologue for human beta-prime-adaptin
gene; CDNA sequence, genomic structure and chromosomal localization
Unpublished
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IVGEYAERIDNADELLESFLEGFHDESTQVQLQLLTAIVKLFLKKPTETGELVQQVLS
LATQDSDNPDLRDRGYIYWRLLSTDPVAAKEVVLAEKPLISEETDLIEPTLLDELLCY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SVLKMEPLNNLQVAVKNNIDVFYFSTLYPLHYLFVEDGKMDROMFLATWKDIANENEA
OFOIRDCPLNTEAASNKLQSSNIFTVAKRNVEGODMLYQSLKLTNGIWYLAELRIQPG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   YATLIKKLAPPLVTLLSAEPELQYVALRNINLIVQKRPEILKHEMKVFFVKYNDPIYV
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                                                                                                                                                                                                                                                                                                                                                                                                                 Guilbaud, C., Fransson, I., Clifton, S.W., Roe, B.A., Carter, N. and
Dumanski, J.P.
                                          Gaps
                                                                                                                                                                                                                                                                                                                                                            Eukaryota; Metazoa; Chordata; Vertebrata; Mammalia; Eutheria;
Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 3885)
                                                                                                                                                                                                            10-SEP-1997
                                          ö
     Length 35;
                                                                                                                                                                                              MMBPRADPR 3885 bp mRNA ROD.
M.musculus mRNA for beta-prime-adaptin protein.
YO7919
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clone_lib="whole mouse embryo"

'clone_lib="mouse brain"
 100.0%; Score 35; DB 5; 100.0%; Pred. No. 0.082;
                                                                           1 agctggcgcctcccgggcggatcggggagccac 35
                                                                                               1 AGCTGGCGCCCTCCCGGGCGGATCGGGAGCCCAC 35
                                     0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /organism-"Mus musculus"
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|b_xref="PID:e266088"
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                                                                                                                                                                                                                                                                                  GI:2398719
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Guilbaud, C.
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                                      35; Conservative
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source

FEATURES

REFERENCE AUTHORS TITLE JOURNAL

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Gaps

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BASE COUNT ORIGIN

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SOURCE

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'clone="cosmid L458"
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                                                                                                                                                                                 CDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eiglmeier,K., Honore,N., Woods,S.A., Caudron,B. and Cole,S.T.
Use of an ordered cosmid library to deduce the genomic organization
of Mycobacterium leprae
Mol. Microbiol. 7 (2), 197-206 (1993)
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Usually the highest scoring match found by fasta -o is given for CDS which show significant similarity to other CDS in the database. The position of possible ribosome binding site sequences are given where these have been used to deduce the initiation codon. All CDS over 100 codons have been analysed. Gene prediction is based on positional base preference in codons especially where there is an increase in the observed/expected third position G + C. CAUTION. We may not have predicted the correct initiation codon. Where
                                                                                                                                                                                                                  acps; CoA.apo-[Acyl Carrier Protein]; DNA polymerase III alpha chain; dnaE; fas; ileS; ilvA; isolencyl-tRNA synthetase; L-asparaginase; L-glutaminase; lipoprotein signal peptidase; lspA; oxidoreductase; pseudogene; pseudouridine synthase; RLEP element; rluC; threonine dehydratase blosynthetic; type I fatty acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Work in Paris is supported by the Heiser Trust, the Association Francaise Raoul Follereau and the Groupement de Recherches et des Etudes des Genomes (GIP-GREG).
Details of M. leprae sequencing at the Sanger Centre are available
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        possible we choose an initiation codon (atg, gtg, or ttg) which is preceded by an upstream ribosome binding site sequence (optimally 5-13bp before the initiation codon). If this cannot be identified
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            on the World Wide Web. (URL, http://www.sanger.ac.uk/Projects/)
CDS are numbered using the following system eg MLCB33.01c. ML (M. leprae), cB33 (cosmid name), .01 (first CDS), c (complementary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The Sanger Centre is funded to complete the sequence of M. leprae by the Heiser Program for Research in Leprosy and Tuberculosis of The New York Community Trust.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The more significant matches with motifs in the PROSITE database are also included but some of these may be fortuitous. The length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Submitted (15-MAR-1998) Mycobacterium leprae sequencing project, Sanger Centre, Wellcome Trust Genome Campus, Hinxton, Cambridge CB10 1SA E-mail: barrell@sanger.ac.uk Cosmids supplied by Dr. Stewart T. Cole, [3] Unite de Genetique Moleculaire Bacterienne, Institut Pasteur, 28 rue du Docteur Roux, 75724 París Cedex 15, France Requests for cosmids should be sent to Karin Eiglmeier (kei@pasteur.fr)
                                                                         24-MAR-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        5-13Dp before the initiation codon). If this cannot be ident we choose the most upstream initiation codon.
IMPORTANT: This sequence MAY NOT be the entire insert of the sequenced clone. It may be shorter because we only sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            sequenced clone. It may be shorter because we only sequence overlapping sections once, or longer, because we arrange for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              3 (bases 1 to 43839)
James, K.D., Parkhill, J., Barrell, B.G. and Rajandream, M.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Bacteria; Firmicutes; Actinobacteria; Actinobacteridae; Actinomycetales; Corynebacterineae; Mycobacteriaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         small overlap between neighbouring submissions. Location/Qualifiers
                                                                         BCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /organism="Mycobacterium leprae"
                                              миссь458 43839 bp DNA
Mycobacterium leprae cosmid L458.
AL049478
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (bases 1 to 43839)
seeger, K.J. and Harris, D.
                                                                                                                                                                                                 GI:4539121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (bases 1 to 43839)
                                                                                                                                                                                                                                                                                                                                                                                                                        Mycobacterium leprae
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mycobacterium leprae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           43839
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             fycobacterium.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                npublished
                                                                                                                                                                                                 AL049478.1
                                                                                                                                                                                                                                                                                                                                                                                                synthase
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                                                                                             DEFINITION
ACCESSION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               source
                                                                                                                                                                                                                                                                                                                                                                                                                                                         ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AUTHORS
JOURNAL
REFERENCE
AUTHORS
TITLE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AUTHORS
TITLE
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MEDLINE
REFERENCE
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KEYWORDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     REFERENCE
RESULT
MLCL458
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COMMENT

/db_xref="taxon:1769"

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translation="MQSLRRHFTCRSTFYHGYISLPAQRAVVRTSTADTHLDSTMTGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AGENORVTNOHPAVDÖVGRLSGSVTVTPAPRSVGRTVŠPADDLLDDSFCHSGTNPFLD
QVAVFPSADLKPQLRNTAKFRAVDHGHEVQPWLDFVAMVIPP"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   'translation="MLEKNRPQIFDSFDRILKARSPEAWLSRRKEIDLHSTIFEYTLK
JABEKRRNPSDDIWRTLASAVITGNDEKPFRLPANELEFFFVLTFTGSNTAKHTTGYW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /translation-"MOLAPEWRQGGEPVFIIAVKVYTILLSGHIONGRTSSHRIEYSL
FLYNHRHLCLSSSEDGQVGGKSDDEPTRREPVSRQRNTGRSELPF"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        unknown function, N-terminus similar to internal sequence of YP22_MYCTU (EMBL:280226) Rv0778 (MTCY369.22) M. tuberculosis hypothetical protein (414 aa), fasta scores; opt: 102 2 <- core: 189.2 E(): 0.0031, 31.4% identity in 102 aa overlap"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /note="MLCB458.03c, hypothetical protein, len: 89 aa;
unknown function, improbable CDS based on frame analysis"
                                                                                                                                                                    aa;
1. .569
/note="overlap with cosmid B1701 from 19932 to 20500"
                                                                                                complement(97...531)
/gene="MLCB485.01c"
/note="MLCB485.01c"
/note="MLCB485.01c, hypothetical protein, len: 114 unknown function, possible CDS based on amino acid composition and frame analysis"
/codon_start=1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  unknown function, possible CDS based on amino acid composition and frame analysis"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             note-"MLCB458.02c, hypothetical protein, len: 127
                                                                                                                                                                                                                                                                                                                product="hypothetical protein MLCB485.01c"
protein_id="CAB39566.1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  product="hypothetical protein MLCB458.02c"
protein_id="CAB39567:1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        label-MLCB458.03c
product-"hypothetical protein MLCB458.03c"
protein_id-"CAB39568.1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 protein MLCB458.04c"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             'gene="MLCB458.04c"
'note="MLCB458.04c, hypothetical
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TAGVHHESRPDKTIPRSGSIAPQRR"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              complement(1581. .1850)
/gene="MLCB458.03c"
/note="MLCB458.03c, hypo
                                                                                                                                                                                                                                                                                                                                                                   db_xref-"PID:e1419859"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                'db_xref="PID:g4539123"
                                                                                                                                                                                                                                                                                                                                                                                           'db_xref-"PID:94539122"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           'db_xref="PID:94539124"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          .2110)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       'gene-"MLCB458.02c".
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       db_xref-"PID:e1419860"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /protein_id="CAB39568...
/db_xref="PID:e1419861
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            .1210)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 'product-"hypothetical
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /db_xref-"PID:e1419862
                                                                                                                                                                                                                                                                                                                                                                                                                        'db_xref-"GI:4539122"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            'protein_id="CAB39569
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /db_xref="PID:q453912
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          'db_xref="G1:4539123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /db_xref="GI:4539124
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /db_xref="GI:4539125
                                                                gene="MLCB485.01c"
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                                                                                                                                                                                                                                                                                          label-MLCB485.01c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            label-MLCB458.02c
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    'gene="MLCB458.02c
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                                                                                                                                                                                                                                                               transl_table=11
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  transl_table=11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       complement(1841.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 complement(158]
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               complement(827
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               complement(827
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         codon_start=1
                                                        complement (9)
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9

'gene="MLCB458.05"

gene

SGS

codon_start=1/transl_table=11

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Eiglmeier, K., Honore, N., Woods, S.A., Caudron, B. and Cole, S.T. Use of an ordered cosmid library to deduce the genomic organization of Mycobacterium leprae Mol. Microbiol. 7 (2), 197-206 (1993)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /tissue_lib="Lorist 6"
/note="The.liver of the armadillo was used to isolate the
Mycobacterium leprae."
i 13528 c 11679 g 8223 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    clone. Coding sequences larger than 60 amino acids were predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               An attempt was
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Beaver St., Waltham, MA, 02154. Please contact Doug Smith (smith@cric,com) for further information. The sequence represents
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          This sequence was generated by the Genome Sequencing Center at
Genome Therapeutics Corporation (Collaborative Research Division),
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  the presence of a Shine-Dalgarno sequence, or overlapping orf tha suggested translational coupling. It is possible that the actual
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Smith, D.R., Richterich, P., Rubenfield, M., Butler, C., Lee, H.-M., Swith, D.R., Richterich, P., Rubenfield, M., Butler, C., Lee, H.-M., K., Q. Gunderson, K., Chung, M., Maher, J. K., Deloughery, C., Aldrich, T., Imrich, J., Tulig, C., Smyth, A., Drill, S., Avruch, A.S., Rice, P., Abendschan, K., Aldredge, T., DeLoughery, C., Kirst, S., Safer, H., Connelly, S., McDougall, S., Eiglmeter, K., Bergh, S., Cole, S., Robison, K., Jaehn, L., Gryan, G., Church, G.M. and Mao, J. Prepublication submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SIMILP 2188 bp DNA BCT 07-FEB-1999 Streptomyces erythraeus gene for trypsin-like protease, complete
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The sequence may not represent the entire cloned insert of
                                    Mycobacterium leprae (clone: cosmid B13) (tissue library: Lorist
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        insert.of a Lorist 6 cosmid clone from a mapped set of clones constructed from M. leprae genomic DNA isolated from armadillo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  cosmid if an overlapping region was previously sequenced from
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                to locate the most probable start site based on codon usage,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ó
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                                                                                                                               Mycobacterium leprae
Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
Actinomycetales; Corynebacterineae; Mycobacteriaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               the basis of codon usage and homology information.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Indels
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/db_xref="taxon:1769"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                62.3%; Score 21.8; DB 1;
llarity 78.8%; Pred. No. 1.4e+02;
Conservative 0; Mismatches 7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /organism-"Mycobacterium leprae"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Db 17290 GCTGGCGCCACCCCGGCACATCGCAAGTCCA 17258
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          site differs from the one selected.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2 gctggcgcgctcccgggcggatcgggagcca 34
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /clone-"cosmid B13'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1. .42923
                                                                                                                                                                                                                                                                       Mycobacterium.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Best Local Similarity
Matches 26; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 9493 a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       homology,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 93188700
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D30760
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /note="MLCB458.06, fas, probable type I fatty acid
synthase, len: 3076 aa; similar to many eubacterial and
sukaryotic FAS e.g. TR:059497 (EMBL:X87822) Brevibacterium
ammoniagenes FAS (3063 aa), fasta scores; opt: 5361
z-score: 5527.0 E(): 0, 44.3% identity in 3106 aa overlap.
N-terminus shows similarity to FASL_CANAL (EMBL:X74952)
candida albicans FAS beta subunit (2037 aa) (27.3%
identity in 1928 aa overlap) and C-terminus to FAS2_CANAL
(EMBL:L29063) Candida albicans FAS alpha subunit (1885 aa)
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KGYTADWLGGATAGLRHAQRGVQLHTAAGGPVSAPIYASIDSNPTYEQYKQQVAPYLR
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RCDTTSYRVDSFDSDFVIDSHQSLSIVAVERSAQIAKQLAISGCS"
                                                                                                                                                                                     3625. .4344

Agone="McCB458.05"

/note="McCB458.05"

/note="McCB458.05"

note="McCB458.05"

note="McCB458.05
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          translation="MSVSRRDVLKFATVTPGLLGLGVAAAALCAVPASTAGSLGTLLD"
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/protein_id="CAB39571.1"
/db_xref="PID:e1419864"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /product="hypothetical protein MLCB458.05"
/protein_id="CAB39570.1"
/db_xref="PID:e1419863"
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Pred. No. 1.3e+02;
0; Mismatches 7; Indels
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table-11

Query Match Best Local Similarity 78.8%; Matches 26; Conservative

GI:1377768

91377768 L78823.1

NID VERSION

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LOCUS DEFINITION RESULT 5 MSGB13GS/c

ACCESSION

VGGVGVDVNT ILKPQFGQWA'

.14186

gene

CDS

/gene="fas" 4956. .1418 4956.

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NID VERSION KEYWORDS SOURCE ORGANISM

REFERENCE AUTHORS TITLE JOURNAL

us-09-037-657-30.rge

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Direct Submission
Submitted (01-APR-1993) Zabarovsky E., Karolinska Institute, Tumor
Biology, S-104 01 Stockholm, Sweden
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Direct Submission
Submitted (03-WAY-1995) Zabarovsky E.R., Microbiology and
Tumorblogy Center, Karolinska Institute, P.O. Box 280, Stockholm,
S-171 77, SWEDEN
                                 1 (bases 1 to 239)
Zabarovsky,E., Kashuba,V., Pettersson,B., Petrov,N., Zakharyev,V., Gizatullin,R., Lebedeva,T., Bannikov,V., Erlandsson,R., Uhlen,M., Kisselev,L. and Klein,G.
Shot-gun sequencing strategy for long range genome mapping: first results
Eukaryota; Metazoa; Chordata; Vertebrata; Mammalla; Eutheria;
Primates; Catarrhini; Hominidae; Homo.
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Eukaryota; Metazoa; Chordata; Vertebrata; Mammalia; Butheria;
Primates; Catarrhini; Hominidae; Homo.
[Dases 1 to 239)
Zabarovsky, E.R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 239;
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H.saliens genomic DNA (chromosome 3; clone NL2273D).
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Pred. No. 6.8e+02;
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Pred. No. 6.8e+02;
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                                                                                                                                                                                                                                                                                                                                      /chromosome="chromosome 3"
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                                                                                                                                                                                                                                                                                               /organism="Homo sapiens"
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/cell_line="MCH903.1"
/clone_lib="NL2"
a 75 c 52 g
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80.6%;
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llarity 80.6%;
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Zabarovsky, E.R.
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Matches 25; Conserve
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Nagamine-Natsuka,Y., Norioka,S. and Sakiyama,F.
Molecular cloning, nucleotide sequence, and expression of the gene encoding a trypsin-like protease from Streptomyces erythraeus J. Biochem. 118 (2), 338-346 (1995)
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ATILGWGNTSEGGQQADHLQKATVPVNSDDTCKQAYGEYTPDAMVCAGVPEGGVDTCQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GGEDANVODHPFTVALVTPDGQQFCGGTLAAPNKVVTAAHCTVGSQPADINVVSGRTV
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                                                                                                                                                                                          Submitted (18-MAY-1994) to the DDBJ/EMBL/GenBank databases. Sh
Norloka, University of Osaka, Institute for protein research;
Yamadaoka, Suita, Osaka 565, Japan (Tel:06-879-8618,
Fax:06-876-2333)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
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                                                        Saccharopolyspora erythraea
Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
Actinomycetales; Pseudonocardineae; Pseudonocardiaceae;
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/organism="Saccharopolyspora erythraea"
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1049. .1867
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Pred. No. 3.8e+02;
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                                                                                                                                                                                                                                                                                                                                                                                                                                       Submitted (18-May-1994) to DDBJ by:
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University of Osaka
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06-876-2533.
Location/Qualifiers
                     trypsin-like protease.
Streptomyces erythraeus DNA
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H.sapiens DNA sequence.
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                                                                                                                                                                                                                                                                                                         Published (1996)
                                                                                                                                                                          Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Suita, Osaka 565
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Shigemi Norioka
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Yamadaoka
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Homo sapiens
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source

CDS

FEATURES

JOURNAL REFERENCE AUTHORS TITLE

JOURNAL MEDLINE

COMMENT

REFERENCE AUTHORS

Gaps

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01-JUL-1996

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/organism="Homo sapiens"
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/clone="NL2273D"
                                                                                                                                                                                                                                                                                      Gaps
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                                                                                                                                                                                                                                            Length 239;
                                                                                                                         /note="genomic DNA surrounding NotI sites"
75 c 52 g 56 t 2 others
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LOCUS DEFINITION ACCESSION RESULT 7 HSDNASGAT/C

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VERSION KEYWORDS SOURCE ORGANISM

BASE COUNT ORIGIN

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FEATURES

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/note="match: cDNA AB010031; match: ESTS AA829582 AA675540 AA270574 AI122433 AA560435 AA007825 AA796578 AA681606 AA270574 AI122433 AA560435 AA007825 AA796578 AA681606 AA322956 H55197 AA349185 AA895042 AA431647 AA278275 AA039963 N42713 AA076578 T48120 W01618 AI182462 AI084123 AA675556 AA427946 AA31283 AA076575 AA13283 AA076575 AA13283 AA076578 AA31283 AA076578 AA31283 AA076578 AA427946 AI287576 AA31283 AA076578 AA31283 AA076578 AA57878 AA076578 AA57878 AA076578 AA781283 AA076578 AA78787 AA78787 AA78787 AA78787 AA78787 AA78787 AA78787 AA78787 AA78787 AA78787 AA78787 AA78787 AA78787 AA78787 AA78787 AA78787 AA78787 AA78787 AA78787 AA78787 AA78787 AA78787 AA78787 AA78787 AA78787 AA78787 AA78787 AA78787 AA78787 AA78787 AA78787 AA78787 AA78787 AA78787 AA78787 AA78787 AA78787 AA78787 AA78787 AA78787 AA78787 AA78787 AA78787 AA78787 AA78787 AA78787 AA78787 AA78787 AA78787 AA78787 AA78787 AA78787 AA78787 AA78787 AA78787 AA78787 AA78787 AA78787 AA78787 AA78787 AA7878 AA7877 AA7878 AA7877 AA7878 AA7877 AA7878 AA7877 AA7878 AA7878 AA7877 AA7878 AA7878 AA7878 AA7878 AA7878 AA7878 AA7877 AA7878 AA7878 AA7878 AA7878 AA7878 AA7878 AA7878 AA7878 AA7878 AA7878 AA7878 AA7878 AA7878 AA7878 AA7878 AA7878 AA7878 AA7878 AA7878 AA7878 AA7878 AA7878 AA7878 AA7878 AA7878 AA7878 AA7878 AA7878 AA7878 AA7878 AA7878 AA7878 AA7878 AA7878 AA7878 AA7878 AA7878 AA7878 AA7878 AA7878 AA7878 AA7878 AA7878 AA7878 AA78 AA7878 AA7878 AA7878 AA7878 AA78 AA7878 AA7878 AA7878 AA7878 AA7878 AA7878 AA7878 AA7878 AA7878 AA787 AA787 AA787 AA787 AA787 AA787 AA78 AA787 AA787 AA78 AA787 AA787 AA787 AA787 AA787 AA787 AA787 AA787 AA787 AA787 AA787 AA787 AA787 AA787 AA787 AA787 AA787 AA787 AA787 AA787 AA787 AA787 AA787 AA787 AA787 AA787 AA787 AA787 AA787 AA787 AA787 AA787 AA787 AA787 AA787 AA787 AA787 AA787 AA787 AA787 AA787 AA787 AA787 AA787 AA787 AA787 AA787 AA787 AA787 AA787 AA787 AA787 AA787 AA787 AA787 AA787 AA787 AA787 AA787 AA787 AA787 AA787 AA787 AA787 AA787 AA787 AA787 AA787 AA787 AA787 AA787 AA787 AA787 AA787 AA787 AA787 AA787 AA787 AA787 AA787 AA787 AA78
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(FSNNNESAAKMIKETMDKKFGSSWHVVIGEGFGFEITHEVKNLLYLYFGGTLAVCVM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /product="dJ327J16.1 (human ortholog of mouse outer arm
Dynein light chain 4)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    complement(join(6902. .7066,8379. .8462,10116. .10184))
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ortholog of mouse outer arm
                                                                                                                                                                                                                                                                                                                                     3819. .3897
/nocte="L2 repeat: matches 2447. .2528 of consensus"
4507. .4583
/note="MIR repeat: matches 103. .182 of consensus"
5473. .5697
/note="L2 repeat: matches 2486. .2709 of consensus"
complement(join(5961. .7066,8379. .8462,10116. .10323,
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'note="L2 repeat: matches 2677. .2707 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    .2698 of consensus"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /note-"Alusx repeat: matches 1. .312 of consensus"
14570. .14681
                                                                                      .2709 of consensus"
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7980, .8010
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     11654. .11835
//note="MIR repeat: matches 4. .210 of consensus"
11960. .12265
                                                                                                                                         109. .1104
note="MIR repeat: matches 90. .144 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /note="MIR repeat: matches 3. .117 of consensus"
14682. .14993
                                                                                                                                                                                                                                                                                             repeat: matches 3. .181 of consensus"
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                                                                                                                                                                                                                                .231 of
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 note="match: proteins 054793 044229" codon_start=1
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/note="L2 repeat: matches 1478.
11159. .11292
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/note="MIR repeat: matches 111.
11253. .11298
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1654. .11835
                                                                                                                                                                                                   240. .2347
note-"MIR repeat: matches 123.
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                                                         note="L2_repeat: matches 2615.
109. .2162
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nein light chain 4)"
rrotein_id="CAA15429.1"
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'product="dJ327J16.1 (huma
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/gene="da327J16.1"
5961..6207
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                     copies 4 mer
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'gene="dJ327J16.1"
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/note="MIR re
                     note="21
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        requests: clonerequestesanger.ac.uk
On Jan 16, 1999 this sequence version replaced gi:3892846
During sequence assembly data is compared from overlapping clones.
Where differences are found these are annotated as variations
together with a note of the overlapping clone name. Note that the
variation annotation may not be found in the sequence submission
corresponding to the overlapping clone, as we submit sequences with
only a small overlap as described above.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           IMPÓRTANT: This sequence is not the entire insert of clone 327J16. It may be shorter because we only sequence overlapping sections once, or longer because we arrange for a small overlap between neighbouring submissions.

The true left end of clone 150C2 (AL022318) is at 111647 in this sequence. The true right end of clone 779B17 (AL021806) is at 50467
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         This sequence has been finished according to sequence map criteria as follows. An attempt is made to resolve all sequencing problems, such as compressions and repeats, but not necessarily within known annotated human repeat sequence elements (e.g. Alu). Where the sequence is ambiguous, there is an annotation using the 'unsure'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ALO08583.1 GI:4160195
HTG; CHROMODOX; CpG island; Neuronal Pentraxin Receptor; outer arm
Dynein light chain 4.
                                                                                                                                                                                                                                                                               HS327J16 111746 bp DNA PRI 15-JAN-1999 Human DNA sequence from clone 327J16 on chromosome 22ql2.3-13.2. Contains three novel genes: the human ortholog of mouse outer arm Dynein light chain 4, the human ortholog of rat Neuronal Pentraxin Receptor and a novel member of of the CHROMODOX protein genes family. Contains ESTs, STSs, a GSS and putative CpG islands,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         32716 is from the library RCCI3 constructed at the Roswell Park Cancer Institute by the group of Pieter de Jong. For further details see http://bacpac.med.buffalo.edu/ VECIOR: pcrPAC2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Submitted (28-DEC-1998) Sanger Centre, Hinxton, Cambridgeshire, CB10 1SA, UK. E-mail enquiries: humquery@sanger.ac.uk Clone
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota; Metazoa; Chordata; Vertebrata; Mammalia; Eutheria;
Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 111746)
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/note="129 copies 2 mer ca 58% conserved"
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/note="71 copies 4 mer tcca 828 885. .1142
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/db_xref="taxon:9606"
/chromosome="22"
                                    ggcgcgcctcccgggcggatcggggagcccac 35
                                                                           Location/Qualifiers
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149. .325
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            complete sequence.
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ote="figger3b repeat: matches 992. .1231 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                               649. .18795
ote="Tigger3b repeat: matches 847. .992 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 te="Tigger3b repeat: matches 584. .847 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    31. .zooo4
te*"Tigger3b repeat: matches 1. .584 of consensus"
                                                                                                                                                                                                         067 . 17413

0cte="L2 repeat: matches 2289. .2620 of consensus"

484 . 17605
                                                                                                                                                                                                                                                              te-"FLAM_C repeat: matches 2. .124 of consensus" 89. .18022
                                                                                                                                                                                                                                                                                    889. 18022
ote="L2 repeat: matches 1739. .1875 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ote="L2 repeat: matches 1618. .2707 of consensus" 599. .26729 of consensus" ote="MLTIJ repeat: matches 356. .499 of consensus" 851. .27002
                                                                                                              .2747 of consensus"
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19. .23559 .23559
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             repeat: matches 550. .691 of consensus'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       .2682 of consensus"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       te="Alusq repeat: matches 1. .313 of consensus" 37. .20604
                                                                                                                                                                                         .298 of consensus"
                                                                                                                                                                                                                                                                                                                                                           339. .18648
Ote-"AluSx repeat: matches 1. .311 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                            .312 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           te="AluSx repeat: matches 1. .297 of consensus"
                                                                                                      note="L2 repeat: matches 2678. .2747 of consensus
5513. 16720
note="MIR repeat: matches 24. .249 of consensus"
 .313 of consensus
                                       .149 of consensus
                                                                     note-"MIR repeat: matches 21. .207 of consensus"
6498. .16566
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ote "MIR repeat: matches 38. .146 of consensus" 22069
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te-"MIR repeat: matches 89. .222 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    repeat: matches 1. .550 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  79. .21776
te="match: CpG island clones 279875 279876"
60. .21158
note="Alusg repeat: matches 2.
14994. 15027
note="MIR repeat: matches 116.
                                                                                                                                                                                       ote="AluJb repeat: matches 1.
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te-"LTR8 re
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Query Match 60.6%; Score 21.2; DB 9; Length 111746; Best Local Similarity 76.5%; Pred. No. 1.6e+02; Matches 26; Conservative 0; Mismatches 8; Indels 0; Gaps

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ö Homo sapiens
Eukaryota; Metazoa; Chordata; Vertebrata; Mammalia; Eutheria;
Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 315)
Gizatuilin,R.Z., Kashuba,V.I., Protopopov,A.I. and Zabarovsky,E.R. Submitted (01 APR-1993) Zabarovsky E., Karolinska Institute, Tumor Biology, S-104 01 Stockholm, Sweden Location/Qualifiers Zabarovsky, E., Kashuba, V., Pettersson, B., Petrov, N., Zakharyev, V., Gizatullin, R., Lebedeva, T., Bannikov, V., Erlandsson, R., Uhlen, M., Kisselev, L. and Klein, G.
Shot-gun sequencing strategy for long range genome mapping: first Submitted (18-APR-1997) Zabarovsky B.R., Karolinska Institute, Microbiology and Tumorbiology Center, P.O. Box 280, Stockholm, Gaps 02-DEC-1997 01-JAN-1995 Sukaryota; Metazoa: Chordata; Vertebrata; Mammalia; Butheria; rimates; Catarrhini; Hominidae; Homo. /lab_host="mouse/human microcell hybrid MCH903.1" ö Length 315; Indels 1S294778 315 bp DNA PRI (clone NLIA177R). /note="sequence surrounding NotI site" 106 c 127 g 36 t 'clone_lib="NL1 Not! linking library PRI Query Match 60.6%; Score 21.2; DB 10; Best Local Similarity 76.5%; Pred. No. 7.3e+02; Matches 26; Conservative 0; Mismatches 8; 133 GCAGCCGCGACCCCCGGGGCGCTCCGGAGCCCAC 166 2 gotggcgcgcctcccgggcggatcggggagcccac 35 .315
 /organism="Homo sapiens" /organism="Homo sapiens" /db_xref="taxon:9606" Microbiology and Tumorbiology S-171 77, Sweden. /db_xref="taxon:9606" /chromosome="3" Location/Qualifiers DNA clone-"NL1A177R" HSDNASIAO 348 bp H.saplens DNA sequence. 222459 GI:2661883 2 (bases 1 to 315) Zabarovsky, E.R. GI:608928 2 (bases 1 to 348) Zabarovsky, E. Direct Submission (bases 1 to 348) Homo sapiens Jnpublished 92661883 294778.1 46. a 222459.1 human. human. misc_feature RESULT 11 HSDNASIAO/C LOCUS DEFINITION ACCESSION NID VERSION KEYWORDS SOURCE ORGANISM DEFINITION ACCESSION NID ORGANISM source BASE COUNT REFERENCE AUTHORS JOURNAL REFERENCE AUTHORS TITLE JOURNAL REFERENCE AUTHORS TITLE VERSION KEYWORDS SOURCE REFERENCE AUTHORS JOURNAL 1SZ94778 FEATURES EATURES TITLE à

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OEPSWNDQQOALAQQLQPATLPLDQAMELLWQAKLAGHSSDYLPQLQGGIEALTPAIV
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FLCTWLQSAKPGGLLAELQQRQLAHSLKATLLYEFAGQALLHLEFDLTSVAASAPVOV
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GFLICYDIEFPENARRLALAGAELILVPTANMIPYDFVADVTIRARAFENQCYVAYAN
YCGHEEQIRYCGOSSIAAPDGSRIALAGLDEALIIGTLDRQLMGESRALNRYLSDRRP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Submitted (18-MAY-1995) U. Schnider, Laboratoire de Biologie Submitted (18-MAY-1995) U. Schnider, Laboratoire de Biologie, UNIVERSITE DE LAUSANNE, CH- 1015 Lausanne-Dorigny, SWITZERLAND Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /translation="IYPKVDIASTIGDPITVSWEADPHFLGAFKGALPGHYRYNQRM
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                                                                                                                                                                                                       Gaps
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                                                                                                                                                          DB 10; Length 348;
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                                                                                                                                                                                                                                                                                                                                                                      FFFQQABCF 5137 bp DNA BCT
P.fluorescens pgqF, pgqA, pgqB, pgqC genes.
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g922799
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Pred. No. 8
                                                                                                                                                                                                                                                    ggcgcctcccgggcggatcgggagcccac 35
                                                                                                                                                                                                                                                                            113 GGGGGCCTGCTGGGGGGGGGGGGGCGCCAC 83
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137 c 155 g
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                                                                  155 g
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Pseudomonas fluorescens
                                                                                                                                                     Query Match 60.0%;
Best Local Similarity 77.4%;
Matches 24; Conservative (
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1276. .3765
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SOURCE

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/product="methionine aminopeptidase"
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Usually the highest scoring match found by fasta -o is given for CDS which show significant similarity to other CDS in the database.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               rpmJ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Bacteria; Firmicutes; Actinobacteria; Actinobacteridae; Actinomycetaceae; Streptomyces.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (URL, http://www.sanger.ac.uk/Projects/S_coelicolor/) CDS are numbered using the following system eg SC787.01c. SC (S. coelicolor), 787 (cosmid name), .01 (first CDS), c (complementary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Redenbach, M., Kieser, H.M., Denapaite, D., Elchner, A., Cullum, J., Kinashi, H. and Hopwood, D.A. A set of ordered cosmids and a detailed genetic and physical map for the B Mb Streptcomyces coelicolor A3(2) chromosome Mol. Microbiol. 21 (1), 77-96 (1996)
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                                                                                                                                                                                                                                                                                                 Gaps
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Direct Submission
Submitted (19-AUG-1998) Streptomyces coelicolor sequencing Sanger Centre, Wellcome Trust Genome Campus, Hinxton, Cambr
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                                                                                                                                                                                                                                     Length 5137;
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                                                                                                                                                                                                                                Score 20.6; DB 1;
Pred. No. 5.4e+02;
0; Mismatches 9;
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                     /db_xref="PID:9929806"
/db_xref="GI:929806"
/db_xref="SWISS-PROT:P55173"
/translation="MTDTPLSAAEF"
                                                                                                                                                                                                                                                                                                                                       1 agctggcgcctcccgggcggatcgggagccac 35
                                                                                                                                900 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SC6G4 41055 bp DNA
Streptomyces coelicolor cosmid 6G4
'protein_id="CAA60734.1"
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RESULT

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correct initiation coden. Where possible we choose an initiation coden (ady, agy, trg or (att)) which is preceded by an upstream colon (ady, ago, trg or (att)) which is preceded by an upstream initiation coden). If this cannot be identified we choose the most upstream initiation coden). If this cannot be identified we choose the most IMPORTANT: This sequence MAY NOT be the entire insert of the sequenced clone. It may be shorter because we only sequence overlapping sections once, or longer, because we arrange for a small overlap between neighbouring submissions. Cosmid 664 lies between D31 and D63 in the Asel-D genomic restriction fragment.
                                                                        prediction is based on positional base preference in codons using a specially developed Hidden Markov Model (Krogh et al., Nucleic Acids Research, 22(22):4768-4778[1994]) and the FramePlot program of Bibs et al., Gene 30:157-66(1984) as implemented at http://www.nih.go.jp/
jun/cgi-bin/frameplot.pl. CAUTION: We may not have predicted the correct initiation codon. Where possible we choose an initiation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  'LTAINS LA LION-" I AGRRVCRNEDKHVFHVTY TPPKKEGVCDVGGGELYQRDDDSEE
VRKRLEVY HTGTEPII DYYKSQGLVATIAATGPVDEVTRRALEALKRDQ"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STRCO adenylate kinase (EC
The position of possible ribosome binding site sequences are given where these have been used to deduce the initiation codon. Gene
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/note-"SC6G4(02, map, methionine aminopeptidase, len: 278
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2.7.4.3) (205 aa) and highly similar to many e.g. 2.7.4.3) (205 aa) and highly similar to many e.g. KAD_BORPE adenylate kinase (EC 2.7.4.3) (218 aa), fasta scores; opt: 2.32 x score; 29.1 E(): 1.2e-16, 50.6% identity in 85 aa overlap. Contains Pfam match to entry PF00406 adenylatekinase, Adenylate kinases, score 136.80,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        adk, adenylate kinase, partial CDS, len:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /note="98.4% match to SCSECYDNA X83011 S.coelicolor secY locus DNA from 4547 to 6154"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (248 aa), fasta scores, opt: 546 z-score: 922.2 E(): 44.5% identity in 256 aa overlap. Also similar to S coelificalor map2 (E(): 3.2e-33, 46.8% identity in 257 overlap). Contains PS00680 Methicoline aminopeptidase subfamily 1 signature and Pfam match to entry PF00557
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     'note-"Pfam match to entry PF00406 adenylatekinase
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E-value 1.4e-54"
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'note="possible RBS upstream of map"
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/protein_id="CAA20379.1"
/db_xref="PID:e1316447"
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/db_xref-"SPTREMBL:086771"
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1736. .1813

misc_feature

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1489. .1506
/standard_name="prostaglandin E receptor EP3 subtype gene"
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Submitted (19-JUN-1996) to the DDBJ/EMBL/GenBank databases. Masato
Submitted (19-JUN-1996) to the DDBJ/EMBL/GenBank databases. Masato
Sotani, Kyoto University Graduate School of Medicine, Dept. of Med.
and Clin. Sci; 54 Shogoin-kawahara-cho, Kyoto, Kyoto 606, Japan
(Tel: 075-751-4285, Fax: 075-771-9452)
2 (bases 1 to 1506)
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The human prostaglandin E receptor EP3 subtype gene
Unpublished (1996)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       3 (sites)
Kotani,M., Tanaka,I., Ogawa,Y., Usui,T., Tamura,N., Mori,K.,
Narumiya,S., Yoshimi,T. and Nakao,K.
Structural organization of the human prostaglandin EP3 receptor
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                                                                 Gaps
                                                                                                                                                                                                                                                                    07-FEB-1999
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Primates; Catarrhin; Hominidae; Homo.
1 (bases 1 to 1506)
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Human DNA for prostaglandin E receptor EP3 subtype, exon 1.
D86087
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                  Length 41055;
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80.0%; Pred. No. 8.5e+02;
tive 0; Mismatches 6;
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ف
                  Score 20.4; DB 1;
Pred. No. 3.6e+02;
0; Mismatches 6;
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prostaglandin E receptor EP3 subtype.
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/organism="Homo sapiens"
/db_xref="taxon:9606"
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Genomics 40 (3), 425-434 (1997)
97230456
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/clone_llb="lEMBL3"
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/gene="EP3-III"
361. .1488
/gene="EP3-III"
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                     58.3%;
80.0%;
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531 c
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Matches 24; Conservative
                                                                 24; Conservative
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                     Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /note="SC664.03, infA, translational initiation factor IF1, len: 73 aa: identical to TR:054209 (EMBL.X83011) translational initiation factor IF1 (fragment) (65 aa) and highly similar to many e.g. IF1_BACSU translation initiation factor IF-1 (71 aa), fasta scores; opt: 384 cortains Pfam match to entry PF00575 s1, s1 RNA binding motif, score 54.10, E-value 3.1e-12"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Anotes "SCGG4.04, rpmJ, 50S ribosomal protein L36, len: 37 aa, highly similar to many e.g. RL36_BACST 50S ribosomal protein L36 (37 aa), fasta scores; opt: 225 z-score: 380.1 E(): 6.6e-14, 78.4% identity in 37 aa overlap. Contains PSO0828 Ribosomal protein L36 signature and Pfam match to entry PF00444 L36, Ribosomal protein L36, score 70.40, E-value 3.1e-22"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /db_xref="PID:g3449237"
/db_xref="GI:3449237"
/tb_xref="GI:3449237"
/translation="MAKKQGAIEIEGTVVESLPNAMFKVELQNGHQVLAHISGKMRMH
                                                                                                                                   WHGDAAYTAFVGSGHSPELVELSRVTEESMWAGIAAMKQGNRLVDVSRAIETYIRRQP
KPGGGKYGIIEDYGGHGIGTEMHMDPHLLNYVDRRRGKGPKLVPGFCLAIEPMVSLGT
PRTEVLPDEWTVITTDGTWSSHWEHSVALTEQGPLVLLSPDGGKAKLAELGITAAPDP
                                                                                         /translation="MVQIKNPEQIAKMREAGLVVAAIHAATREAAVPGATTKDLDQVA
RKVLAEHDAKPNFLGYGGFPATICTSVNEVVVHGIPSDDVVLKDGDVISIDCGAIIDG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /note="Pfam match to entry PF00444 L36, Ribosomal protein L36, score 70.40, E-value 3.1e-22" L1819
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1422. .1634
/gene="infA"
/note="Piam match to entry PF00575 S1, S1 RNA binding
motif, score 54.10, E-value 3.1e-12"
                                                                                                                                                                                                                                                                                                                                                           /gene-"map"
/note-"PS00680 Methionine aminopeptidase subfamily 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /translation="MKVKPSVKKICDKCRVIRRHGRVMVICDNPRHKQRQG"
                                                                                                                                                                                                                                            /gene="map"
/note="Pfam match to entry PF00557 pep_M24,
metallopeptidase family M24, score 194.80, E-value
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       'trans1_table-11
product-"translational initiation factor IF1"
protein_id-"CAA20381.1"
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'note="possible RBS upstream of rpmJ"
                                                                                                                                                                                                                                                                                                                                                                                                                                 405. .1408
note="possible RBS upstream of infA"
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product="50S ribosomal protein L36"
/protein_id="CAA20382.1"
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                                                                 /db_xref="SPTREMBL:054208"
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/db_xref="GI:3449238"
/db_xref="PID:e1316448"
/db_xref="PID:93449236"
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                                            /db_xref-"GI:3449236
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gene="infA"
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/qene="rpmJ
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954. .10
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'note-"L2 re
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5760, 2591
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'note="17
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Murer differences are found these are annotated as variations together with a note of the overlapping clone name. Note that the corresponding to the overlapping clone name. Note that the corresponding to the overlapping clone, as we submit sequences submission or responding to the overlapping clone, as we submit sequences with The following abbreviations are used to associate primary accession numbers given in the feature table with their source databases:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Emi. EMBL: Sw., SWISSPROT; Tr:, TREMBL
This sequence is the entire insert of clone 333A15. This sequence
has been finished according to sequence map criteria as follows. An
attempt is made to resolve all sequencing problems, such as
compressions and repeats, but not necessarily within known
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           This sequence was generated from part of bacterial clone contigs of human chromosome 1, constructed by the Sanger Centre Chromosome 1 Mapping Group. Further information can be found at http://www.sanger.ac.uk/HGP/Chri 333A15 is from the library RPCI3 constructed at the Roswell Park Cancer Institute by the group of Pieter de Jong. For further details see http://www.ac.uk/horpac.med.buffalo.edu/ VECTOR: pCYPAC2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           annotated human repeat sequence elements (e.g. Alu). Where the sequence is ambiguous, there is an annotation using the 'unsure'
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/note="LlME3A repeat: matches 5600. .5863 of consensus
                      133221 bp DNA PRI 12-MAY-1999 sequence from clone 333A15 on chromosome 1p31.1-31.3
                                                                                                                                                                                                                                                                                                                               Submitted (12-MAY-1999) Sanger Centre, Hinxton, Cambridgeshire,
CB10 1SA, UK. E-mail enquiries: humquery@sanger.ac.uk Clone
requests: clonerequest@sanger.ac.uk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1083. 1237
note="MER41B repeat: matches 481, .635 of consensus"
                                                                                                                                                                                                                          Vertebrata; Mammalia;
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note="Alusx repeat: matches 1. .267 of consensus"
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'note="AluJb repeat: matches 1. .303 of consensus'
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/note="8 copies 4 mer acac 94% conserved"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   678. 4132
note-"L2 repeat: matches 1453. 1965 of
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'note="48 copies 2 mer at 83% conserved"
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'note="19 copies 2 mer ac 87% conserved"
                                                                                                                                                                                                               Eukaryota; Metazoa; Chordata; Craniata; Vertebra
Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 133221)
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Note="LIP repeat: matches 3493.
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/db_xref="taxon:9606"
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HTG; CpG Island.
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                                                                    complete sequence.
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Mrect Submission
                                                                                                                                                                                               Homo sapiens
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note="HERVFH21 repeat: matches 9. .99 of consensus'
                                                                                                                                                                         note="12 repeat: matches 2424, .2497 of consensus"
1924, .9283
Mote="30 copies ? ...
                                                                                                                                               8760. .9114
Anote-"THELA repeat: matches 1. .354 of consensus" 9153. .9222
Anote-"L2 repeat: matches 2424. .2497 of consensus"
                                                                                                                                                                                                                                                                                                                                consensus
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note="THEIA-internal repeat: matches 1. .1580 of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        .390 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             note="THELA repeat: matches 1. .354 of consensus"
1510. .24869
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10989
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /note="MIR repeat: matches 34. .192 of consensus"
31453. .31661.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    note-"MIR repeat: matches 4. .113 of consensus"
2488. .22559
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           .188 of consensus"
                                                                                                                                                                                                                                                                                    copies 4 mer caca 77% conserved"
copies 4 mer tata 80% conserved'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   conserved
                                                                                                                                                                                                                                                                                                                                                                                              note="9 copies 4 mer atat 89% conserved"
                                                                                                                                                                                                                                                                                                                            .2710 of
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              .2710 of
                                                                                         185. .8759
note="THE1A-internal repeat: matches 1.
                                     ta 82% conserved"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             .2416 of
                                                                                                                                                                                                                                                                                                                                                                  conserved"
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                                                                                                                                                                                                                                                                                                                                                                                                                      2473. .12626
note⇒"MER5A repeat: matches 6.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           4867. .15211
note="THE1A repeat: matches 3.
                                                                     note="THE1A repeat: matches 1.
                                                                                                                                                                                                                                                                                                                          repeat: matches 2550.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 copies 4 mer ttaa 77%
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       repeat: matches 1643.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     6793. .17146
note="THE1A repeat: matches 1.
7835. .18314
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          note "L2 repeat: matches 1705.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2 repeat: matches 2245.
19353
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      note="MLT1B repeat: matches 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              note "MER3 repeat: matches 38.
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                                   9 copies 2 mer
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te-"LIPB1 repeat: matches 6046. .6155 of consensus"
40. .43411
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       repeat: matches 6265. .6322 of consensus"
                                                                                                                   te-"LLMA6 repeat: matches 4491. .6300 of consensus"
91. .35998
                                                                                                                                                                                                    "LIMA6 repeat: matches 4456. .4491 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             repeat: matches 2688. .2742 of consensus"
                                                                                                                                                                 te-"AluSg1 repeat: matches 1. .295 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 te-"L2 repeat: matches 1935. 2486 of consensus"
                                                                                                                                                                                                                                                                                                                                  -"MER5A repeat: matches 40. .164 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    repeat: matches 2649. .2705 of consensus"
                                                                                                                                                                                                                                                                                         "MERSA repeat: matches 1. .187 of consensus"
                                                                                                                                                                                                                                         "MLTIC repeat: matches 1. .465 of consensus" .37439
                                                                                                                                                                                                                                                                                                                                                                                                                 IB repeat: matches 1. .364 of consensus"
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                                                                   "Alusx repeat: matches 7. .284 of consensus" 35690
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32. .41828
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repeat: matches 11. .213 of consensus"
                                                                                                                                                                                                                                                                                                                                                                            "MIR repeat; matches 3. .196 of consensus"
                                       copies 4 mer agga 73% conserved"
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Query Match 58.3%; Score 20.4; DB 10; Length 133221; Best Local Similarity 80.0%; Pred. No. 2.7e+02; Matches 24; Conservative 0; Mismatches 6; Indels 0; 6 gcgcgcctcccgggcggatcgggagcccac 35 ò

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Gaps

Db 124320 GCCTGCTCCTGGCCGGACCGGGAGCCCAC 124349

Search completed: September 28, 1999, 16:46:27 Job time: 7374 sec

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GenCore version 4.5
Copyright (c) 1993 - 1998 Compugen Ltd.
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10614 10614 10614 6530 5092 4698 7218	-	c 72	ല് ന എ	že Š	SOFTWARE: Wordperfect RREENT APPLICATION DARA: APPLICATION NUMBER: US/ FILING DARE: 19911212 CLASSIFICATION: 424 KIOR APPLICATION DATA: APPLICATION NUMBER: 07-	ING DATE: 23-SEPTEMBER-1 ALCATION DATA: ALCATION NUMBER: 07/728, ING DATE: 9-JULY 1991 APPLICATION DATA: ALCATION NUMBER: 07/705, ING DATE: 23-May-1991	ATTORNEY AGENT INFORMATION: NAME: Hanson, No. 5342774m REGISTRATION NUMBER: 30,94 REFERENCE/DOCKET NUMBER: 10,19 TELECOMMUNICATION INFORMATION TELEPHONE: (212) 838-3884 FORMATION FOR SEQ ID NO: 5:	rics pai gula	1.5%; larity 80.6%; Conservative	ttgtatttggttttggttttggttttgtttatttgggacagggcttcttgttgt
00000000		cat 74 710N 7110N	TITLE OF INVENTION: F NUMBER OF SEQUENCES: CORRESPONDENCE ADDRESS ADDRESSEE: Felfe & STREET: 805 Third CITY: New YORK CIEV	YO YOU IN TO SEE	SOFTWARE: Wordperf RRENT APPLICATION D APPLICATION NUMBER: FILING DATE: 19911 CLASSIFICATION: 42 ION APPLICATION DAT APPLICATION NUMBER:	FILING DATE: 23-SE IOR APPLICATION DAT APPLICATION NUMBER: FILING DATE: 9-JUL IOR APPLICATION DAT APPLICATION NUMBER: APPLICATION NUMBER: FILING DATE: 23-WB	TORNEY/AGENT INFORMATION NUMBER: Hanson, No. 5 REGISTRATION NUMBER: REFERENCE/DOCKET NUMBER: (212) 68 TELEPHONE: (212) 68 TELEFRAX: (212) 68 REATION FOR SEQ ID N	1 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	similarity 9; Conser	igttt TTT
		143B-5 5, Applicat 5, 5342774 INFORMATION OF INVENTIO	INVE SEQUENCI EE: 80:	New YOL 10022 READABLE TYPE: D ER: IBM ING SYSTE	E: PPLIC	DATE PLICATION DATE PLICATION ATION	AGENTALION NICALION NE:	CHARACT 4698 NUCLEIC IDNESS: Y: lin TYPE:	겯	attte
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800HUW4N		ULT 1 07-807-0 Sequence Patent No GENERAL APPLIC	ITLE TOMBE CORRE ADD STR CIT	STATE: 2IP: COMPUTER MEDIUM COMPUTI	SOFTW CURRENT APPLIC FILINC CLASS: PRIOR AI	PRIOR APPI FILI PRIOR APPI	ATTORNEY AGENT IN NAME: Hanson, REGISTRATION NO REFERENCE/DOCKE TELECOMMUNICATION TELEPHONE: (212) INFORMATION FOR SEQ	SEQUENCE LENGTH: TYPE: STRANDE TOPOLOG MOLECULE	Query Ma Best Loca Matches	364
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APPLICANT: Murata, Yoshiyuki
TITLE OF INVENTION: Human And Murine Interleukin-5 Receptor
UNMER OF SEQUENCE: 18
CORRESPONDENCE ADDRESS:
                                                                                                                                                                               E: Floppy disk
IBM PC compatible
PC CDOS/MS-DOS
PatentIn Release #1.0, Version #1.25
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APPLICATION NUMBER: US/07/757,390
FTIING DATE: 19910910
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1155 Avenue of the
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REGISTRATION NUMBER: 18,87.
REFERENCE/DOCKET NUMBER: 7,
TELECOMMUNICATION INFORMATION
TELEPHONE: 212 790-9090
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Best Local Similarity 78.4%;
Matches 131; Conservative
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MEDIUM TYPE: Floppy
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APPLICANT: De Plaen, Etienne; Boon-Falleur, Thierry;
APPLICANT: Leth, Bernard; Szikora, Jean-Pierre; De Smet, Charles;
APPLICANT: Chomez, Patrick
APPLICANT: Chomez, Patrick
TITLE OF INVENTION: Isolated Nucleic Acid Molecules Useful In
TITLE OF INVENTION: Determining Expression Of A Tumor Antigen Precursor NUMBER OF SEQUENCES: 48
1599 CCCTGGCTGTCC-TGGCACTCACTCTGTAGACCAGGCTGGCCTCAAACTCAGAAATCTGC 1657
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MEDIUM TYPE: Diskette, 5.25 inch, 360 kb storage
                                                                                   1658 CIGCCICIGCCICCCAAAIGCIGGGAITAAAGGCIIGCAC 1697
                                        484 ctgcttgtgcttcccaagtgcttagattaaaggtgtgcac 523
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 100; DB;
Pred. No. 2.7e-1
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICATION NUMBER: PCT/US92/04354
FILING DATE: 22-MAY-1992
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FILING DATE: 23-SEPTEMBER-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/728,838
APPLICATION NUMBER: 9-JULY-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/705,702
FILING DATE: 23-May-1991
ATTORNEY/AGENT INFORMATION:
NAME: HANSON, NO. 5612201man D.
REGISTRATION NUMBER: 30,946
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ELLING DATE: 26-MARCH-1993
PRIOR APPLICATION DATA:
FITTER
                                                                                                                                                                                      Sequence 5, Application US/08299849B Patent No. 5612201
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         JMBER: 07/807,043
12-DECEMBER-1991
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER: 07/764,364
FILING DATE: 23-SEPTEMBER-1991
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      OPERATING SYSTEM: PC-DOS
SOFTWARE: Wordperfect
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                 ADDRESSEE: Felfe & Lynch STREET: 805 Third Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       genomic DNA
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Best Local Similarity 80.65
Matches 129; Conservative
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PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                        CORRESPONDENCE ADDRESS: ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                       SITY: New York City STATE: New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ; MOLECULE TYPE:
US-08-299-849B-5
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1295 AGCTCTGGCTGTCC-TGGAACTCACTTTATAGACCAAGCTGGCCTCGAACTCAGAAATCC 1237
                                                                                           362 gtttgtatttggtttggtttggtttgagttttgtttatttgagacagggtttctgtgt 421
                                                                                                                                                                                            422 agteetggetgteettggaacteactetgtagaecaggetggeettgaacteagaaatee 481
Length 1355;
                                                                                                                                                                                                                                                                                                                                             1236 TCCCGTCTGTGCATCCCAGGTGCTGGTATTAAAGGCGAGCTCTACCA 1190
                                                35; Indels
                                                                                                                                                                                                                                                                                             482 gcctgcttgtgcttcccaagtgcttagattaaaggtgtgcactgcca 528
Score 99; DB 1;
Pred. No. 2.3e-17;
0; Mismatches 35
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364 ttgtatttggtttggtttggtttgagttttgtttatttgagacagggcttctctgtgtag 42

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TITLE OF
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                                                                                                                                                                                                                                                                                                                                                                                       MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/757,390
FILING DATE: 19910910
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Pred. No. 2.3e-17;
0; Mismatches 35;
                                                                                                                                                                                                                                      ADDRESSEE: Pennie & Edmonds
STREET: 1155 Avenue of the Americas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 4, Application US/08442282
Patent No. 5760204
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NAME: Misrock, S. Leslie
REGISSRATION NUMBER: 18,872
REFERENCE/DOCKET NUMBER: 700
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELEFAX: 212 869864/9741
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 16:
SEQUENCE CHARACTERISTICS:
                                                                                                       APPLICANT: Tominaga, Akira
APPLICANT: Takagi, Satoshi
Murata, Yoshiyuki
TITLE OF INVENTION: Human Am
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity 78.4%;
Matches 131; Conservative
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APPLICANT: Takatsu, Kiyoshi
APPLICANT: Tominaga, Akira
                                                                                                                                                                                                                                                                                                      STATE: New YORK
COUNTRY: U.S.A.
ZIP: 10036-2711
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy di
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: NUCLEIC ACID
STRANDEDNESS: single
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                                                                                                                                                                                                                                                                                 New York
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; LOCATION: 13.
US-07-757-390-16
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1355 GIGITCALTITGITIGITIGITIGITIGITITTICGAGACAGGGITTCICIGI 1296
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: Takagi, Satoshi
: Murata, Yoshiyuki
INVENTION: Human And Murine Interleukin-5 Receptor
SEQUENCES: 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human And Murine Interleukin-5 Receptor
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                                                                                                                                                                                                                                                                                                                                                                              SOFTWARE: Patentin Release #1.0, Version #1.25
JURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/442,282
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/757,390
FILING DATE: 10-SEP-1991
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                               MEDIUM TYPE: Floppy disk COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NAME: Misrock, S. Leslie
REGISTRATION NUMBER: 18,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                REFERENCE/DOCKET NUMBER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity 78.4
Matches 131; Conservative
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                                                                                                 CORRESPONDENCE ADDRESS:
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STRANDEDNESS: sing
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Takag1,
APPLICANT: Murata,
TITLE OF INVENTION:
                                                                                                                                                                                                   E: New York
FRY: U.S.A.
10036-2711
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CLASSIFICATION:
                                                                                                                           ADDRESSEE:
                                                                                                                                                                                                                        COUNTRY:
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1295 AGCTCTGGCTGTCC-TGGAACTCACTTTATAGACCAAGCTGGCCTCGAACTCAGAAATCC 1237
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COMPUTER: IBM PC Compatible
OPERATUNG SYSTEM: PC-DOS/MS-DOS.
SOFTWARE: Patentin Release #1.0, Version #1.25
PatentIn Release #1.0, Version #1.25
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Pred. No. 2.3e-17;
0; Mismatches 35
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                        CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/442,281
                                                                                        CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/757,390
FILING DATE: 10-SEP-1991
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 16, Application US/08442281 Patent No. 5807991 GENERAL INFORMATION:
                                                                                                                                                                                                         NAME: MISTOCK, S. Leslie
REGISTRATION NUMBER: 18,872
REFERENCE/DOCKET NUMBER: 7005
TELECOMMULCATION INFORMATION:
TELEFAX: 212 790-9090
TELEFAX: 212 869864/9741
TELEX: 66141 PENIE
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Takatsu, Kiyoshi
APPLICANT: Tominaga, Akira
APPLICANT: Takagi, Satoshi
APPLICANT: Murata, Yoshiyuki
TITLE OF INVENTION: Human And
NUMBER OF SEQUENCES: 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 1.5%;
Best Local Similarity 78.4%;
Matches 131; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                            LENGTH: 1355 base pairs
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ADDRESSEE: Pennie 6 |
STREET: 1155 Avenue 6
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MEDIUM TYPE: Floppy
COMPUTER: IBM PC com
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GENERAL INFORMATION:
APPLICANT: Takatsu, Kiyoshi
APPLICANT: Tominaga, Akira
APPLICANT: Takata, Akira
APPLICANT: Takata, Yoshiyuki
APPLICANT: Hawata, Yoshiyuki
TITLE OF INVENTION: Human And Murine Interleukin-5 Receptor
NUMBER OF SEQUENCES: 18
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie & Edmonds
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 1355;
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Pred. No. 2.3e-17;
0; Mismatches 35; Indels
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                                         MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRET APPLICATION DATA:
APPLICATION NUMBER: US/08/442,282
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1155 Avenue of the Americas
                                                                                                                                                                                                    CLASSIFICATION: 536
PRIOR APPLICATION: 536
APPLICATION NUMBER: 07/757,390
FILING DATE: 10-SEP-1991
ATTORNEY/AGENT INFORMATION:
NAME: MISTOCK, 5. Leslie
REGISTRATION NUMBER: 18,72
REFERENCE/DOCKET NUMBER: 7005-030
TELEPHONE: 212 790-9090
TELEPHONE: 212 790-9090
TELEFAX: 212 8698864/9741
TELEFAX: 212 8698864/9741
TELEFAX: 212 BENNIE
INFORMATION FOR SEQ ID NO: 16:
SEQUENCE CHARACTERISTICS:
LENGTH: 1355 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 4, Application US/08442281
Patent No. 5807991
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 1.5%;
Best Local Similarity 78.4%;
Matches 131; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: nucleic acid
STRANDEDNESS: single
                        COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER READABLE FORM
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13..1008
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TOPOLOGY: 11
MOLECULE TYPE:
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; LOCATION:
US-08-442-282-16
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Length 1355;

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US-08-686-878A-38
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            362 gtttgtatttggtttggtttggtttgattttgtttatttgagacagggcttctctgtgt 421
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Indels
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Patentin Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEE: Genetics Institute, Inc.: 87 CambridgePark Drive
Cambridge
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICATION NUMBER: US/08/686,878A
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-
                                                                                    REFERENCE/DOCKET NUMBER: 7(
FELECOMMUNICATION INFORMATION
TELEPHONE: 212 790-9090
                                                                                                                                           TELEFAX: 212 8698864/9741
TELEX: 66141.PENNIE
INFORMATION FOR SEQ ID NO: 16:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                      1.5%;
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LaVallie, Edward
Racie, Lisa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Herberg, David
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ATTORNEY/AGENT INFORMATION:
                                                        . Leslie
                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match ... 1.55
Best Local Similarity 78.45
Matches 131; Conservative
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Spaulding, V
                                                                                                                                                                                                                                         TYPE: nucleic acid
STRANDEDNESS: single
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13..1008
APPLICATION NUMBER:
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; LOCATION:
US-08-442-281-16
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374 tttggtttggttttgatttgtttatttgagacagggcttctctgtgtagtcctggctgt 433
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                                                                                                            Length 535;
                                                                                                                                                         Indels
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CURRENT APPLICATION DATA:
CURLICATION NUMBER: US/07/757,390
FILING DATE: 19910910
                                                                                                          Score 96.2; DB 2;
Pred. No. 7.6e-17;
1; Mismatches 19;
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SYSTEM: PC-DOS/MS-DOS
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: 66141 PENNIE
ON FOR SEQ ID NO: 2:
E CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                517 CTCCCAAGTGCTGGGATTA 535
                                                                                                          Query Match
Best Local Similarity 84.9°
Matches 118; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NAME: Misrock, S. Lesl REGISTRATION NUMBER: 1
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ADDRESSEE: Pennie &
STREET: 1155 Avenue
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linea
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APPLICANT: Murata
TITLE OF INVENTION
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10036-2711
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1808 GITIGITIGITIGITIGITITITICGAGACAGGGTTICTCTGTGTAGCTCTGGCTGTC-T 1750
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378 gtttggtttgagttttgtttatttgagacagggcttctctgtgtagtcctggctgtcctt 437
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APPLICANT: Tominaga, Akira
APPLICANT: Takagi, Satoshi
APPLICANT: Murata, Yoshiyuki
TITLE OF INVENTION: Human And Murine Interleukin-5 Receptor
CORRESPONDENCE: 18
CORRESPONDENCE ADDRESS:
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APPLICATION NUMBER: US/08/442,282
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1.4%; Score 94.2; DB 3; 1
Best Local Similarity 80.8%; Pred. No. 5.7e-16;
Matches 122; Conservative 0; Mismatches 28;
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/757,390
FILING DATE: 10-SEP-1991
ATTORNEY/AGENT INFORMATION:
NAME: MISTOCK, S. Leslie
                                                                                                                                                                                                                                                                                                                                                Sequence 2, Application US/08442282
Patent No. 5760204
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Pennie & Edmonds
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THE FEHONE: 212 790-9090
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TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
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REGISTRATION NUMBER: 18,
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COUNTRY: U.S.A.
ZIP: 10036-2711
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy di
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.7e-16;
                                                                                            Length 1808;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Tominaga, Akira
APPLICANT: Takagi, Satoshi
APPLICANT: Murata, Yoshiyuki
TITLE OF INVENTION: Human And Murine Interleukin-5 Receptor
                                                                                                                                      Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
OPENATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/757,390
FILING DATE: 19910910
                                                                                     1.4%; Score 94.2; DB 1;
80.8%; Pred. No. 5.7e-16;
tive 0; Mismatches 28;
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ADDRESSEE: Pennie & Edmonds
STREET: 1155 Avenue of the Americas
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REGISTRATION NUMBER: 18,872
REFERENCE/COCKET NUMBER: 700
TELECOMMUNICATION: INFORMATION:
TELEPHONE: 212 790-9090
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TELEX: 66141 PENNIE
INFORMATION FOR SED ID NO: 15:
SEQUENCE CHARACTERISTICS:
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TTORNEY/AGENT INFORMATION:
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                                                                                       Query Match
Best Local Similarity 80.8%
Matches 122; Conservative
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Best Local Similarity 80.8
Matches 122; Conservative
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TYPE: NUCLEIC ACID
STRANDEDNESS: single
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; MOLECULE TYPE: CDNA US-07-757-390-2
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US-07-757-390-15/C
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US-07-757-390-15
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Sequence 2, Application US/08442281
Patent No. 5807991
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ADDRESSEE: Pennie &
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UNRRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/442,282
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Best Local Similarity 80.8%; Pred. No. 5.7e-16;
Matches 122; Conservative 0; Mismatches 28;
                                              1689 CAGGTGCTGGTATTAAAGGCGAGCTCTACCA 1659
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498 caagtgcttagattaaaggtgtgcactgcca 528
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STREET: 1155 Avenue of the Americas
CITY: New York
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IBM PC compatible
SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                   Sequence 15, Application US/08442282
Patent No. 5760204
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PRIOR APPLICATION DATA:
PAPLICATION NUMBER: 07/757,39
FILING DATE: 10-SEP-1991
ATTORNEY/AGENT INFORMATION:
NAME: MSIOCK, S. Leslie
REFERENCE/DOCKET NUMBER: 18,872
REFERENCE/DOCKET NUMBER: 7005
                                                                                                                                                                                                                                  APPLICANT: Takatsu, Kiyoshi
APPLICANT: Tominaga, Akira
APPLICANT: Takagi, Satoshi
APPLICANT: Murata, Yoshiyuki
TITLE OF INVENTION: Human And
NUMBER OF SEQUENCES: 18
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TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 15
SEQUENCE CHARACTERISTICS:
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STRANDEDNESS: single
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303..1547
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; LOCATION:
US-08-442-282-15
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1808 GTTTGTTTGTTTGTTTTTTCGAGACAGGGTTTCTCTGTAGCTCTGGCTGTCC-T 1750
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APPLICANT: Takatsu, Kiyoshi
APPLICANT: Tominaga, Akira
APPLICANT: Takaqi, Satoshi
APPLICANT: Murata, Yoshiyuki
TITLE OF INVENTION: Human And Murine Interleukin-5 Receptor
NUMBER OF SEQUENCES: 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 1808;
                                                                                                                                                                                                                                                                                                                                                                                                                OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATCHTIN Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/442,281
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
1.4%; Score 94.2; DB 3;
Best Local Similarity 80.8%; Pred. No. 5.7e-16;
Matches 122; Conservative 0; Mismatches 28;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/757,390
FILING DATE: 10-SEP-1991
ATTORNEY/AGENT INFORMATION:
NAME: MAJSTOCK, S. Leslie
REGISTRATION NUMBER: 18,872
REFERENCE/DOCKET NUMBER: 7005-030
                                                                                                                                                                                                                                                                                       Sequence 15, Application US/08442281
Patent No. 5807991
                                                                                                                                                                                          E: Pennie & Edmonds
1155 Avenue of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELECOMMUNICATION INFORMATION TELEPHONE: 212 790-9090
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TELEFAX: 212 869864/9741
TELEX: 66141 PENNIE
INFORMATION FOR SEO ID NO: 2:
SEQUENCE CHARACTERISTICS:
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APPLICANT:
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Search completed: September 28, 1999, 16:41:07 Job time: 7053 sec bcl-1 probe G13b. Hepatitis C virus

50.9

17.8

C 44 45

ALIGNMENTS

GenCore version 4.5 Copyright (c) 1993 - 1998 Compugen Ltd.

OM nucleic - nucleic search, using sw model

September 28, 1999, 16:50:24; Search time 303.81 Seconds (without alignments) 28.823 Million cell updates/sec Run on:

Title: Perfect score: Sequence:

US-09-037-657-30 35 1 agctggcgcgcctcccgggcggatcgggagcccac 35

IDENTITY_NUC Scoring table:

311585 seqs, 125096042 residues Searched:

N_Geneseq_36:* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	Description		NR6.1 prim	1ced muri	haemopoiet	1 haemopoie	sotide sequ	encoding ra	nomologue	oxygen	ance encoc	CONA encouring GALA	TETO	2 C-7.76	avultaerus	vcobacterium	eading f	uman alpha3/TX	2 0	΄ Δ	ြင်	ric	0	enome. Aden	VP1 capsi	VP2 coat	coat	otide seg	myosin L-	secreted p	ley injury a	NA encoding a	actens	e.	todextr	dUTPase of bovine	lobiase gene f	usculu	RAD1. New cycli	yclin Dl qene.	n D1 promote	uman cyclin Dl.	itamin D hydro	3 derived bcl-
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217 CICGGGGIGCCICGGGGGGGGATCGGGAGCCCAC 249

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us-09-037-657-30.rng

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for modulatiny from the modulating form of the movel HR NR6. Claim 5; Page 84-87; 182pp; English.

Claim 5; Page 84-87; 182pp; English.

The haemopoletin receptor (HR) NR6.2 is a form of the movel HR NR6.

The haemopoletin receptor (HR) NR6.2 is a form of the movel HR and it's differentiation between the movel HR and a light of cells. The HR and it's differentiation and survival of a wide variety of cells. The HR and it's derivatives can be used for modulating the activity of the receptors e.g. to regulate development, maintenance or regeneration in an array of different cells and tissues in vitro and in vivo. They can be present in therapeutics used for modulating neuronal proliferation, differentiation and survival. The products can also be used for detection and diagnosis, e.g. for cancers or predisposition to cancers, or for drug screening.
                                                                                                                                                                           Novel hemopoletin receptor NR6.2 gene. Haemopoletin receptor; cell proliferation; cell differentiation; cancer; cell survival; therapeutic; neuronal proliferation; drug screening; ss;
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Nucleotide sequence of the murine U4 gene.
Murline; U4 protein; haematopoletin receptor superfamily;
cell proliferation; immune response; antibody; cell differentiation;
autoimmune disease; cancer; allergy; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   New isolated haemopoietin receptor - used for developing products for modulating proliferation, differentiation and survival of cells,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DB 1; Length 1673;
                                                                                                                                                                                                                                                                                                                                                                          /product= "Haemopoietin receptor NR6.2"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Alexander W, Fabri L, Farley A, Hilton DJ, Kikuchi Y, Kojima I, Maeda M, Nash A, Nicola NA, Rakar S, Willson
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15-JAN-1998: U00334.
16-JAN-1997: US-784863.
GOILINS M. DONALGSON DD. Neben T, Whitters M:
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1. .1278
/*tag= a
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(AMRA-) AMRAD OPERATIONS PTY LTD.
(DZIE/) DZIEGLEWSKA H E.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  V41688 standard; cDNA; 1656 BP
                                                                                                         V27141 standard; cDNA; 1673
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                                                                                                                                                         (first entry)
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Best Local Similarity
Matches 25; Conserva
                                                                                                                                                                                                                                                                                                                                                                                                                               19-MAR-1998.
11-SEP-1997; G02479.
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                                                                                                                                  V27141;
29-SEP-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Zhang J;
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Claim 4: Page 77-81: 182pp; English.
The haemopotetin receptor (HR) NR6.1 is a form of the novel HR NR6.
The haemopotetin receptor (HR) NR6.1 is a form of the novel HR NR6.
Interaction between the novel HR and a ligand facilitates proliferation, differentiation and survival of a wide variety of cells. The HR and it's derivatives can be used for modulating the activity of the receptors e.g. to regulate development, maintenance or regeneration in an array of different cells and tissues in vitro and in vivo. They can be present in therapeutics used for modulating neuronal proliferation, differentiation and survival. The products can also be used for detection and diagnosis,
                                                                                                                                                                                                                                                                                                                                                                                                                                                          ö
                                                                                                         NRG as a novel haemopoietin receptor (HR). Interaction between the novel HR and a ligand facilitates proliferation, differentiation and survival of a wide variety of cells. The HR and it's derivatives can be used for modulating the activity of the receptors e.g. to regulate development, naintenance or regeneration in an array of different cells and tissues in vitro and in vivo. They can be present in therapeutics used for modulating neuronal proliferation, differentiation and survival. The products can also be used for detection and diagnosis, e.g. for cancers or predisposition to cancers, or for drug screening.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Novel haemopoletin receptor NR6.1 gene.
Haemopoletin receptor; cell proliferation; cell differentiation; cancer;
cell survival; therapeutic; neuronal proliferation; drug screening; ss;
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New isolated haemopoietin receptor - used for developing products
for modulating proliferation, differentiation and survival of cells,
                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
WPI; 98-260970/23.

New isolated haemopoietin receptor - used for developing products for modulating proliferation, differentiation and survival of cells, e.g. neuronal cells

Example 8; Page 99-100; 182pp; English.
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Sequence 1629 BP; 336 A; 541 C; 453 G; 299 T;
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(DZIEZ/) DZIEGEWSKA H. E.
ADLYANGA T. FERLEY A. Hilton DJ, KIKUCHI Y.
AAJAXANGA T. FERLEY A. HILON DJ, KIKUCHI Y.
KOJIMA T, Maeda M, Nash A. Nicola NA, Rakar S, Willson
                                                                                                                                                                                                                                                                                                                                                                                                          DB 1;
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Pred. No. 46;
0; Mismatches
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Pred. No. 45;
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llarity 75.8%;
Conservative
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29-SEP-1998 (first entry)
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Best Local Similarity 75.8
Matches 25; Conservative
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11-SEP-1996; AU-002246.
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Matches 25; Conserv
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WO9811225-A2

Matches

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Mus sp. Mouse.

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Gaps

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Length 1724;

DB 1;

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                                             New nucleic acid encoding U4 haematopoietin receptor superfamily chain - potentially useful, e.g. for modulating cell proliferation or immune response, for treating cancer and auto:immune.disease Claim 1; pages 25-26; 38pp; English.

This is the nucleotide sequence encoding the murine U4 protein from the haematopoietin receptor superfamily, used in the method of the invention for the modulation of cell proliferation, or the immune response. Transformed mammalian cells are used to produce recombinant U4 protein. The U4 protein is used to screen for specific binding as tissue markers for isolation of cognate ligands and receptors, and in pharmaceutical compositions which may modulate cell proliferation, cell differentiation, and the immune system (e.g. for treating immune diseases,
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Disclosure; Page 72-75; 55pp; English.

The present sequence encodes a protein designated Zeytor5, which is a cytokinin-like receptor. Soluble Zeytor5 may be administered to down-regulate the effects of a growth and/or maintenance factor in thyroid, heart, and skeletal muscle for example to lessen the effect of cardiotrophin-1 on cardiac pathologies, so preventing heart of cardiotrophin-1 on cardiac pathologies, so preventing heart blood, and to discover other possible Zeytor5 ligands. A probe comprising Zeytor5 DNA or RNA can be used to determine the presence and integrity of the Zeytor5 gene on chromosome 19. Antibodies and the candidotypic antibody could be used to purify Zeytor5 and therapeutically to modify Zeytor5 ligand effects.

Sequence 1724 BP; 350 A; 550 C; 500 G; 324 T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            17-MAR-1999 (first entry)
CDNA encoding rat Zcytor5.
Zcytor5; cytokinin-like receptor; down-regulation; growth factor;
maintenance factor; thyroid; heart; skeletal muscle; cardiotrophin-1;
cardiac pathology; heart enlargement; Zcytor5 ligand; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               New mammalian cytokinin-like receptor Zcytor5 - useful for, e.g. down-regulating Zcytor5 natural ligands or detecting cardiotrophin-l
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DB 1; Length 1656;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            308 T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CAYMO, ZYMOGENETICS INC.
Adams RL, Foster DC, Gilbert T, Jelmberg AC, Lehner JM,
Lok S, Presnell SR, Whitmore TE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         478 G;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         .;
8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 57.7%; Score 20.2; F
Best Local Similarity 75.8%; Pred. No. 46;
Matches 25; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       215 CTCGGGGTGCCTCGGGGCGGATCGGGAGCCCAC 247
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   3 ctggcgcgctcccgggcggatcgggagcccac 35
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         552 C;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Location/Qualifiers
159. .1436
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /*tag= a
/product= 2cytor5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   318 A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      V70896 standard; cDNA; 1724
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     cancer, and allergy).
Sequence 1656 BP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-MAY-1997; US-045287
01-MAY-1997; US-850030
13-FEB-1998; US-023890
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WPI; 99-034662/03.
P-PSDB; W70862.
                                 P-PSDB; W59804
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V70896
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Gaps
                                                                                                                                                                                                              078165/c
ID 078165 standard; DNA; 1496 BP.
AC 078165;
DT 07-JUN-1995 (first entry)
DE U149 homologue gene of bovine herpes virus 1 (BHV-1)
KW Cattle pathogen; infectious bovine rhinotracheitis; nucleocapsid;
KW VIV: Promoter: 18.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Vaccine, also with replacement bacterial or viral pathogen immunogens and/or cytokine(s), inserted at deletion arample; Fig 11, 109pp; English.

O'8165/R63461 are the nucleotide sequence and deduced AA sequence of BHV 1 UL49 homologue gene. The complete DNA sequence between UL48 homologue gene. The complete DNA sequence bresented. Putstive G-C box, TATA box and polyA signal sequence are indicated in FT. The boundaries of UL50, UL 49.5 and UL48 oRFs surrounding the UL 49 homologue gene are also indicated. Signal Sequence Sequence 1496 BP; 212 A; 535 C; 517 G; 237 T;
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Human oxygen regulated protein ORP 150 gene promoter.
Oxygen regulated protein; ORP 150; stress protein; ischaemia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DB 1; Length 1496;
                                                                                                                                                                                                                                                                                                                                                                                                                             /*tag= a
/label= dUTPase (UL50) ORF start codon
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mutant bowine herpes type 1 virus with deleted gene(s)
                                                                  0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 19.6; DE
Pred. No. 73;
0; Mismatches
                            Score 20.2;
Pred. No. 46;
                                                                                                                            252 CTCGGGGTGCCTCAGGCGGGATCGGGAGCCCAC 284
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                557 GCTAGGGGGGGCGCCGCTCGGCTCGGGTC 524
                                                                                                 3 ctggcgcctcccgggcggatcgggagccac 35
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2 gctggcgcgctcccgggcggatcgggagcccac 35
                                                                                                                                                                                                                                                                                                                                                                                      Location/Qualifiers
complement (28. .26)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     *tag- b
label- UL49.5 gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /label= ŭ148 ORF
                        57.7%;
75.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Liang X, Rabulk LA, Zamb T; WPI; 94-341875/42.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            T64785 standard; DNA; 2861 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       333. 335
/*tag= e
1226. 1231
/*tag= f
Query Match
Best Local Similarity 75.88,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          .1496
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 56.0%;
Best Local Similarity 73.5%;
Matches 25; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            256. .258
/*tag= c
294. .300
/*tag= d
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                .266
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         19-APR-1994; CA0201
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        P-PSDB; R63461
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                polya_signal
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ID T6 T6 AC T6 DT 03 DE HU CX
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Length 6306;

DB 1;

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C A genomic DNA molecule (164785) comprises the promoter region of the human oxygen regulated protein ORP 150 gene. It was obtd. from a human placenta genomic library using probes based on human and c a human placenta genomic library using probes based on human and c rat ORP 150 cDNA clones (see also T64783 and T64784). The sequence covers the 5' untranslated region to just before the translation in initiation codon in exon 2. It is able to promote translation in cells when exposed to hypoxla, and will be useful for analysis of the corresponding human gene, partic. for facilitating its appln. C to the treatment of ischaemia diseases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            claim 24, Page 56-66, 93pp; English.

Claim 24, Page 56-66, 93pp; English.

MI and MT2 proteins were isolated from malignant cells essentially following the method of Penman and Fey described in US Pat. Nos. 4, 2010 and 4, 885,236. DNA sequences encoding these proteins were cloned by probing expression librates using monoclonal antibodies raised against the isolated INM proteins. The genetic sequence cooling MT2 has been disclosed by Yang et al. 1992, J. Cell Biol. 116:1395-1408, and is referred to by them as 'NuMA'. The nucleotide sequence encoding MT1 has not been described previously. Both the MT2 proteins are distributed throughout the nucleus (with the exception of the nucleolus) in non-mitotic cells, and localise to the exception of the nucleolus) in non-mitotic cells, and localise cell type in a sample which uses a mRNA complementary to 254841 is claimed.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    15-701-1994 (first entry)
Sequence encoding inner nuclear matrix (INM) protein MT2
Malignant cell type marker; interior nuclear matrix; MT2; NuWA; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Novel malignant cell type markers of the interior nuclear matrix - used for detecting abnormal cell types e.g. malignant breast, prostate, lung, etc., for determining deg. of cell death in
                                                                                                                                                                                       Human and rat oxygen regulated protein ORP 150 coding sequences useful in diagnosis and treatment of ischaemic diseases such as
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               924 T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DB 1; Length 2861;
hypoglycaemia; hypoxia; gene therapy; diagnosis; promoter;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         9; Indels
                                                                             20-DEC-1996; 120662.
20-DEC-1995; JP-349661.
23-UL-1996; JP-213181.
(HSP-T) HSP RES INST INC.
Heda J, Kaneda S, Matsumoto M, Yanagi H, Yura T;
WPI; 97-322148/30.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2010 G;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2053 AGCGTGCGAGCTCCGGGGGGGGGGGGGGGGGCGCA 2086
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 19.6; DE Pred. No. 69; 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 agotggcgcctcccgggcggatcgggagccca 34
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1749 C;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Location/Qualiflers
1. .6306
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1623 A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Bb
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity 73.5%;
Matches 25; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Q54841 standard; cDNA; 6306
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (MATR.) MATRITECH INC.
Lidgard GP. Toukatly G;
WPI; 94-026210/03.
P-PSDB; R47143.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               U06160.
US-901701.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 is claimed.
e 6306 BP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Homo sapiens
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The sequences given in T77782-83 encode fusion proteins which contain TWAM (nuclear mitotic apparatus).

The sequences given in T77782-83 encode fusion proteins were used in the identification of NuMA interecting proteins (NIP's) (see also W21729-30).

W21729-30).

W21729-30).

W21729-30).

W21729-30).

Ab, raised conventionally using NIP-1 or -2 as immunogen, are used to detect NIP (or their complexes) and to block their activity for detect NIP (or their complexes) and to block their activity for which may be markers for a berrant (including malignant) cell growth (which can also be detected by nucleic acid sequencing). Also where
                                ö
                                                                                                                                                                                                                01-0CT-1997 (first entry) cDNA encoding GAL4/HA/NuMA fusion protein. NuMA interacting protein; NPP-1; NIP-2; NUMA; nuclear mitotic apparatus; NuMA interacting protein; cell division; proliferation; antibody; Ab; detection; malignant cell growth; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                malignancy is related to defects in NuMA or NIP, it can be treated by administration of the appropriate functional protein. Sequence 6819 BP: 1796 A; 1841 C; 2136 G; 1046 T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        New nucleic acid encoding nuclear mitotic appts. interacting proteins - useful for modulating cell division and proliferation and
                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ö
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                                 Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /product= Residues 18-2116 of NuMA
                                                                                                                                                                                                                                                                                                                                                                          /product GAL4 DNA binding domain
442. 522
/*tag b
/product hemaglutinin tag
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                                 0; Mismatches
   Score 19.2;
Pred. No. 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-OCT-1997 (first entry)
CDNA encoding LexA/NuMA fusion protein.
                                                                                                                                                                                                                                                                                                                            Location/Qualifiers
1. .441
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                     Pred.
                                                                                                  3459 ecedecriccedecreAcceda 3482
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                                                                  6 gegegetecegggeggateggga 29
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                                                                                                                                                                                         I77782 standard; cDNA; 6819 BP.
ch 54.9%;
1 Similarity 87.5%;
21; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                .6819
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WPI; 97-077270/07.
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07-JUN-1996; U09504.
07-JUN-1995; US-478408.
                                                                                                                                                                                                                                                                                                                                                               *tag=
   Query Match
Best Local Similarity
Matches 21; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (UYYA ) UNIV YALE.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           in diagnosis
                                                                                                                                                                                                       T77782;
01-0CT-1997
                                                                                                                                                                                                                                                                                                               Homo sapiens
                                                                                                                                                                                                                                                                                                                                             misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                   misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WO9640917-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                 mat_peptide
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411 T;

672 G;

751 C;

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associated multi-protein complexes, chimeric proteins, antibodies, nucleic acid, etc., involved in nuclear-cytoplasmic protein transport

Disclosure; Page 58-61; 112pp; English.

Disclosure; Page 58-61; 112pp; English.

The nucleotide and deduced as sequences of human transducin-like chancer of split proteins TLE-1 (962175, R51476), TLE-2 (062176, R51477), TLE-3 (062177, R81478) and TLE-4 (062178, R51479) were determined. The as sequences were compared with that of Drosophila (R5147), TLE-3 (062177, M81478). Comparison of the WD-40 domains of these proteins defined the consensus residues shown in R51480. The CN motifs of the proteins were compared with those of the SY40 T antigen, human c-myc, human p53, human A-myb and doirsal proteins with respect to nuclear localization site, and caseln-kinase II and cdc-kinase plosphorylations tites (sequences R51482-96). TLE can be need to the contact of 
                                                                                                                                                                                                                                                                                                                                                                                                                                                             11arity 71.4%; Score 19; DB 1; Length 2271; 71.4%; Pred. No. 1.1e+02; Conservative 0; Mismatches 10; Indels
                                                                                                                                                                                                                                                                                                                                                used to treat or diagnose (pre)neoplastic conditions, or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1896 AGCTGGCGGCCCTCCGGAGGTCCCAGCAGCCCAC 1862
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 agctggcgcgcctcccgggcggatcggggagccac 35
                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity
Matches 25; Conserva
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The dagemons as Claim 16; Page 42-50; 78pp; English.

Claim 16; Page 42-50; 78pp; English.

The sequences given in T77782-83 encode fusion proteins which contain the sequences given in T7778-83 encode fusion proteins were used in the identification of NuMA interecting proteins (NIP'S) (see also W21729-30). Compounds which interfere with the interaction of NuMA of NIP are used to modulate cell division and/or proliferation. Ab, raised conventionally using NIP-1 or -2 as immunogen, are used to detect NIP (or their complexes) and to block their activity for detect of dagnostic or therapeutic use, e.g. to detect defective NIP (or their complexes) and to block their activity for diagnostic or therapeutic use, e.g. to detect defective NIP (which can also be detected by nucleic acid sequencing). Also where complexe malignancy is related to defects in NUMA or NIP, it can be treated by sequence 6579 BP; 1691 A; 1806 C; 2107 G; 975 T;
NIP-1; NIP-2; NUMA; nuclear mitotic apparatus; NuMA interacting protein; cell division; proliferation; antibody; Ab; detection; malignant cell growth; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           New nucleic acid encoding nuclear mitotic appts. Interacting proteins – useful for modulating cell division and proliferation and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ILB-2; transducin-like enhancer of split protein; differentiation;
protein transport; cervix cancer; dysplasia; malignancy;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DB 1; Length 6579;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Indels
                                                                                                                                                                                                                                                                                                       /product- Residues 18-2116 of NuMA
                                                                                                                                                                  /product Lexa DNA binding domain 262. .283
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87.5%; Pred. No. 87;
tive 0; Mismatches
                                                                                               Location/Qualifiers
1. .261
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/note= "Polylinker"
284. .6579
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062176/C
ID 062176;
AC 062176;
DT 10-SEP-1994 (first entry)
DE Human TLE-2 gene.
KW TLE-2; transducin-like enhancer of protein transport; cervix cancer;
KW TLE-2; transducin-like enhancer of protein transport; cervix cancer;
KW TLE-2; transducin-like enhancer of protein transport; cervix cancer;
KW TLE-2; transducin-like enhances of protein transport; cervix cancer;
KW TLE-2; transducin-like enhances

KW TLE-2; transducin-like enhances

KW TLE-2; transducin-like enhances
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                                                                                                                                          /*tag= a
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07-JUN-1995; US-478408.
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Best Local Similarity
Matches 21; Conserv
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                                                                         Homo sapiens.
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                                                                        Human TLE-2 gene.
TLE-2: transducin-like enhancer of split protein; cell fate;
differentiation; cervix cancer; breast cancer; psoriasis; baldness;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           kinase phosphorylation sites (sequences R52956-70).
Sequence 2271 BP; 437 A; 751 C; 672 G;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 54.3%; Score 19; DB 1; Best Local Similarity 71.4%; Pred. No. 1.1e+02; Matches 25; Conservative 0; Mismatches 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1896 AGCIGGCGCCCTCCCGCAGGTCCCAGCAGCCCAC 1862
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   35
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 agctggcgcgctcccgggcggatcgggagcccac
                                                                                                                                                Location/Qualifiers
26. .2257
                                                                                                                                                                                                                                                            Artavanis-tsakonas S, Stifani S;
RESULT 13
Q45334/c
ID Q45334 standard; cDNA; 2271
                                                            (first entry)
                                                                                                                                                                              /*tag= a
                                                                                                                                                                                                                   30-SEP-1993; U09339.
30-SEP-1992; US-954813.
(UYYA.) UNIV YALE.
                                                                                                                                                                                                                                                                           WPI; 94-135221/16.
P-PSDB; R51110.
                                            Q45334;
10-SEP-1994
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us-09-037-657-30.rng

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New Particle of Mycobacterial infections, wontcring used for diagnosis of mycobacterial infections, monitoring used for diagnosis of mycobacterial infections, monitoring used for diagnosis of mycobacterial infections, monitoring used for diagnosis of mycobacterial agents

T vaccination and development of anti-mycobacterial agents
Claim 1; Fig 9; 55pp; English.

Claim 1; Fig 9; 55pp; English.

Claim 2; Fig 9; 55pp; English.

Claim 3; Fig 9; 55pp; English.

Claim 4; Fig 9; 55pp; English.

Claim 4; Fig 9; 55pp; English.

Claim 5; Fig 9; 55pp; English.

Claim 6; Fig 9; F
                                                                                                                                                                                      Mycobacterium tuberculosis genomic DNA fragment (I). Tuberculosis, mycobacteria, infection; diagnosis; antimycobacterial; antibiotic; vaccine; ss.
                                                                                                                                                                                                                                                                                                                                                                                                   06-NOV-1997.
18-APR-1997; E01973.
18-APR-1996; DE-017184.
(GBPB) GBF GES BIOTECH FORSCHUNG GMBH.
ESPITIA C, Honlsch C, Moreno C, Singh M;
                                                                        T93610 standard; DNA; 3946 BP.
                                                                                                                                                                                                                                                                                                                      Mycobacterium tuberculosis WO9741252-A2.
                                                                                                                                                         27-APR-1998 (first entry)
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P-PSDB; W31852-55
RESULT
                                          r93610,
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                                                                                                                       naturally produce clavarance.
Disclosure; Fig.2; 41pp; English.
A library of S. clavuligerus NRRL 5741 genomic DNA fragments (15-22 A library of S. clavuligerus NRRL by screened for the cla gene using two constructed in cosmid plakFR3 was screened for the cla gene using a probe based on a partial N-terminal sequence from the CLA enzyme.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              P-ESDB: R77856; R77859; R77860; R77861; R77862; R77863; R77864; R77865; R77866; R77866
R77865; R77866; R77867
R77865; R77866; R77867
R77865; R77866; R77867
R77865; R77866; R77867
R77865; R77863; R77869; R77861; R77861; R77862; R77863; R77864; R77864; R77864; R77862; R77863; R77864; R77863; R77864; R77863; R77864; R77863; R77864; R77863; R77864; R77
                                                                                                                                                                                           13-NOV-1995 (first entry)
S. clavulinidgerus cla gene region.
Clavulinic acid: clavulinate; antibiotic; beta-lactamase-inhibitor;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             5324 G;
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given in Q91580 that included the cla gene (ORF4)
Sequence 15079 BP; 2097 A; 5488 C; 532
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           complement (12662. .13365)
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complement (49. .1745)
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WPI; 95-207301/28.
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611. .7588
                                                                                                                                        Q91580 standard; DNA; 15079 BP.
Q91580;
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/label= ORF10
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13769. .14995
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label= ORF8
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08-OCT-1993; 108113.
08-OCT-1993; CA-108113.
(UYAL-) UNIV ALBERTA.
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                                                                                                       Length 3946;
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as for epidemiological studies, for monitoring vaccinations development of anti-mycobacterial drugs and vaccines Sequence 3946 BP; 518 A; 1541 C; 1345 G; 5
                                                                                                       53.7%; Score 18.8; DB 1;
76.7%; Pred. No. 1.2e+02;
Live 0; Mismatches 7;
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Job time: 7613 sec
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Matches 23; Conserva
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Gaps

Length 15079;

Ouery Match 53.7%; Score 18.8; DB 1; Length 1 Best Local Similarity 76.7%; Pred. No. 1.1e+02; Matches 23; Conservative 0; Mismatches 7; Indels

Db 13682 GCGCCCCCCCGGCGGACCGGCCACCCGC 13711 6 gegegeeteeegggeggategggageeeae 35

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)7; Search time 152.56 Seconds (without alignments)
21.032 Million cell updates/sec
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/cgn2_6/ptcdata/2/ina/5B_COMB.seq:*
/cgn2_6/ptcdata/2/ina/5D_COMB.seq:*
/cgn2_6/ptcdata/2/ina/5D_COMB.seq:*
/cgn2_6/ptcdata/2/ina/FCTUS9_COMB.seq:*
/cgn2_6/ptcdata/2/ina/FCTUS9_COMB.seq:*
GenCore version 4.5
Copyright (c) 1993 - 1998 Compugen Ltd.
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                                                                                                                                                     OM nucleic - nucleic search, using sw model
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Match Length DB
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Perfect score:
Sequence:
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					SOUNDEN	MARNERS			•			#1.25														INTRANICIERR	r FOR				2; Length 6306;	3; Indels
US-08-961-240-13 US-08-665-501-3 US-08-605-501-13 US-08-136-277-1 US-08-136-277-1 US-08-136-277-1 US-08-136-277-1 US-08-136-277-1 US-08-136-277-1	ALIGNMENTS		2390		GRAHAM P NOVEL MALIGNANT CRIL TYP	INTERIOR NUCLEAR MATRIX 6	& THIBEAULT				v	S-DOS #1.0, Version	166 390	06-JUN-1995		ജത	MTP-013									Ä	VEL P	•			Score 19.2; DB 2	Mismatch
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7.0044 7.0044 7.0044 7.0044 1.004			plication		LIDGARD, G	TITLE OF INVENTION: NUMBER OF SEQUENCES:	NCE ADDRES		USA	COMPUTER READABLE	PE: Floppy IBM PC com	OPERATING SYSTEM: SOFTWARE: Patent	CURRENT APPLICATION DATA:	TE: 06	ENT INF	NAME: PITCHER ESO, EDMUND R REGISTRATION NUMBER: 27,829	REFERENCE/DOCKET NUMBER: MT TELECOMMUNICATION INFORMATION:	(617)	INFORMATION FOR SEC	96	ESS: S	TOPOLOGY: Linear LECULE TYPE: CDNA	CDS	16306 INFORMATION:	SZILAK,	CLEVELA PRIMARY S	PROTEIN THAT DEFINES A NC SEGREGATION OF PROTEINS A	J. Cell	395-1408 32		larity	21; Conserv
44444444	٠.		390-3 3, Appl:	INFOR	APPLICANT: TITLE OF IN	OF S	RRESPONDEN ADDRESSEE: GTDEET.		COUNTRY: US	SR SE	JTER:	ATING VARE:	CATI	NG DA	X/AG	TRAT	ENCE	TELEPHONE:	ON	5 : E	STRANDEDNESS	MOLECULE TYPE:	ATURE: NAME/KEY:	LOCATION: PUBLICATION	AUTHORS: AUTHORS:	. RS:		••	199	e-0	ՏՀան	21;
adaadaa		,- 1	56-3 1ce		i i i i i i	TITLE	CRES	CITY: E	OUN.	POT	OMP	PER	PPL	ILII	ORN	REGIS	EFER	ELER	MAT	LENGIH:	TRAN	ECUI	FEATURE: NAME/K	LICA	OT HO	AUTHO	TITLE	JOURNAL VOLUME:	PAGES: DATE:	5-39	Match Ocal	m
86444444 800112,644		្ន	S-08-466-3 Sequence	atent NC GENERAL APPLIC	AFI	E E	Ö T	100	,0	, S	2 0 0	OM	CUR	E4 C	ATT	Z (X)	TEL	HH	TOR.	ŭ. ZHE	4 Ø E	MOL	Z Z	P G	4 4	ÆΗ	HH	ŠΣ	22.	-08-466	Query Matc Best Local	Matches
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APPLICANT: TOUKATLY, GARY
APPLICANT: LIDGARD, GRAHAM
TILLE OF INVENTION: NOVEL MALIGNANT CELL TYPE MARKERS OF THE
TITLE OF INVENTION: INTERIOR NUCLEAR MATRIX
NUMBER OF SEQUENCES:
CORRESPONDENCE ADDRESS:
ADDRESSEE: TESTA, HURMIT2 & THEREAULT
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                                                                                                                                                                                                                                                                                                                                                                                                    SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/467,781
FILING DATE: 06-JUN-1995
CLASSIFICATION: 424
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0; Mismatches
                                                                                                                                                                                        E: TESTA, HURWITZ & THIBEAULT
125 HIGH STREET
                                                                                                                                                                                                                                                                                                                                             MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    3459 GCGGCCTCCCGGGCTGAGCGGGA 3482
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FILING DATE: 06-JUN-1995
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: PITCHER ESQ, EDMUND R
RELISTRATION NUMBER: 27,829
REFERENCE/DOCKET NUMBER: MTP-
TELECOMMUNICATION INFORMATION:
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Sequence 3, Application US/08467781 Patent No. 5780596
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Best Local Similarity 87.5%;
Matches 21; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELEPHONE: (617) 248-700
TELEFAX: (677) 248-7100
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 6306 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LOCATION: 1.6306
PUBLICATION INFORMATION:
                                                                                                                                                                                                                                                                        COUNTRY: USA
ZIP: 02110
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TOPOLOGY: . linear MOLECULE TYPE: CDNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: LIDGARD TITLE OF INVENTION:
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                                                                                                                                                                                                                                  BOSTON
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NAME/KEY:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AUTHORS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        US-08-195-487-3
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PRIMARY STRUCTURE OF NUMA, AN INTRANUCLEAR
PROTEIN THAT DEFINES A NOVEL PATHWAY FOR
SEGREGATION OF PROTEINS AT MITOSIS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/470,950
FILING DATE: 06-JUN-1995
CLASSIFICATION: 536
                                                                                                                                                                                                          APPLICANT: TOUKATLY, GARY
APPLICANT: LIDGARD, GRAHAM P
TITLE OF INVENTION: NOVEL MALIGNANT CELL TY
TITLE OF INVENTION: INTERIOR NUCLEAR MATRIX
                                                                                                                                                                                                                                                                                                                                        E: TESTA, HURWITZ & THIBEAULT 125 HIGH STREET
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Db 3459 GCGGCCTCCCGGGCTGAGCGGGA 3482
                                       3459 cccccccccccccccccc3482
                                                                                                                                              Sequence 3, Application US/08470950
Patent No. 5698439
  6 gcgcgcctcccgggcggatcggga 29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NAME: PITCHER ESQ, EDMUND R REGISTRATION NUMBER: 27,829
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         REFERENCE/DOCKET NUMBER: N
TELECOMMUNICATION INFORMATION
TELEPHONE: (617) 248-7000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ATTORNEY/AGENT INFORMATION:
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LOCATION: 1..6306
PUBLICATION INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                          ZIP: 02110
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
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SOFTWARE: PatentI
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Best Local Similarity
Matches 21; Conserve
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AUTHORS:
AUTHORS:
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US-08-470-950-3
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DB 3; Length 6306; Indels

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TITLE:

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Sequence 3, Application US/08483924
Patent No. 5882876
GENERAL INFORMATION:
APPLICANT: TOUKATLY, GARY
APPLICANT: LIDGARD, GRAHAM P
TITLE OF INVENTION: NOVEL MALIGNANT CELL TYPE MARKERS OF THE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 6306;
                                                                                                                                                                                                                                                                SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/195,487
INTERIOR NUCLEAR MATRIX
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRIMARY STRUCTURE OF OF NUMA, AN INPROTEIN THAT DEFINES A NOVEL PATHWISEGREGATION OF PROTEINS AT MITOSIS JOURNAL OF CELL BIOLOGY
                                                                                                                                                                                                                                                                                                                                FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/07/901,701
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: PITCHER ESQ, EDMUND R
REGISTRATION NUMBER: 27,829
REFERENCE/DOCKET NUMBER: MTP-013
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617/248-7000
INFORMATION FOR ESQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 6306 base pairs
                                                       ADDRESSE: TESTA HURWITZ & THIBEAULT
STREET: 53 STATE STREET
CITY: BOSTON
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TESTA, HURWITZ & THIBEAULT
                                                                                                                                                                                                       MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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Best Local Similarity 87.5%;
Matches 21; Conservative (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LOCATION: 1..6306
PUBLICATION INFORMATION:
AUTHORS: COMPTON, DUA
                                   CORRESPONDENCE ADDRESS:
                                                                                                                                                          ZIP: 02109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TOPOLOGY: linear MOLECULE TYPE: CDNA FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ; DATE: MAR-1992
US-08-195-487-3
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Sequence 3, Application PC/TUS9306160
GENERAL INFORMATION:
APPLICANT:
TITLE OF INVENTION: INTERIOR NUCLEAR MATRIX
TITLE OF INVENTION: INTERIOR NUCLEAR MATRIX
CORRESPONDENCE ADDRESS:
ADDRESSE: TESTA HURWITZ & THIBEAULT
STREET: 53 STATE STREET
CITY: BOSTON
STATE: MA
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Indels
                                                                                 COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFWWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/483,924
FILING DATE: 07-JUN-1995
CLASSIFICATION: 435
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Pred. No. 44;
0; Mismatches
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                                                                                                                                                                                   FILING DATE: 07-70N-1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: PITCHER ESQ. EDMUND R
REGISTRATION NUMBER: 27,829
RETEREORMONGET NUMBER: MTP-
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 248-7000
                                                                                                                                                                                                                                                                                                                      TELEPHONE: (617) 248-7000
TELEFAX: (617) 248-7100
INFORMATION FON SEQ ID NO: 3.
SEQUENCE CHARACTERISTICS:
LENGTH: 6306 base pairs
ZIP: USA
ZIP: 02110
COMPUTER READABLE FORM:
MEDIUM TYPE: F)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity 87.5
Matches 21; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LOCATION: 1.6306
PUBLICATION INFORMATION
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          IBM PC CO
                                                                                                                                                                                                                                                                                                                                                                                                                                                        TOPOLOGY: linear
MOLECULE TYPE: CDNA
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER: IBM PC
OPERATING SYSTEM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NAME/KEY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              QQ
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Length 1578;
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APPLICANT: Mayne, Richard
TILE OF INVENTION: TYPE IX COLLAGEN AND FRAGMENTS THEREOF
NUMBER OF SEQUENCES: 32
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA: APPLICATION NUMBER: US/08/555,669 FILING DATE: 13-NOV-1995 CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                           DB 3;
                                                                                                                                                                                                                                                                                                                                                                                               0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        200 AGCIGGGGGCCTCGGCCGCGCGTGGGCCGCCC 232
                                                                                                                                                                                                                                                                                                                                                         53.1%; Score 18.6; 72.7%; Pred. No. 81;
                                                                                                                                                                                                                                                                                                                                                                                                                                    1 agctggcgcctcccggggcggatcggggagcc 33
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ADDRESSEE: Pennie & Edmonds
STREET: 1155 Avenue of the Americas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 11, Application US/08555669 Patent No. 5773248
                                                                                                                                                                                                                                                                Pseudorables virus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     REFERENCE/DOCKET NUMBER: 83
TELECOMMUNICATION:
TELEPHONE: 415-854-3660
                                                                                                                                                                                                   TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LENGTH: 2543 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME: Halluin, Albert F
REGISTRATION NUMBER: 25
                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity 72.73
Matches 24; Conservative
                               NAME: GOTMLEY, MARY E. REGISTRATION NUMBER: 3. TELECOMMUNICATION INFORMA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                415-854-3694
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELEX: 66141 PENNIE INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS
                                                                                                                                                                TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ZIP: 10036
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                    TELEPHONE: (301) 258 INFORMATION FOR SEQ ID NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TOPOLOGY: unknown MOLECULE TYPE: CDNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CITY: New York
STATE: New York
                                                                                                                                                                                                                                                                                  Kaplan
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NAME/KEY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ;
US-08-555-669-11
                                                                                                                                                                                                                                                                    ORGANISM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELEFAX:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COUNTRY
                                                                                                                                                                                                                                                                                STRAIN:
US-08-681-129-1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GENERAL INFORMATION:
APPLICANT: Mettenleiter, Thomas Cristoph
TITLE OF INVENTION: Pseudorables virus vaccine
NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
ADDRESSEE: Organon Teknika Corporation
STREET: 1330 Piccard Drive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 19.2;
Pred. No. 44
                                                                                                                                                                                                                                                                                                                                                                                                                                        : SZILAK, ILLYA
: CLEVELAND, DON W
: RILARY STRUCTURE OF OF NUMA, A
PROTEIN THAT DEFINES A NOVEL PA
19930621
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER: US/08/681,129
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ITLE: SEGREGATION OF PROTEINS POURNAL: JOURNAL OF CELL BIOLOGY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    3459 ecedecrecedecreaeceda 3482
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/244,446
FILING DATE: 02-JUN-1994
CLASSIFTCATION: 424
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               6 gegegeeteeegggeggateggga 29
                                                                       ATTORNEY/AGENT INFORMATION:
NAME: PITCHER ESQ, EDMUND R
REGISTRATION NUMBER: 27,829
REFRENCE/DOCKET NUMBER:
TELECOMMUNICATION INFORMATION:
TELEFAX: 617/248-7000
TELEFAX: 617/248-7100
INFORMATION FOR SEQ ID NO: 3:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 1, Application US/08681129 Patent No. 5738854
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           21; Conservative
URRENT APPLICATION DATA
                                                                                                                                                                                                                                                                nucleic acid
EDNESS: single
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                               LOCATION: 1..6306
PUBLICATION INFORMATION
                     APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                          linear
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                                                                                                                                                                                                                                                                              STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                          MOLECULE TYPE:
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LOCATION:
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Matches

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           Length 2543;
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         DB 3;
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                                                                                                         1048 criccidecerceredaceaceaceacea 1080
Query Match
53.1%; Score 18.6; I
Best Local Similarity 72.7%; Pred. No. 76;
Matches 24; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 18.4; DE
Pred. No. 93;
0; Mismatches
                                                                                                                                                                                                                                                                           TITLE OF INVENTION: CONSTITUTIVE
TITLE OF INVENTION: EXPRESSION OF P450SOY
TITLE OF INVENTION: AND FERREDOXIN-SOY IN
NUMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESS:
                                                                        2 gctggcgcctcccgggcggatcgggagccca 34
                                                                                                                                                                                                                                                                                                                                                                                          ADDRESSEE: E. I. DU PONT DE NEMOURS
ADDRESSEE: AND COMPANY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FILING DATE:
ATORNEY/AGENT INFORMATION:
NAME: GALLEGOS, R. THOMAS
REGISTRATION NUMBER: 32,692
REFERENCE/DOCKET NUMBER: CR-9000
TELECOMUNICATION INFORMATION:
TELEPHONE: 302-892-7942
INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             738 GCGACTCCTGCGCGCCCGGGAGCCGAC 765
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/102,863
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/07/807,001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             8 gcgcctcccgggcggatcggggagcccac 35
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 10, Application PC/TUS9210885 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ZIP: 19898
COMPUTER READABLE FORM:
ABDIUM TYPE: Floppy disk
CMMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SOFTWARE: Patentin Release #1.0
SOFTWARE: Version #1.25
                                                                                                                                                                                                      Sequence 10, Application US/08102863 Patent No. 5466590
                                                                                                                                                                                                                                                                                                                                                                                                                             1007 MARKET STREET
                                                                                                                                                                                                                                                              SARIASLANI, SIMA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        52.6%;
78.6%;
                                                                                                                                                                                                                                                                                                                                                                                                               AND COMPANY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity 78.6°
Matches 22; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                  COUNTRY: ""
                                                                                                                                                                                                                                                                                                                                                                                                                                                WILMINGTON
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US-08-102-863-10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RESULT 10
PCT-US92-10885-10
                                                                                                                                                                                 -08-102-863-10
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APPLICANT: Ryan, Michael J.
APPLICANT: Lotvin, Jason A.
APPLICANT: Lotvin, Jason A.
APPLICANT: Lotvin, Jason A.
APPLICANT: Strathy, Nancy
APPLICANT: Fartini, Susan E.
TITLE OF INVENTION: Cloning of the biosynthetic pathway for
TITLE OF INVENTION: useful therein
NUMBER OF SEQUENCES: 1
CORRESPONDENCE ADDRESS:
ADDRESSEE: American Cyanamid Company
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ö
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Pred. No. 93;
                                                                                                                                                                                                                                                                                                                                COMPUTER: Macintosh
OPERATING SYSTEM: Macintosh System, 6.0
SOFTWARE: Microsoft Word, 4.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US92/10885
FILING DATE: 19921216
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 52.6%; Score 18.4; I Best Local Similarity 78.6%; Pred. No. 93; Matches 22; Conservative 0; Mismatches
TITLE OF INVENTION: CONSTITUTIVE
TITLE OF INVENTION: EXPRESSION OF P450SO
TITLE OF INVENTION: STREPTOMYCES
NUMBER OF SEQUENCES: 11
CORRESPONDENCE ADDRESS: 12
ADDRESSEE: E. I. DU PONT DE NEMOURS
ADDRESSEE: AND COMPANY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                738 GCGACTCCTGCGCGGCCCGGGAGCCGAC 765
                                                                                                                                                                                                                                                     ZIP: 19898
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.50 inch,
MEDIUM TYPE: 1.0 MB
                                                                                                                                         ADDRESSEE: AND COMPANY
STREET: 1007 MARKET STREET
CITY: WILMINGTON
STATE: DELAWARE
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                        CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: GALLEGOS, R. THOMAS
REGISTRATION NUMBER: 32,692
REFERENCE/DOCKET NUMBER: GR-5
TELECHONE: 302-892-7342
INFORMATION FOR SEQ ID NO: 10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 1, Application US/08125468
Patent No. 5589385
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NUCLEIC ACID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STREET: One Cyanamid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CITY: Wayne
STATE: New Jersey
COUNTRY: USA
ZIP: 07470
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STRANDEDNESS:
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DB 4; Length 30001;
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                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 7, Application US/07947120
Patent No. 5538846
GENERAL INFORMATION:
APPLICANT: Meeker, Timothy C.
TITLE OF INVENTION: BCI-1 Locus Nucleic Acid Probes and
TITLE OF INVENTION: Assay Methods
                                                                                                                                                                                                               Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ......um TYPE: Floppy disk COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: Patentin Release #1.0, Version #1.25 CURRENT APPLICATION DATA: APPLICATION NUMBER: US/07/947,120 FILING DATE: 19920917 CLASSIFICATION: 435 ATTORNEY APPLICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ADDRESSEE: Leona L. Lauder
STREET: Steuart Street Tower, 18th Fl., One Market
STREET: Plaza
                                                                                                                                                                                                               0; Mismatches
                                                                                                                                                                                                                                                                                                Db 26694 Accresacecercesseacescenses 26664
                                                                                                                                                                  Score 18.2;
Pred No. 7
                                                                                                                                                                                                                                                          1 agctggcgcctcccgggcggatcgggagc 31
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME: Lauder, Leona L.
REGISTRATION NUMBER: 30,863
REFERENCE/DOCKET NUMBER: 91
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-777-9257
TELEFAX: 415-543-4219
                                                                                    DNA (genomic)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match . 50.9%;
Best Local Similarity 75.9%;
Matches 22; Conservative
                                                                                                                                                                     52.0%;
ilarity 74.2%;
Conservative
30001 base pairs
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NUMBER OF SEQUENCES: 1(
CORRESPONDENCE ADDRESS:
ADDRESSEE: Leona L. 1
                                            single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     San Francisco
                        nucleic acid
                                                                                                                                                                     Query Match
Best Local Similarity
Matches 23; Conserva
                                                                  inear
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                                        STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MOLECULE TYPE: HYPOTHETICAL:
                                                                TOPOLOGY: 11: MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STRANDEDNESS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ; NAME/KEY:
; LOCATION:
US-07-947-120-7
                                                                                                                                                                                                                                                                                                                                                                                         JS-07-947-120-7/c
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                                                                                                      US-08-474-933-1
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                                                                                                                                                                                                                                                            δ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Ryan, Michael J.
APPLICANT: Lotvin, Jason A.
APPLICANT: Strathy, Nancy
APPLICANT: Fantini, Susan E.
TITLE OF INVENTION: Chlorid of the biosynthetic pathway for
TITLE OF INVENTION: Chlorietracycline and tetracyline Formation and cosmids
TITLE OF INVENTION: useful therein
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CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/474,933
                        PatentIn Release #1.0, Version #1.25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ; Score 18.2; DE; Pred. No. 77; 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Db 26694 AGCIGGAGCGCCTCGGGCACCGAGCGGTAGC 26664
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 agctggcgcgcctcccggggcggatcgggagc 31
    OCHERAL
SOFTWARE: Patentim ACCURENT APPLICATION DATA:
APPLICATION NUMBER: US/08/125,468
FILING DATE: 22-SEP-1993
CLASSIFICATION: 435
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: TSevdos, Estelle J
REGISTRATION NUMBER: 31,145
RECISTRATION NUMBER: 31,145
RECENENCE/DOCKET NUMBER: 31,255-02
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/125,468
FILING DATE: 22-SEP-1993
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 1, Application US/08474933 Patent No. 5866410
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-
                                                                                                                                                                                                                                                                                                                                                                                                               MOLECULE TYPE: DNA (genomic)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                52.0%;
74.2%;
                                                                                                                                                                                                                                                                                                                          : 30001 base pairs
nucleic acid
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                                                                                                                                                                                                                                                     TELEFANCE (201)831-3305
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   REGISTRATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CORRESPONDENCE ADDRESS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                New Jersey
: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity
Matches 23; Conserv
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US-08-474-933-1/C
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STRAINS FOR EXPRESSION OF PEPTIDES AND
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                                                                                                                                                                APPLICANT: Meeker, Timothy C.
TITLE OF INVENTION: BCl-1 Locus Nucleic Acid Probes and
TITLE OF INVENTION: Assay Methods
NUMBER OF SEQUENCE: 10
CORRESPONDENCE ADDRESS:
ADDRESSEE: Leona L. Lauder
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COUNTRIES.

ZIP: 94105
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION NUMBER: US/07/947,120

TTTING DATE: 1920917
                                                                                                                                                                                                                                                                                                                                                                                                      ADDRESSEE: Leona L. Lauder
STREET: Steuart Street Tower, 18th Fl., One Market
STREET: Plaza
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Patent No. 5616485
GENERAL INFORMATION:
APPLICANT: Barffeld, Daniel
APPLICANT: Butler, Michael J.
APPLICANT: Hadary, Dany
APPLICANT: Jenish, David
APPLICANT: Krieger, Timothy
TITLE OF INVENTION: STREPTOMYCES PRITILE OF INVENTION: STREPTOMYCES STREATMENT OF STREPTOMYCES STREATMENT OF STREPTOMYCES STREATMENT OF STREA
                                             Sequence 9, Application US/07947120
Patent No. 5538846
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REGISTRATION NUMBER: 30,863
REFERENCE/DOCKET NUMBER: 91
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-777-9257
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MOLECULE TYPE: DNA (genomic) HYPOTHETICAL: NO
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SEQUENCE CHARACTERISTICS:
LENGTH: 476 base palrs
TYPE: NUCLEIC ACID
STRANDEDNESS: single
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Best Local Similarity 75.9
Matches 22; Conservative
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ADDRESSEE: Foley & LA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NUMBER OF SEQUENCES:
                                                                                                                           GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ; ANTI-SENSE: YES US-07-947-120-9
S-07-947-120-9/c
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Search completed: September 28, 1999, 16:41:09 Job time: 7055 sec

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                                                            SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/173,508
FILING DATE: 23-DEC-1993
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: BENT, Stephen A.
REGISTRATION UNMBER: 19,768
REFERENCE/DOCKET NUMBER: 18740/125/CACO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1.4e+02
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Pred. No. 1.
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              MEDIUM TYPE: Floppy disk COMPUTER: IBM PC COMPATIBLE OPERATING SYSTEM: PC-DOS/MS
                                                                                                                                                                                                                     TELECOMMUNICATION INFORMATION:
TELEPHONE: 202 672 5300
TELEFAX: 202 672 5399
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      50.9%;
                                                                                                                                                                                                                                                   TELEFAX: 202 672 5399
TELEX: 904136
INFORMATION FOR SEQ ID NO: 7
SEQUENCE CHARACTERISTICS:
LENGTH: 1820 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Ouery Match
Best Local Similarity 75.9
Matches 22: Conservative
COMPUTER READABLE FORM:
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NAME/KEY:
LOCATION:
FEATURE:
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LOCATION:
FEATURE:
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US-08-173-508-7
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Wed Cep 29 14:40:35 1999

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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                                                                                                               SUMMARIES
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W82073
AA052662
AA105248
AA116255
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AA695430
AA695938
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AA275781
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AA392321
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Match 1
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W63911.1
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W63911/c
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VERSION
                                                                                                                                  Result
No.
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                                                                      8 ; Search time 2095.87 Seconds (without alignments) 32.940 Million cell updates/sec
     GenCore version 4.5
Copyright (c) 1993 - 1998 Compugen Ltd.
                                                                                                                                     1 agctggcgcgcctcccggggcggatcgggagcccac
                                                                                                                                                                                2546578 seqs, 986266752 residues
                                                                     September 28, 1999, 15:38:38
                                              nucleic search, using sw model
                                                                                                             US-09-037-657-30
35
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gb_est1:*
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gb_est4:
gb_est5:
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em_est3:
em_est4:
em_est5:
em_est6:
em_est7:
em_est8:
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                                                                                                               Title:
Perfect score:
Sequence:
                                                                                                                                                           Scoring table:
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                                                                     Run on:
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AA889310 ak27805.3 A1197884 q148901.x A1355982 ac914017.x A1355982 ac914017.x A135255 tg09c07.x A1401119 tgo6b06.x A1470829 t189f02.x A1640129 wa29e01.x A1640362 wa17602.x W46604 zc32110.s1

AI016400 ov59h10 T84586 yd50d04.r1 W30648 mc14d08.r1

W46604 ZC32h10.81 AA555903 nm65903.8 AA622624 np55f03.8 AA091921 mm1518.se AA880407 vx40401.r AI575060 UI-R-G0-u

T31953 EST41425 Hu W57897 zd17d12.s1 AA042972 zk56d06.r AA201099 LD03671.5

nr35g12. GM02819.

AA052662 mf41c04.r AA105248 mp45hil.r AA12465 mp96e12.r AA518890 v102h06.r AA51889 v102h06.r AA883131 alcog08.s W74180 zd75e07.sl AIS73568 UI-R-GG-U

W63911 md90e12.r1 W82073 me96f06.r1

Description

ORGANISM

KEYWORDS SOURCE

REFERENCE AUTHORS

TITLE JOURNAL

COMMENT

FEATURES

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13'), on equal amounts of mRNA from 2 13.5dpc and 2
14.5dpc embryos [total RNA provided by Minoru Ko, Wayne
State Univ., from 2 ]; double-stranded cDNA was ligated to
Eco RI adaptors (Pharmacla), digested with Not I and
cloned into the Not I and Eco RI sites of the modified
pT7T3 vector. Library went through one round of
DT7T3 weathen, and was constructed by Bento Soares and
M FATTIMA BOARDA A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /note="Vector: pT7T3D-Pac (Pharmacia) with a modified bolylinker; Site_1: Not I: Site_2: Eco RI: 1st strand cDNA was primed with a Not I - Oligo(dT) primer [5' refraccaarcigaagrages of the contraction of
                                                            Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 834)
Marra,M., Hillier,L., Allen,M., Bowles,M., Dietrich,N., Dubuque,T., Gelsel,S., Kucaba,T., Lacy,M., Le,M., Martin,J., Morris,M., Schellenberg,K., Steptoe,M., Tan,F., Underwood,K., Moore,B., Theising,B., Wylle,T., Lennon,G., Soares,B., Wilson,R. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Contact: Marra M/Mouse EST Project
WashU-HMIM Mouse EST Project
WashIngton University School of MedicineP
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
Email: mouseest@watson.wustl.edu
This clone is available royalty.free through LLML; contact the IMAGE Consortium (info@image.llnl.gov) for further information.
MGI:247195
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Eukaryota; Metazoa; Chordata; Cranlata; Vertebrata; Mammalia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1. .834
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/clone="IRAGE:403427"
/clone="Ib="Soares mouse embryo NbME13.5 14.5"
/sex="unknown"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 834;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /tissue_type="embryo"
/dev_stage="13.5-14.5dpc total fetus"
/lab_host="DH108"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ..
%
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High quality sequence stop: 476.
Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 22.2; DF
Pred. No. 83;
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 agctggcgcctcccgggcggatcgggagccac 35
                                                                                                                                                                                                                                                                                                                          Waterston, R.
The WashU-HHMI Mouse EST Project
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        M.Fatima Bonaldo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        g1543535
AA052662.1 GI:1543535
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77.18;
                                                                                                                                                                                                                                                                                                                                                                                                      Unpublished (1996)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Conservative
                                     Mus musculus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity
Matches 27; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          house mouse.
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AAO52662/c
LOCUS
DEFINITION
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KEYWORDS
SOURCE
ORGANISM
                                  ORGANISM
                                                                                                                                                                                                                                                                                                                                                        TITLE
JOURNAL
COMMENT
                                                                                                                                            REFERENCE
AUTHORS
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SOURCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    T 3'], on equal amounts of mRNA from 2 13.5dpc and 2
14.5dpc embryos [total RNA provided by Minoru Ko, Wayne
State Univ., from 2 ]; double-stranded cDNA was ligated to
Eco RI adaptors (Pharmacla), digested with Not I and
cloned into the Not I and Eco RI sites of the modified
pT7T3 vector. Library went through one round of
mormalization, and was constructed by Bento Soares and
M.Fatima Bonaldo. " 93 t
                                                                                       Eukaryota: Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases I to 404)
Marra,M., Hillier,L., Allen,M., Bowles,M., Dietrich,N., Dubuque,T., Schellenberg,K., Steptoe,M., Tan,F., Underwood,K., Moore,B., Theising,B., Wylle,T., Lennon,G., Soares,B., Wilson,R. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Contact: Marra M/Mouse EST Project
WashD-HHMI Mouse EST Project
WashIndron University School of MedicineP
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1810
Fax: 314 286 1810
Email: mouseest@watson.wustl.edu
This clone is available royalty-free through LLNL; contact the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ;
0
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Unpublished (1996)
On May 9, 1995 this sequence version replaced gi:802631
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /clone="IMAGE:385294"
/clone_lib="Soares mouse embryo NDMEl3.5 14.5"
/sex="unknown"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 22.2; DB 26; Length 404; Pred. No. 74; 0; Mismatches 8; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /tissue_type="embryo"
/dev_stage="13.5-14.5dpc total fetus"
/lab_host="DH108"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          High quality sequence stop: 358.
High quality sequence stop: 358.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /organism="Mus musculus"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/map="19"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 g1393024
W82073.1 GI:1393024
EST.
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Best Local Similarity 77.1%;
Matches 27; Conservative (
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Gaps

DEFINITION

ACCESSION

VERSION KEYWORDS

RESULT 2 W82073/c LOCUS

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BASE COUNT ORIGIN

m

TITLE JOURNAL COMMENT

REFERENCE

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Score 22.2; DB 28;
Pred. No. 72;
                                                                                                                                                                                                                                                                                                                                                                                     Seq primer: -28ml3 rev2 ET from Amersham
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /clone="IMAGE:572229"
/clone_lib="Barstead MPLRB1"
/sex="mixed"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 agctggcgcctcccgggcggatcgggagccac 35
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /organism-"Mus musculus"
                                                                                                                                                                                                                                                                                                                                                                                                      High quality sequence stop: 317.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /db_xref-"taxon:10090"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /tissue_type="Kidney
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /dev_stage="6 weeks"
/lab_host="DH10B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /strain="BALB/c"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                63.4%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AA116255.1 GI:1671348
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Best Local Similarity 77.1
Matches 27; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      house mouse.
Mus musculus
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                                                                                                            TITLE
JOURNAL
COMMENT
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KEYWORDS
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ORGANISM
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LOCUS
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                  AUTHORS
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Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases I to 256)
Marra,M., Hillier,L., Allen,M., Bowles,M., Dietrich,N., Dubuque,T.,
Gelsel,S., Kucaba,T., Lacy,M., Le,M., Martin,J., Morris,M.,
Schellenberg,K., Steptoe,M., Tan,F., Underwood,K., Moore,B.,
Theising,B., Wylle,T., Lennon,G., Soares,B., Wilson,R. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           T 3'), on equal amounts of mRNA from 2 13.5dpc and 2 state Univ. from 2 ]; double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of the modified normalization, and was constructed by Bento Soares and M.Fatima Bonaido. "
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AA105248 341 bp mRNA EST 13-FEB-1997
mp45hll.rl Barstead MPLRB1 Mus musculus cDNA clone IMAGE:572229 5',
                                                                                                                                                                                                                                                                                                                             Email: mouseest@watson.wustl.edu
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 341)
                                                                                                                                The WashU-HHMI Mouse EST Project
Unpublished (1996)
On May 8, 1995 this sequence version replaced gi:800265.
                                                                                                                                                                                                               Contact: Marra M/Mouse EST Project
WashU-HHMI Mouse EST Project
Washington University School of MedicineP
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                clone_lib="Soares mouse embryo NbME13.5 14.5"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /tissue_type="embryo"
/dev_stage="13.5-14.5dpc total fetus"
/lab_host="DH10B"
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6
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High quality sequence stop: 81.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 63.4%; Score 22.2; DB 77.1%; Pred. No. 69; Live 0; Mismatches
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/organism="Mus musculus"
/strain="C57BL/6J"
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/clone="IMAGE:407622"
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73 c 69
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /sex="unknown
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AA105248
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                                                                                                                                                                                                                                                                                                                                                                                          MGI:251390
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Matches 27; Conser
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                                                                                                                    Waterston,
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RESULT 4
AA105248/c
LOCUS
DEFINITION

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SOURCE ORGANISM

VERSION KEYWORDS

REFERENCE

BASE COUNT ORIGIN

source

FEATURES

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Dubuque, T.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                This clone is available royalty-free through LLNL ; contact the IMAGE Consortium (info@image.llnl.gov) for further information. MGI:346877
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Marra,M., Hillier,L., Allen,M., Bowles,M., Dietrich,N., Dubh
Gelsel,S., Kucaba,T., Lacy,M., Le,M., Martin,J.; Morris,M.,
Schellenberg,K., Steptoe,M., Tan,F., Underwood,K., Moore,B.,
Theising,B., Wylle,T., Lennon,G., Soares,B., Wilson,R. and
                                                                                                           Waterston, R.
The WashU-HHMI Mouse EST Project
Unpublished (1996)
On Sep 12, 1996 this sequence version replaced g1:1282726.
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                                                                                                                                                                                                                                               Contact: Marra M/Mouse EST Project
WashU-HHMI Mouse EST Project
WashIngton University School of MedicineP
4444 Forest Park Parkway, Box 8501, St. Louis, 1
Tel: 314 286 1800
Fax: 314 286 1810
Email: mouseest@watson.wustl.edu
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Washu-HHMI Mouse EST Project
Washington University School of MedicineP
Washington University School of MedicineP
Washington University School of MedicineP
Tel: 314 286 1800
Fax: 314 286 1810
Fax: 314 286 1810
Fax: 316 286 1810
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                                                                                                                                                                                                                                                                                                                                                                                                                  /organism="Mus musculus"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="IMAGE:575462"
/clone_lib="Soares 2NbMT"
/sex="male"
/tissue_type="Thymus"
/dev_stage="4 weeks"
/lab_host="DH10B"
                                          Marra M/Mouse EST Project
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AA518890.1 GI:2259433
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Best Local Similarity 77.1%;
Matches 27; Conservative
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AA518890/c
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                                                                                                                                                                                                                                                                                                            This clone is available royalty-free through LLNL; contact the IMAGE Consortium (info@image.llnl.gov) for further information. MGI:352614
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AA124665 525 bp mRNA EST 17-FEB-1997 mp79e08.r1 Soares 2NbHT Mus musculus cDNA clone IMAGE:575462 5' similar to TR:6203113 G203113 BETA'-CHAIN CLATHRIN ASSOCIATED PROTEIN COMPLEX AP-1. ; mRNA sequence.
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Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 525)
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On Sep 12, 1996 this sequence version replaced gi:1290543.
                                                                 On Sep 12, 1996 this sequence version replaced g1:1293995.
                                                                                                                                          WashU HHMI Mouse EST Project
Washington University School of MedicineP
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
Email: mouseest@watson.wustl.edu
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High quality sequence stop: 435,
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Pred. No. 75;
0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="IMAGE:577966"
/clone_lib="Soares_2NbMT"
                                                                                                                 Contact: Marra M/Mouse EST Project

    .441
    /organism="Mus musculus"

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The WashU-HHMI Mouse EST Project
The WashU-HHMI Mouse EST Project
Unpublished (1996)
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/dev_stage="4 weeks"
/lab_host="DH10B"
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Best Local Similarity 77.1%;
Matches 27; Conservative
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Gaps

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Length 525; Indels

DB 29; .; 6

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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (Dases 1 to 423)
Marra, M., Hillier, L., Allen, M., Bowles, M., Dietrich, N., Dubuque, T., Gelsel, S., Kucaba, T., Lacy, M., Le, M., Martin, J., Morris, M., Schellenberg, K., Steptoe, M., Tan, F., Underwood, K., Moore, B., Theisling, B., Wylle, T., Lennon, G., Soares, B., Wilson, R. and
                                                                                                                                                               AA518890 423 bp mRNA EST 16-JUL-1997 v102h06.rl Barstead mouse myotubes WPLRB5 Mus musculus cDNA clone IMAGE:902651 5' similar to TR:G203113 G203113 BETA'-CHAIN CLATHRIN ASSOCIATED PROTEIN COMPLEX AP-1.;, mRNA sequence.
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236 Arcagegaeccrccreegreerrcagaecccac 202
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WashU-HHMI Mouse EST Project
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AA885331
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                                                                                                                                                                                                                                                                                                                                                                                                                      3'); double-stranded cDNA was ligated to Eco RI adaptors [AATTCGGATCCTTG], digested with Not I and cloned into the Not I and Eco RI sites of the modified p7713 vector. Library constructed by Bob Barstead. The C2cl2 cell line (available from ATCC, catalog # CRL-1772) differentiates rapidly, forming contractile myotubes and producing characteristic muscle proteins.
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Marra,M., Hillier,L., Allen,M., Bowles,M., Dietrich,N., Dubuque,T., Schellenberg,K., Steptoe,M., Tan,F., Underwood,K., Morris,M., Tan,E., Wastan,M., Moris,M., Tan,E., Underwood,K., Morris,M., Tan,E., Underwood,K., Morre,B., Theising,B., Wylle,T., Lennon,G., Soares,B., Wilson,R. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           vs13f12.rl Barstead mouse irradiated colon MPLRB7 Mus musculus cDNA clone IMAGE:1138127 5' similar to SW:ADB1_RAT P52303 BETA-ADAPTIN 1
                                                                                                                                                                                                                                                                                                                                             Washington University School of MedicineP
444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
Email: mouseest@watson.wustl.edu
This clone is available royalty.free through LLNL; contact the IMAGE Consortium (info@lmage.llnl.gov) for further information.
Seq primer: -28ml3 rev2 Er from Amersham.
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Unpublished (1996)
On Sep 12, 1996 this sequence version replaced g1:1393359.
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Washington University School of MedicineP
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
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                                                                                                                                                                                                                                                                /clone="IMAGE: 902651"
/clone_lib="Barstead mouse myotubes MPLRB5"
/cell_line="C2C12"
/lab_host="DH10B"
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Pred. No. 75;
0; Mismatches
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                                                                                                                                                                                                             /organism="Mus musculus"/strain="C3H"
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Email: mouseest@watson.wustl.edu
                                                                                                                                                                                                                                                     /db_xref-"taxon:10090"
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77.1%;
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Best Local Similarity 77.1;
Matches 27; Conservative
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AA691737/c
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AUTHORS
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KEYWORDS
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al60g08.s1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone
IMAGE:1461758 3' similar to contains Alu repetitive element;, mRNA
This clone is available royalty-free through LLNL; contact the IMAGE Consortium (info@image.llnl.gov) for further information. MGI:619399
MGI:619399
MGI:619399
Seq primer: -28m13 rev2 ET from Amersham
High quality sequence stop: 222
Location/qualifiers
1.346
/organism="Mus_musculus"
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National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Contact: Robert Strausberg, Ph.D.
Tel: (301) 496-1550
Email: Robert_Strausberg@nih.gov
This clone is available royalty-free through LLNL; contact the IMAGE Consortium (info@image.llnl.gov) for further information.
INSERT Length: 597 Std Error: 0.00
Seq primer: -40ml3 fwd. ET from Amersham
High quality sequence stop: 470.
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Eukaryota; metazoa; Chordata; Craniata; Vertebrata; Mammalia;
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I (bases I to 473; Catarrhini; Hominidae; Homo.
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Pred. No. 73;
0; Mismatches 8;
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Best Local Similarity 77.1
Matches 27; Conservative
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                                       /ncce="Order in pooled; Vector: p7773D-Pac (Pharmacia) with a modified polylinker; Site_1: Not I; Site_2: Eco RI; Equal amounts of plasmid DNA from three normalized libraries (fetal lung NbHL19W, testis NHT, and B-cell NCI_CGAP_GCBI) were mixed, and ss circles were made in vitro. Following HAP purification, this DNA was used as tracer in a subtractive hybridization reaction. The driver was PCR-amplified CDNAs from pools of 5,000 clones made from the same 3 libraries. The pools consisted of I.M.A.G.E. clones 297480-302087, 682632-687239, 726408-728711, and 729096-731399. Subtraction by Bento Soares and M. Fatima Bonaldo.

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/dav_bost="bHiOB (ampicillin resistant)"
/note="Organ: heart; Vector: pT773D (Pharmacia) with a
modified polylinker; Site_1: Not I; Site_2: Eco RI; 1st
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Contact: Wilson RK
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1810
Fax: 314 286 1810
Email: est@watson.wustl.edu
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
Insert Length: 575 Std Error: 0.00
Seq primer: mob.REGA+ET
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       W74180 435 bp mRNA EST 17-0CT-1996 zd75e07.s1 Soares_fetal_heart_NDHH19W Homo sapiens cDNA clone IMAGE:346500 3', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 (bases 1 to 435)
Hillier, L., Clark, N., Dubuque, T., Elliston, K., Hawkins, M., Holman, M., Hultman, M., Kucaba, T., Le, M., Lennon, G., Marra, M., Parsons, J., Rifkin, L., Rohlfing, T., Soares, M., Tan, F., Trevaskis, E., Waterston, R., Williamson, A., Wohldmann, P. and
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Eutheria; Primates; Catarhini; Hominidae; Homo.
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On Nov 29, 1993 this sequence version replaced gi:430390.
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                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 60.6%; Score 21.2; DB 39; Best Local Similarity 76.5%; Pred. No. 1.6e+02; Matches 26; Conservative 0; Mismatches 8;
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W74180.1
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Eutherla; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 447)
NCI-CGAP http://www.ncbl.nlm.nih.gov/nclogap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Contact: Robert Strausberg, Ph.D.
Tel: (301) 496-1550
Email: Robert_Strausberg@nih.gov
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@lmage.llnl.gov) for further information.
Insert Length: 715 Std Error: 0.00
Seq primer: -40ml3 fwd. ET from Amersham.
                                                                                                                                                                                                                                                                                                                                                                                                 AI191353 447 bp mRNA EST 29-OCT-1998 qe32c09.s1 Soares_fetal_lung_NDHL19W Homo sapiens CDNA clone IMAGE:1740688 3', mRNA sequence.
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Unpublished (1997)
On May 8, 1995 this sequence version replaced g1:801250.
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Pred. No. 1.9e+02;
0; Mismatches 5; Indels
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                                                                                                                                                                                                                                                                                      2 gctggcgccctcccgggcggatcgggag 30
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AI191353.1 GI:3742562
                                                                                                                                                                                                                         Query Match
Best Local Similarity 82.8%;
Matches 24; Conservative (
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RESULT 12 AI574687

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DEFINITION

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NID VERSION KEYWORDS SOURCE ORGANISM

REFERENCE AUTHORS TITLE

JOURNAL MEDLINE COMMENT

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University of Iowa 451 Eckstein Medical Research Building Iowa City, IA 52242, USA 7e1: 119 315 8250
Fax: 319 315 8250
Email: msoarces@blue.weeg.uiowa.edu
Oligo-dT track not found, Not I site shown in beginning of sequence is likely internal to the message. cDNA Library Preparation: M.B. Soarces Lab Clone distribution: clones will be available through
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Cote 1 Note 2 Note 2 Note 2 Note 2 Note 2 Note 2 Note 2 Note 2 Note 2 Note 2 Note 2 Note 2 Note 2 Note 2 Note 2 Note 2 Note 2 Note 2 Note 2 Note 2 Note 2 Note 2 Note 2 Note 2 Note 2 Note 2 Note 2 Note 2 Note 2 Note 2 Note 2 Note 2 Note 2 Note 2 Note 2 Note 2 Note 2 Note 2 Note 2 Note 2 Note 2 Note 2 Note 2 Note 2 Note 2 Note 2 Note 2 Note 2 Note 2 Note 2 Note 2 Note 2 Note 2 Note 2 Note 2 Note 2 Note 2 Note 2 Note 2 Note 2 Note 2 Note 2 Note 2 Note 2 Note 2 Note 2 Note 2 Note 2 Note 2 Note 2 Note 2 Note 2 Note 2 Note 2 Note 2 Note 2 Note 2 Note 2 Note 2 Note 2 Note 2 Note 2 Note 2 Note 2 Note 2 Note 2 Note 2 Note 2 Note 2 Note 2 Note 2 Note 2 Note 2 Note 2 Note 2 Note 2 Note 2 Note 2 Note 2 Note 2 Note 2 Note 2 Note 2 Note 2 Note 2 Note 2 Note 2 Note 2 Note 2 Note 2 Note 2 Note 2 Note 2 Note 2 Note 2 Note 2 Note 2 Note 2 Note 2 Note 2 Note 2 Note 2 Note 2 Note 2 Note 2 Note 2 Note 2 Note 2 Note 2 Note 2 Note 2 Note 2 Note 2 Note 2 Note 2 Note 2 Note 2 Note 2 Note 2 Note 2 Note 2 Note 2 Note 2 Note 2 Note 2 Note 2 Note 2 Note 2 Note 2 Note 2 Note 2 Note 2 Note 2 Note 2 Note 2 Note 2 Note 2 Note 2 Note 2 Note 2 Note 2 Note 2 Note 2 Note 2 Note 2 Note 2 Note 2 Note 2 Note 2 Note 2 Note 2 Note 2 Note 2 Note 2 Note 2 Note 2 Note 2 Note 2 Note 2 Note 2 Note 2 Note 2 Note 2 Note 2 Note 2 Note 2 Note 2 Note 2 Note 2 Note 2 Note 2 Note 2 Note 2 Note 2 Note 2 Note 2 Note 2 Note 2 Note 2 Note 2 Note 2 Note 2 Note 2 Note 2 Note 2 Note 2 Note 2 Note 2 Note 2 Note 2 Note 2 Note 2 Note 2 Note 2 Note 2 Note 2 Note 2 Note 2 Note 2 Note 2 Note 2 Note 2 Note 2 Note 2 Note 2 Note 2 Note 2 Note 2 Note 2 Note 2 Note 2 Note 2 Note 2 Note 2 Note 2 Note 2 Note 2 Note 2 Note 2 Note 2 Note 2 Note 2 Note 2 Note 2 Note 2 Note 2 Note 2 Note 2 Note 2 Note 2 Note 2 Note 2 Note 2 Note 2 Note 2 Note 2 Note 2 Note 2 Note 2 Note 2 Note 2 Note 2 Note 2 Note 2 Note 2 Note 2 Note 2 Note 2 Note 2 Note 2 Note 2 Note 2 Note 2 Note 2 Note 2 Note 2 Note 2 Note 2 Note 2 Note 2 Note 2 No
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Bonaldo,M.F., Lennon,G. and Soares,M.B.
Normalization and subtraction: two approaches to facilitate gene
                                                                                            J32 bp mRNA EST 05-APR-1999
UI-R-GO-ut-h-08-0-UI.83 UI-R-GO Rattus norvegicus cDNA clone
AI579568
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Contact: Soares, MB
Program for Rat Gene Discovery and Mapping
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Pred. No. 3.3e+02;
0; Mismatches 8;
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Seq primer: M13 Forward,
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97044477
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ilarity 75.8%;
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Oligo-dT track not found, Not I site shown in beginning of sequence
is likely internal to the message. cDNA Library Preparation: M.B.
Soares Lab Clone distribution: clones will be available through
Segarch Genetics (www.resgen.com)
Seg primer: M13 Forward.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             mixture of rat tissues (nodose ganglia, dorsal root ganglia, and trigeminal ganglia). The tag is a string of oncleotides present between the Not I site and the oligo-dr track. The library was constructed as described by Bonaldo, Lennon and Soares.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ö
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Bonaldo,M.F., Lennon,G. and Soares,M.B.
Normalization and subtraction: two approaches to facilitate gene
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/lab_host="PHIDB (Life Technologies)"
/lab_host="PHIDB (Life Technologies)"
/note="vector: pT73D-Pac (Pharmacla) with a modified
polylinker; Site_1: Not I; Site_2: Eco RI; The UI-R-GO
library is a normalized library constructed from a
mixture of rat tissues (nodose ganglia, dorsal root
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     University of lowa 451 Eckstein Medical Research Building lowa City, IA 52242, USA 7e1: 319 335 9250 Fax: 319 335 9565 Eax: 319 335 9565 Eax: 319 335 9565
                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                 AI574687 319 bp mRNA EST 30-MAR-1999
UI-R-GO-uc-b-11-0-UI.SI UI-R-GO Rattus norvegicus CDNA clone
UI-R-GO-uc-b-11-0-UI.3', mRNA sequence.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    On May 18, 1998 this sequence version replaced gi:3138307
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ö
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                   Length 447;
   60.0%; Score 21; DB 43; Length 44
82.8%; Pred. No. 1.96+02;
.ive 0; Mismatches 5; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Contact: Soares, MB
Program for Rat Gene Discovery and Mapping
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 20.2; DB 48;
Pred. No. 3.3e+02;
0; Mismatches 8;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /strain="Sprague-Dayley"

(db_xref="taxon:10116"

/map="fp21.3; 5q33"

/clone="U1-R-G0-uc-b-11-0-UI"

/clone="lib="U1-R-G0"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /organism="Rattus norvegicus"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Genome Res. 6 (9), 791-806 (1996)
97044477
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                                                                                                                          2 gctggcgcgctcccgggcggatcgggag
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llarity 75.8%;
Conservative (
                                                                  24; Conservative
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Query Match
Best Local Similarity
Matches 24; Conserv
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Best Local Similarity
Matches 25; Conserv
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FEATURES

Gaps

52 crcedeGreccrcaeGeceGarceGeaGeceae 84

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BASE COUNT

ORIGIN

Length 332; Indels

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Search completed: September 28, 1999, 15:38:41 Job time: 3309 sec
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Best Local Similarity
Matches 24; Conserv
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ORIGIN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 209 bp mRNA .EST 27-AUG-1998 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:1641667 to contains MER22.t3 MER22 repetitive element ;, mRNA
                                                                       Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; euphyllophytes; Spermatophyta; Magnollophyta; Liliopsida; Poales;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Homo sapiens
Eukaryota: Metazoa: Chordata: Craniata: Vertebrata: Mammalia:
Eutheria: Primates: Catarrhin: Hominidae: Homo.
1 (bases 1 to 209)
NCI-GAP http://www.ncbi.nlm.nih.gov/nciogap.
NCI-GAP http://www.ncbi.nlm.nih.gov/nciogap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Email: Robert_Strausberg@nih.gov
cDNA Library Preparation: M. Bento Soares, Ph.D., M. Fatima
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Tumor Gene Index
Unpublished (1997)
On Nov 29, 1993 this sequence version replaced gi:636002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ö
                                                                                                                                                                                                           On May 8, 1995 this sequence version replaced g1:801536.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  10 15.6%; Score 19.8; DB 36; Length 335; Indity 75.0%; Pred. No. 4.5e+02; Conservative 0; Mismatches 8; Indels 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       National Institute of Agrobiological Resources
Rice Genome Research Program
2-1-2 Kannondai, Tsukuba
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      163 TGGCGCTCTTCNCCGTCGGATCGGAGTCCCAC 194
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                4 tggcgcgcctcccgggcggatcgggagcccac 35
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Contact: Robert Strausberg, Ph.D. Tel: (301) 496-1550
                                                                                                                                                                                                                                                                                                                        Ibaran.
Japan 305
Tel: 0298-38-7441
Fax: 0298-38-7468
Email: tsasaki@abr.affrc.go.jp.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                         1. .335
/organism-"Oryza sativa"
                                                                                                                                               Sasaki,T. and Yamamoto,K.
Rice cDNA from panicle
Unpublished (1997)
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                                                                                                                                                                                                                                              Contact: Takuji Sasaki
C74272.1 GI:2442501
                                                                                                                             (bases 1 to 335)
                                                                                                             Poaceae, Oryza.
                                     Oryza sativa.
Oryza sativa
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Matches 24; Conserv
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ov59h10.s1 8
3' similar t
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q3230736
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KEYWORDS
SOURCE
ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               15
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                                                     ORGANISM
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AUTHORS
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AUTHORS
TITLE
JOURNAL
COMMENT
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LOCUS
VERSION
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/note-"Vector: pr713D-Pac (Pharmacia) with a modified polylinker; Site_1: Not I; Site_2: Eco RI; 1st strand cDNA was prepared from mNNA obtained from Clontech Laboratories, Inc., and primed with a Not I - oligo(dT)
                                                                                                                                                                                                                                                                                                                                                                                                                                           Double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not and Eco RI sites of the modified pT7T3 vector. Library went through one round of normalization to Cot5, and was constructed by Bento Soares and M. Fatima Bonaldo."
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found through the I.M.A.G.E. Consortium/LLNL at: www-bio.llnl.gov/bbrp/image/image.html
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Pred. No: 4.2e+02;
): Mismatches 7;
                                                               Insert Length: 349 Std Error: 0.00
Seg primer: -40ml3 fwd. ET from Amersham
Location/Quallflers
                                                                                                                                                                                                        /clone="IMAGE:1641667"
/clone_lib="Soares_testis_NHT"
/sex="male"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mismatches
                                                                                                                                                            /organism="Homo sapiens"
/db_xref="taxon:9606"
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ilarity 77.4%;
Conservative (
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